



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 194203**

**TO: Sheela Huff**  
**Location: rem/3A15/3C18**  
**Art Unit: 1643**  
**Friday, June 30, 2006**  
**Case Serial Number: 10/671054**

**From: Willis McCumber**  
**Location: Biotech-Chem Library**  
**REM-1A75**  
**Phone: (571)272-2697**

**[willis.mccumber@uspto.gov](mailto:willis.mccumber@uspto.gov)**

### **Search Notes**

Examiner Huff,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services.

Willis McCumber  
ASRC Aerospace Corporation  
Library Technician  
STIC Biotech/Chem Library  
(571)272-2697

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71973

194203

my

STIC-Biotech/ChemLib

From: Huff, Sheela  
Sent: Tuesday, June 27, 2006 5:27 PM  
To: STIC-Biotech/ChemLib  
Subject: 10671054--search request

Please search and interference search SEQ ID No. 1-2 of the above.

Thanks-

Sheela Huff  
Art Unit 1643  
571-272-0834  
Remsen 3A15  
mailbox Remsen 3C18

FOR  
SCANNING  
ONLY

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

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# STIC SEARCH RESULTS FEEDBACK FORM

## Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor  
571-272-2507 Remsen E01 D86

## Voluntary Results Feedback Form

➤ I am an examiner in Workgroup:  Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature  
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library Remsen Bldg.

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 29, 2006, 11:10:56 ; Search time 44 Seconds  
(without alignments)  
1500.107 Million cell updates/sec

Title: US-10-671-054-1

Perfect score: 3675  
Sequence: 1 MAPSLSPGPAALRRAPQLLT.....AHSCPPVEPAADYKDDDDK 686

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3628	98.7	678	2 B48089	growth arrest-spec
2	2993	81.4	674	2 I55476	growth potentiatin
3	2955.5	80.4	673	2 A48089	growth arrest-spec
4	1543	42.0	676	1 KXHU5	plasma protein S p
5	1512.5	41.2	642	2 S53434	plasma protein S p
6	1479	40.2	675	1 KXBO5	plasma protein S p
7	1477.5	40.2	642	2 S53433	plasma protein S p
8	1460.5	39.7	646	2 S38819	plasma protein S p
9	1452	39.5	675	1 KXMS	plasma protein S p
10	1448	39.4	675	1 KXRTS	plasma protein S p
11	600	16.3	346	2 I59618	protein S - rat (f
12	362	9.9	685	2 S78040	fibulin, splice fo
13	362	9.9	705	2 S34968	fibulin, splice fo
14	352	9.6	3002	2 A47221	fibritilin 1 precu
15	351	9.6	2871	2 A55567	fibritilin 1 - bovl
16	351	9.6	2871	2 A55624	fibritilin-1 precu
17	345.5	9.4	1221	2 A49457	fibulin-2 precuro
18	344.5	9.4	589	2 T43210	fibulin-1D precurs
19	344.5	9.4	689	2 T42760	fibulin, splice fo
20	344.5	9.4	712	2 T42990	fibulin 1, splice
21	344.5	9.4	798	2 T22793	hypothetical prote
22	341.5	9.3	1184	2 A55184	transforming growt
23	339.5	9.2	1394	2 A35626	fibulin-2 precuro
24	339	9.2	601	2 B36346	fibulin 1 precuro
25	339	9.2	683	2 C36346	fibritilin-1 precu
26	331.5	9.0	2918	2 A54105	fibritilin-2 precu
27	327.5	8.9	2907	2 A57278	fibritilin-2 precu
28	327	8.9	2907	2 A57278	masking protein pr
29	326.5	8.9	1820	2 A55494	latent transformin

30	324	8.8	443	2 I46932	coagulation factor
31	321	8.7	387	2 I38449	extracellular prot
32	320.5	8.7	475	1 EXCH	coagulation factor
33	320	8.7	493	2 JC5621	epidermal growth f
34	319.5	8.7	1251	2 A57293	latent transformin
35	319.5	8.7	1620	2 T27283	hypothetical prote
36	318	8.7	482	1 EXRT	coagulation factor
37	318	8.7	488	1 EXHU	coagulation factor
38	315.5	8.6	741	2 T46488	hypothetical prote
39	315	8.6	492	1 EXBO	coagulation factor
40	312	8.5	886	2 A57172	probable hormone r
41	310.5	8.4	1574	2 T13954	MEGF6 protein - ra
42	308	8.4	452	1 A30351	coagulation factor
43	303	8.2	459	2 J00419	coagulation factor
44	303	8.2	2321	2 S78549	notch3 protein - h
45	297.5	8.1	2139	2 A35672	crumbs protein - f

#### ALIGNMENTS

RESULT 1  
B48089  
growth arrest-specific protein gas6 - human  
C:Species: Homo sapiens (man)  
C:Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 09-Jul-2004  
C:Accession: B48089  
R:Manfioletti, G.; Brancolini, C.; Avanzi, G.; Schneider, C.  
Mol. Cell. Biol. 13, 4976-4985, 1993  
A:Title: The protein encoded by a growth arrest-specific gene (gas6) is a new member of  
A:Reference number: A48089; MUID:93330291; PMID:8336730  
A:Accession: B48089  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-678 <MAN>  
A:Cross-references: UNIPROT:Q14393; UNIPARC:UPI0000073CA; CB:LI3720; NID:9401766; PIDD  
C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat ho  
F:41-92/Domain: Gla domain homology #status atypical <GLA>  
F:120-153/Domain: EGF homology <EG1>  
F:160-195/Domain: EGF homology <EG2>  
F:201-236/Domain: EGF homology <EG3>  
F:242-277/Domain: EGF homology <EG4>  
F:311-671/Domain: sex hormone-binding globulin homology <SHB>  
F:321-473/Domain: laminin G repeat homology <LGR>

Query Match 98.7%; Score 3628; DB 2; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1e-246;  
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MAPSLSPGPAALRRAPQLLTLLLAACALAAALPAREATQFLPRPRRAFOVEEAKQGH 60		DB	1	MAPSLSPGPAALRRAPQLLTLLLAACALAAALPAREATQFLPRPRRAFOVEEAKQGH 60
QY	61	LERECVEELCSREAREVEFENDETDYFYPRYDCKNTKGSPTKSGFATCYQNLPDQC 120		DB	61	LERECVEELCSREAREVEFENDETDYFYPRYDCKNTKGSPTKSGFATCYQNLPDQC 120
DB	61	LERECVEELCSREAREVEFENDETDYFYPRYDCKNTKGSPTKSGFATCYQNLPDQC 120		QY	121	TPNPCDRKGTQACODLMGNFCLCKAGWGRLCDKDVNCSQENGGCLQICHNKPSFPG 180
DB	121	TPNPCDRKGTQACODLMGNFCLCKAGWGRLCDKDVNCSQENGGCLQICHNKPSFPG 180		QY	121	TPNPCDRKGTQACODLMGNFCLCKAGWGRLCDKDVNCSQENGGCLQICHNKPSFPG 180
QY	181	SCHSGFELSSDRTCCDIDECADSEACGEARCNLPFGSYSCLCDEGFAVSSQEKARVDV 240		DB	181	SCHSGFELSSDRTCCDIDECADSEACGEARCNLPFGSYSCLCDEGFAVSSQEKARVDV 240
DB	181	SCHSGFELSSDRTCCDIDECADSEACGEARCNLPFGSYSCLCDEGFAVSSQEKARVDV 240		QY	241	ECLQGRCEQVCVNSPGSYTCHCDGRGGLKLSQDMPTCEPILPCVPSVAKSVSYLYLGM 300
QY	241	ECLQGRCEQVCVNSPGSYTCHCDGRGGLKLSQDMPTCEPILPCVPSVAKSVSYLYLGM 300		DB	241	ECLQGRCEQVCVNSPGSYTCHCDGRGGLKLSQDMPTCEPILPCVPSVAKSVSYLYLGM 300
DB	241	ECLQGRCEQVCVNSPGSYTCHCDGRGGLKLSQDMPTCEPILPCVPSVAKSVSYLYLGM 300		QY	301	FGTPIVIRLRFYRLQPTRLVAEFDFRTDPESILLFAGGHQSTWIVIALRAGRLELQLR 360
QY	301	FGTPIVIRLRFYRLQPTRLVAEFDFRTDPESILLFAGGHQSTWIVIALRAGRLELQLR 360		DB	301	FGTPIVIRLRFYRLQPTRLVAEFDFRTDPESILLFAGGHQSTWIVIALRAGRLELQLR 360



```

QY 187 ELSSDGRTCODIDECADSEAGSEARCKNLPGSYSLCDEGFAYSSOEAKACDVDECIOGR 246
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 184 SLASDGTCTCDDIBCTDSDTCGDARCKNLPGSYSLCDEEGTYSKERTCODVDECQDR 243
QY 247 CEQVCVNSPGSYTCHCDGRGGLKLSQDMTCEDILPCVPSPVAKSVKSLYIGRMFGSTPV 306
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 244 CEQVCVNSPGSYTCHCDGRGGLKLSQDMTCEDILPCVPSPVAKSVKSLYIGRMFGSTPV 303
QY 307 IRLRFKLOPTRLVAEPDFPTEDEGILLPFGGHQSDTWIVLARARLEQLARVNGVR 366
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 304 IRLRFKLOPTRLVAEPDFPTEDEGILLPFGGHQSDTWIVLARARLEQLARVNGVR 363
QY 367 VTSSGPVINGMMQTTISVEELARLVKVRDAVMKIAVAGDLPQPERGLYHMLTYGGI 426
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 364 ITSSGPTINNGMOTTISVEELERLVKVRDAVMKIAVAGDLPQPERGLYHMLTYGGI 423
QY 427 PFHEKLDVQPNPLDGCMSWMNLNGEDTTIOETKVNTRMOCFSVTERGSEFYSGGFA 486
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 424 PFHESELVQPINPLDGCMSWMNLNGEDSAIQETVAKNTKMQCFSTVERGSEFPFGGFA 483
QY 487 FYSLDVWRPFLDVGTSSTWVEVVAHTRPADGCVLFALMAPDLRAVPLSVLVVDYHSTK 546
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 484 TYRLNTRISLDVGTEETWVKVARIPTDGVLLALVGD--DVVISVALVDYHSTK 541
QY 547 KLRKQVLVAVENTALALMEIKVCDGQEHVTVSLRDGEATLEVDTGRGSEVSAQLOE 606
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 542 KLRKQVLVAVENTALALMEIKVCDGQEHVTVSLRDGEATLEVDTGRGSEVSAQLOE 601
QY 607 RLAVLERHRLSPVLTRAGSLPDVPTVSAPVTAFFYRCGMLTEVNRLLDDEAAVYKSHDIT 666
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 602 RLDTTLTFLHQSGVHTVYGVLPVSVISAPVTAFFYRCGMLTEVNRLLDDEAAVYKSHDIT 661
QY 667 AHSCEPVEPA 676
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 662 SHSCPEVEPA 671

```

## RESULT 4

KXHU

Plasma protein S precursor - human

M:Alternate names: vitamin K-dependent protein S

C:Species: Homo sapiens (man)

C:Date: 21-Sep-1990 #sequence revision 26-Jan-1996 #text change 09-Jul-2004

R:Accession: A35610; A35611; A26157; A25891; A35612; A60903; S02424; S09519

R:Schmidel, D.K.; Tatro, A.V.; Phelps, L.G.; Tomczak, J.A.; Long, G.L.

Biochemistry 29, 7845-7852, 1990

A:Title: Organization of the human protein S genes.

A:Reference number: A35610; MUID:91084444; PMID:2148110

A:Accession: A35610

A:Molecule type: DNA

A:Residues: 1-676 &lt;SCH&gt;

A:Cross-references: UNIPROT:P07225; UNIPARC:UPI000013238; GB:M57853; NID:g190547; PIDN:

A:Note: the authors translated the codon TTT for residue 26 as Leu

R:Piocos van Amstel, H.K.; Reitsma, P.H.; van der Logt, C.P.E.; Bertina, R.M.

Biochemistry 29, 7853-7861, 1990

A:Title: Intron-exon organization of the active human protein S gene Psalpa and its pse

A:Reference number: A35611; MUID:91084445; PMID:2148111

A:Accession: A35611

A:Molecule type: DNA

A:Residues: 1-25 &lt;Pl3&gt;

A:Cross-references: UNIPARC:UPI0000173343; GB:j02918

Proc. Natl. Acad. Sci. U.S.A. 84, 349-353, 1987

A:Title: Cloning and characterization of human liver cDNA encoding a protein S precursor

A:Reference number: A26157; MUID:87092407; PMID:3467362

A:Accession: A26157

A:Molecule type: mRNA

A:Residues: 1-10; 'P', 12-25; 'L', 27-676 &lt;HOS&gt;

A:Cross-references: UNIPARC:UPI000014279B; GB:M15036; NID:g190288; PIDN:AAA36479.1; PID:

R:Lundwall, A.; Dackowski, W.; Cohen, E.; Shaffer, M.; Mahr, A.; Dahlback, B.; Stenflo,

Proc. Natl. Acad. Sci. U.S.A. 83, 6716-6720, 1986

A:Title: Isolation and sequence of the cDNA for human protein S, a regulator of blood co

A:Reference number: A25891; MUID:86313649; PMID:2944113

A:Accession: A25891

A:Molecule type: mRNA

A:Residues: 27-220; 'L', 222-262; 'H', 264-344; 'Y', 346-676 &lt;LUN&gt;

A:Cross-references: UNIPARC:UPI0000070664; GB:M4338; NID:g190448; PIDN:AAA60181.1; PID

A:Note: part of this sequence, including the amino end of the mature protein, was deter

Biochemistry 29, 7861-7868, 1990

A:Title: Molecular analysis of the gene for vitamin K dependent protein S and its pseud

A:Reference number: A35612; MUID:91084446; PMID:2148112

A:Accession: A35612

A:Molecule type: DNA

A:Residues: 284-676 &lt;EDR&gt;

A:Cross-references: UNIPARC:UPI0000173344; GB:j02919

R:Piocos van Amstel, J.K.; van der Zanden, A.L.; Bakker, E.; Reitsma, P.H.; Bertina, R.M.

Thromb. Haemost. 58, 982-987, 1987

A:Title: Two genes homologous with human protein S cDNA are located on chromosome 3.

A:Reference number: A60903; MUID:88178564; PMID:2895503

A:Accession: A60903

A:Molecule type: mRNA

A:Residues: 351-676 &lt;PLO&gt;

A:Cross-references: UNIPARC:UPI0000173345

R:Piocos van Amstel, H.K.; van der Zanden, A.L.; Reitsma, P.H.; Bertina, R.M.

FEBS Lett. 222, 186-190, 1987

A:Title: Human protein S cDNA encodes Phe-16 and Tyr 222 in consensus sequences for the

A:Reference number: S02424; MUID:88005138; PMID:2820795

A:Accession: S02424

A:Molecule type: mRNA

A:Residues: 1-676 &lt;PL2&gt;

A:Cross-references: UNIPARC:UPI000013238; EMBL:Y00692; NID:g36578; PIDN:CAA6687.1; PI

C:Gene: GDB:PROS1, PROS

A:Map position: 3p11.1-3q11.2

A:Intons: 26/1; 78/3; 87/1; 116/1; 157/1; 201/1; 243/1; 283/3; 322/2; 385/3; 441/3; 49

C:Complex: in plasma forms a complex with C4b binding protein

C:Function:

A:Description: a cofactor for activated protein C (EC 3.4.21.69); thrombin cleavage des

C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat ho

C:Keywords: beta-hydroxyaspartate; beta-hydroxyaspartic acid; blood coagulation; carbo

F:1-24/Domain: signal sequence #status predicted &lt;SIG&gt;

F:25-41/Domain: propeptide #status predicted &lt;PRO&gt;

F:42-66/Domain: Gla domain homology &lt;GLA&gt;

F:121-154/Domain: EGF homology &lt;EG1&gt;

F:161-199/Domain: EGF homology &lt;EG2&gt;

F:205-241/Domain: EGF homology &lt;EG3&gt;

F:247-282/Domain: EGF homology &lt;EG4&gt;

F:315-667/Domain: sex hormone-binding globulin homology &lt;SHB&gt;

F:325-478/Domain: laminin G repeat homology &lt;LGR&gt;

F:47-48,55,57,60,61,66,67,70,73,77/Modified site: gamma-carboxyglutamic acid (Glu) #sta

F:58-63,88-113,121-134,126-143,145-154,161-175,171-184,186-199,205-217,212-226,228-241,

F:111-112/Cleavage site: Arg-Ser (thrombin) #status predicted

F:137/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted

F:177,219,258/Modified site: erythro-beta-hydroxyaspartic acid (Asn) #status predicted

F:99,509,530/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 42.0%; Score 1543; DB 1; Length 676;

Best local Similarity 44.4%; Pred. No. 2e-100;

Matches 298; Conservative 127; Mismatches 218; Indels 28; Gaps 14;

QY 18 LLLLLLAAECALAAALLPAREATQFLRPRORRAFOVEEAKOGHLEECYEBUCSREARE 77

Db 12 LACLLLVLPVSBANFLSKOASQVL-VRKRANSLLEETKQNLRECEBECNKEARE 70

QY 78 VFENDPDTYFYPRVYDCTINKY-----GSPYTKNS--GFATCVQVLPPOGCPNPPCDRGG 129

Db 71 VFENDPDTYFYPRVYDCTINKY-----GSPYTKNS--GFATCVQVLPPOGCPNPPCDRGG 130

QY 130 TQACODLMGNFCLCKAGNGRLCDKDVNEC---SQENGCLQIQCHNKGSPHSCGSHG 186

Db 131 YMSCKDGRKASFTCTCKPQGWGKECFDINECKDPSNINNGSGQICDNTGSHGCKNGF 190

[illegible]

Db 4 RKRRAISMLEETQGNLIERCEIBELCNKEARAVFENDEPDTDFYKRYLVLCARF----- 58

Qy 105 KNSGFAT-----CYQNLPDCTPNCCKRGTQACODLGNFCTCKAGWG 150

Db 59 -QGGLFTFAQTGSDAYPDLRSVNAIPDQSPFCPNEDGYSCKDGKASFTCTCKPMDG 117

Qy 151 RLCDKDVNEC---SQENGGCLOI CHNKPQSGFHSCSHSGFELSDGRTCCDIDSCA -DSEA 206

Db 118 ERCEFDINECKDPSNINNGCSQICDNTPGSYHSCSKSGFWMLSNKKDCKDQVDESLKPNM 177

Qy 207 CGEARCINLPGSYSLCDEGFAYSQEKACRDVDECLQGRCEQVCAVNSPGSYTCHCDGRG 266

Db 178 CGTAVCKNITGDECECEPEGRYRNLSKSCSEVDDEGEMNCAQLCVNYPGGYTCYDGGK 237

Qy 267 GLKLSQDMDCEDILPCVPPSVAKSVKSLYLGMFGSTPVIRLPFKRLQPTRLVAEFDR 326

Db 238 GFLTAQDQKSCNAVSVCLPLNLDPTKELLVLAQPAQV -VLVLEKFLRLPEISRESAEFDR 296

Qy 327 TFPDEGILLFAGGHODSTWLVALLRAGRLELQLRVNGCVGVNVSQVYINNGMQTISVEE 386

Db 297 TYDSOGVILYAESIDHSAMLLIALRGKLEVLQKNEHTSKITGGDITNGGNMWSVEE 356

Qy 387 IARNLVYKNVRDVMKKAIVAGDLPFQPERGLYHNLFTVGGIPIFH -EKDLVQIPNRLDGM 445

Db 357 LEHSITIKIAKEAVMDINKRPFLEKPNGLLETKYVFAGRPRVBSLLIPINPRLDGCI 416

Qy 446 RSNWNLNGEDTTIOETKVTNMQCPSVTERSGSFYPSGFAFYSLDMRTPLDVTEST- 504

Db 417 RSNWNLNQASGIKEIIQEKQNHKCLVTVAEKGSGYYPGSGIAEFHIDY-----NNGSNVAG 471

Qy 505 WEVEVAHPIPADTGYLFLMAPDLRAVLPSALVDYHSTKTLKQLVLAVENTL-A 563

Db 472 WHINVTNINIPSGTGTGMLALVSN -NTVPPAVSLVD -STSE -KSQDIVISENTVIYR 527

Qy 564 IMELKVCDDGEHVVTVSLRQGEATLEVDTRGQSEVSAQLOERLAVENTLSSPVLTFA 623

Db 528 IQALSLCSYQRS -HLEFRVNRNLELLTFLPKETTSIQEELQYQALDLDAKMKQVATYL 585

Qy 624 GGLPDVEVTSAPVATAFYRGCTLEVNRRLLDLDEAAVKHSDITAHSCPPV 673

Db 586 GGLPDVPFSATPVNAFVNGMEVNINGVELDLDEAISKHNDIRAHSCPSV 635

RESULT 6

KKBOS

plasma protein S precursor - bovine

N:Alternate names: vitamin K-dependent protein S

C:Species: Bos primigenius taurus (cattle)

C:Date: 08-Aug-1967 #sequence\_revision 26-Jan-1996 #text\_change 09-Jul-2004

C:Accession: A24759; A23888

R:Dahlback, B.; Lundwall, A.; Stenflo, J.

R:Proc. Natl. Acad. Sci. U.S.A. 83, 4199-4203, 1986

A:Title: Primary structure of bovine vitamin K-dependent protein S.

A:Reference number: A24759; PMID:66233400; PMID:2940558

A:Accession: A24759

A:Molecule type: mRNA

A:Residues: 1-675 <DB>

A:Cross-references: UNIPROT:P07224; UNIPARC:UPI00001333E7; GB:M13044; NID:G163697; PIDN

A:Note: parts of this sequence, including the amino end of the mature protein, were det

R:Dahlback, B.; Lundwall, A.; Stenflo, J.

U: Biol. Chem. 261, 5111-5115, 1986

A:Title: Localization of thrombin cleavage sites in the amino-terminal region of bovine

A:Reference number: A23888; PMID:86168236; PMID:2937785

A:Accession: A23888

A:Molecule type: protein

A:Residues: 42-141 <DB>

A:Cross-references: UNIPARC:UPI0000173346

C:Function:

C:Complex: in plasma forms a complex with C4b binding protein

C:Superfamily: a cofactor for activated protein C (EC 3.4.21.69); thrombin cleavage des

C:Keywords: beta-hydroxyaspartine; beta-hydroxyaspartic acid; blood coagulation; carbo

F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:25-41/Domain: propeptide #status predicted <PRO>  
 F:26-85/Domain: Gla domain homology <Gla>  
 F:42-675/Product: plasma protein S #status experimental <MAT>  
 F:131-154/Domain: EGF homology <EG3>  
 F:151-199/Domain: EGF homology <EG2>  
 F:205-241/Domain: EGF homology <EG3>  
 F:247-282/Domain: EGF homology <EG3>  
 F:315-666/Domain: sex hormone-binding globulin homology <SHB>  
 F:325-478/Domain: laminin G repeat homology <LGR>  
 F:47-48, 55-57, 60, 61, 66, 67, 70, 73, 77/Modified site: gamma-carboxyglutamic acid (Glu) #stat  
 F:58-63, 88-113, 121-134, 126-143, 145-154, 161-175, 171-184, 186-199, 205-217, 212-226, 228-241, 2  
 F:93-94/Cleavage site: Arg-154 (thrombin) #status experimental  
 F:111-112/Cleavage site: Arg-Ser (thrombin) #status experimental  
 F:136/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F:177, 219, 258/Modified site: erythro-beta-hydroxyasparagine (Asn) #status experimental  
 F:288-567, 449-475, 638-665/Dsulfide bonds: #status experimental  
 F:499/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:509/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 40.2%; Score 1479; DB 1; Length 675;  
 Best Local Similarity 41.6%; Pred. No. 6, 2e-96;  
 Matches 280; Conservative 132; Mismatches 225; Indels 36; Gaps 13;

22 LLAECALALPAREATOPLRP-----RORRAFOVEERAKOGLHRECEBELCSREE 74  
 11 LLA---CLALVLPVLEANPLSRHQAQVLIARRRANLLEBTKKGNLECEBELCKKEE 67  
 75 AREVFENDERTDFYPRYLDCINKYSPYTKNSGFAT-----CYQNLPDQCTPNPCD 126  
 68 AREIFENNPTETEFYPRYLDCINKYSPYTKNSGFAT-----CYQNLPDQCTPNPCD 127  
 127 RKTOACODLMGNPFCLCKAGMGRGLCDKDVNECSQE---NGGLOICHNKPFSFHCSC 183  
 128 EDGFMTCKDQATFTCTCKSGMOGCKESDINECKDPVNINNGSGQICENTPGSHCSCK 187  
 184 SGFELSDGRTCODIDBCA--DSEACGARCNUFGSYCLDEGFAVSSEKACRDVDEC 242  
 188 NGFVMLSNKKDCQDVDECVALKPSICGTAVCNKIPGDEPCABEGYKKNPNVSKSDVDDEC 247  
 243 LQGRCEOVCNVSGSYTCHCDGRGLKLSQDMTCEDILPCVPFSVAKSVKSYLYLGMFS 302  
 248 AENLCAQOLCVNPGVSGSYCYCDGKKGFLADOKSCENAVPVCLPLDLDKNELLYLEQFV 307  
 303 GTFVIRLRFKRLPTLRVAEFDRTPEBGLILPAGGHODSTWIVALARGLLEQLRYN 362  
 308 GV-VLYLKFRLPETTFPSAEFDRTYDSBGVILYAESSDHSAMFLALARGKLEIQKNE 366  
 363 GVGRTVSSGPIVNHGMQOTISVEELANLVIKVNRDAVMKIAVAGDLFQPERGLYHLNLT 422  
 367 KTKMTTGKVINIDGLMHWVSVELEBSISVKIAKEAVNMINKPSLFRKTNGFLETKVY 426  
 423 VGGIPRH-EKDLVQPINRPLDGMKRSNMWINGEDTTIQETVKNTRMQCSVTERGSFYP 481  
 427 FAVVPKRMKVALRPIINPRDGCIRGMWLNQGTSGVKEIIQEKONKGLVNEKESYYP 486  
 482 GSGFAFYSLDYMKTPLDVGESTWEVYVAHIRPADDTGLPALMAPDLRAVLSVALVD 541  
 487 GTCVAPFSINVK---NESNPEAKQINVSINIRPSAGTGMALVDSN--TVFPALSLVD 540  
 542 YHSTKLKQQLVLAVEHTALME--IKVCDQGEHVTVSLRDGEATLEVDGTRGQSEVS 600  
 541 -SATEKL--QDILVSVESVWIGRIEALISCSDDQ--TFLEIRVNRNLELSTQLRDSEH 595  
 601 AAOQLRLAVLEHLRSPLYTEAGGILPDVPTVSAPVATPYRGCMTLEVNRLILDLDEAV 660  
 596 SEDFOQAFILDEAMGVTVTYLGILPDVPSATPVNAFYQGMVENVINGVQVLDLEAIS 655  
 661 KHSIDITAHSCPPV 673  
 656 KKNIDIRAHSCPSV 668

## RESULT 7

553433

plasma protein S precursor, vitamin K dependent - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 01-Aug-1995 #sequence\_revision 18-Jul-1997 #text\_change 09-Jul-2004

C:Accession: S53433

R:Greengard, J.S.; Fernandez, J.A.; Radtke, K.P.; Griffin, J.H.

Biochem J. 305, 397-403, 1995

A:Title: Identification of candidate residues for interaction of protein S with C4b bin

A:Reference number: S53433; MUID:95134217; PMID:7832752

A:Accession: S53433

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-642 &lt;GBR&gt;

A:Cross-references: UNIPROT:Q20904; UNIPARC:UPI0000176515; EMBL:L31379

A:Experimental source: tissue type liver

C:Genetics:

A:Gene: PROS

C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat ho

F:1-51/Domain: Gla domain homology (fragment) &lt;Gla&gt;

F:1-7/Domain: signal sequence (fragment) #status predicted &lt;SIG&gt;

F:8-642/Product: plasma protein S #status predicted &lt;MAT&gt;

F:87-120/Domain: EGF homology &lt;EG1&gt;

F:127-165/Domain: EGF homology &lt;EG2&gt;

F:171-207/Domain: EGF homology &lt;EG3&gt;

F:213-248/Domain: EGF homology &lt;EG4&gt;

F:261-633/Domain: sex hormone-binding globulin homology &lt;SHB&gt;

F:231-444/Domain: laminin G repeat homology &lt;LGR&gt;

Query Match 40.2%; Score 1477.5; DB 2; Length 642;  
 Best Local Similarity 43.5%; Pred. No. 7, 4e-96;  
 Matches 280; Conservative 125; Mismatches 213; Indels 25; Gaps 11;

45 RORRAFOVEERAKOGLHRECEBELCSREAREVFENDERTDFYPRYLDCINKYSPYT 104  
 4 RKRANSMLERKOGNLERECIEBELCSKEAREVFENDERTDFYPRYLDCINKYSPYT 63  
 105 KNSGFAT-----CYQNLPDQCTPNPCDCKRQKTOACODLMGNPFCLCKAGMGRGLCDK 156  
 64 TAARLSTNAVPLDRSCVNALPDQCNPLPCNEDPFMTCKDQAMFTCTCKSGWEEKELD 123  
 157 VNECSQE---NGGLOICHNKPFSFHCSCSGFELSDGRTCODIDBCA--DSEACGARC 212  
 124 INECKPPTNNGGCSQICDTPPSYHSCSKSGFIMLSNKKDCQDVDECSYKPSICDTAVC 183  
 213 KNLPSYSCLDEGFAVSSQEKACRDVDECLQGRCEOVCNVSGSYTCHCDGRGLKLSQ 272  
 184 KNIPGDFECCEPGEYRNPFLTKSCEDVDECSNMCAQLCVNPGVSGSYCYCDGKRGFLAQ 243  
 273 DMOTCEDILPCVPFSVAKSVKSYLYLGMBSGTVILRFKRLQPTRLVAEFDRTPEEG 332  
 244 DQSCENAVPVCLPLNDKVEYELLYLAQFVG-VLYLKFRLPETTFPSAEFDRTYDSBG 302  
 333 ILTFAGGHODSTWIVALARGLLEQLRYNGVGRVTSVSGPIVNHGMQOTISVEELANLV 392  
 303 VILYAESSDHSAMFLALADDKIEIOPKNEHTTKITTGGRVINIDGLMHWVSVELEBSIS 362  
 393 IKVNRDAVMKIAVAGDLFQPERGLYHLNLTVGGIPIH-EKDLVQPINRPLDGMKRSNMWL 451  
 363 VKIAKEAVNMINKPSLFRKTNGFLETKVYFAGLPKRVENALIKPIINPRDGCIRGMWLN 422  
 452 NGEEDTTIQETVKNTRMQCSVTERGSFYPGSGFAFYSLDYMKTPLDVGESTWEVYVAH 511  
 423 NQASGVKEIIDIQNHKCLVTEKESYYPGSSVAFOSIDYK---NVSSAGAMQVNVSL 478  
 512 HIRPADDTGLPALMAPDLRAVPLSVALVDYHSTKLKQQLVLAVEHTALA-LMEIKVC 570  
 479 NIRPSAGTGMALVDSN--NTVPFALSLVD-SATEKL--QDILVSVESVWIGRIEALISCS 534  
 571 DQGEHVTVSLRDGEATLEVDGTRGQSEVSAOQLRLAVLEHLRSPLYTEAGGILPDV 630  
 535 SSG--LSLLEWVSVNSLELITQFEKRRISSEEDYQOFAILDKAMGVTATYLGILPDV 592

QY 631 VTSAPTAFYRCMTLEVNRRLLDLEAAYKHSIDITAFHSCPPV 673  
 DB 593 FSATPVNAFYNGCMVDVITINGVPLDLDEALAKINDIRAHSCPSV 635

## RESULT 8

S38819  
 plasma protein S - rabbit (fragment)

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 18-Feb-1994 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004

C/Accession: S38819; S37238

R/He, X.; Dahlback, B.

Eur. J. Biochem. 217, 857-865, 1993

A/Title: Molecular cloning, expression and functional characterization of rabbit anticon

A/Reference number: S38819; MUID:94039141; PMID:8223642

A/Accession: S38819

A/Status: preliminary

A/Molecule type: mRNA

A/Cross-references: UNIPROT: P98118; UNIPARC: UP10000176514; EMBL: Z26485

R/He, X.; Dahlback, B.

submitted to the EMBL Data Library, September 1993

A/Description: Molecular Cloning and Expression of Rabbit Anticoagulant Vitamin K-depend

A/Reference number: S37238

A/Accession: S37238

A/Molecule type: mRNA

A/Residues: 1-502, 'L', 504-646 <HE2>

A/Cross-references: UNIPARC: UP1000013238A; EMBL: Z26485; NID: g403306; PIDN: CAA81259.1; PI

C/Superfamily: Plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom

F:1-56/Domain: Gla domain homology (fragment) <GLA>

F:132-125/Domain: EGF homology <EG1>

F:176-212/Domain: EGF homology <EG2>

F:218-253/Domain: EGF homology <EG3>

F:286-637/Domain: sex hormone-binding globulin homology <SHB>

F:296-449/Domain: laminin G repeat homology <LGR>

Query Match 39.7%; Score 1460.5; DB 2; Length 646;

Best Local Similarity 42.7%; Pred. No. 1.2e-94; Matches 277; Conservative 117; Mismatches 230; Indels 25; Gaps 11;

QY 38 ATQFLRPRORRAFOVFEAKQGLERECEVEELCSREAREVFENDEDTFYPRYLDGIN 97  
 DB 3 AQQVL-VRRKRANSMLEFTRKGNLEKECELECNKEAREVFENDEDTFYPRYLCGCG 61  
 QY 98 KTGSPT---TKNSG-----PATVQNLPDQCTPNPCDRKCTQACODLMGNFCLCKAKMG 149  
 DB 62 SFRAKLFTATRRSANGYPDLRSQVNAIPQCNPFLPCESEGYLNCKQGOATFTICRKGWQ 121  
 QY 150 GRLCDVDVACSGE---NGGCLQICHNKGSGFHSCGSGPELSDGRTCODIDEGCA-DSE 205  
 DB 122 GEKCELDINECKDPTNINSGSQICDVTAGSHSCSGFVMLANEKCDKMDCECVKRS 181  
 QY 206 ACGEARCKNLPGSYGLCDGFAYSOQEKARCDVDECTQRCQVQCVNPSGYTCHCDGR 265  
 DB 182 VCGTAVCKMTPGDFECESGGRYNNPAPKASCEBIDECSENMCAQLCTVNGYGVGSCYCDK 241  
 QY 266 GGLKLSQMDTGCDDILPCVPFSAKYSKSYLGRMSGTVITLRFKRLQPTFLVAFDF 325  
 DB 242 KGFKLADKKSCSAVPCPLDLDKVQQLYLAEQFQGA-VLYLKFPLPEITFRSSEFDF 300  
 QY 326 RTDPREGIILFAGGHDSSTWIVLALRAGRLELRLRVGVGRVSSGPFVNHGMQITISVE 385  
 DB 301 RTTDSRQVILYASLDHSTWFLIALRQKKEIQKNDYAAQITGGQVINDGIMNWSVE 360  
 QY 386 ELARNLVITKVRDAVMKIAVAGDLFQPERGILYHLNLTVGSI PRH-EKDLVQPINRLDGC 444  
 DB 361 ELHSHVSITKIAQEPVNMINKPGLFKPTNGFLETKYVFAGLPRVNEALIRPINRLDGC 420  
 QY 445 MRSWMNLGDDTTIQTETVKYNTRMQCSVTERRGSFFYGGGFATYSLDYMETPLDVGTST 504  
 DB 421 MRGMNLMKQAGASVKETIIQOKKQKGLVTEVKGSGYPSGSIAGQPHIDYN---NLSEYED 476

QY 505 WEVEVAHIRPADTGVFLMAPDLRAVPLSVLVDYHSTKGLKKQDLVLAVENTALAL 564  
 DB 477 MQVNTLNIIRSTGTGWLTLVSGN--TVFALSLV--QSTSETSQDLIVSENRVLYQL 532  
 QY 565 MEIKVCDQGEHVTVSLDGEATLEVDGTGQSEVSAALOQERLAVLERHLRSPULTFPG 624  
 DB 533 ESISLCSGQSQSLERFSVRNH--LELSTPLVDVTVYSBDLQRHLAVLDEAMKGVTTYLG 590  
 QY 625 GLPDYPTVASPYTAFYRCMTLEVNRRLLDLEAAYKHSIDITAFHSCPPV 673  
 DB 591 GLPEVPNATPVNAFYNGCMVEVINGVQDLDEALSKINDIRAHSCPSV 639

## RESULT 9

KXMS  
 plasma protein S precursor - mouse

N/Alternate names: vitamin K-dependent glycoprotein S

C/Species: Mus musculus (house mouse)

C/Date: 13-Jan-1995 #sequence\_revision 26-Jan-1996 #text\_change 09-Jul-2004

C/Accession: S43504; S59616; S35962

R/Chu, M.D.; Sun, J.; Bird, P.

Biochim. Biophys. Acta 1217, 325-328, 1994

A/Title: Cloning and sequencing of a cDNA encoding the murine vitamin K-dependent protei

A/Reference number: S43504; MUID:94198297; PMID:8148380

A/Accession: S43504

A/Molecule type: mRNA

A/Residues: 1-675 <CHU>

A/Cross-references: UNIPROT: Q08761; UNIPARC: UP1000002204D; EMBL: Z25469; NID: g396426; PID

R/Chu, D.; Schmidl, D.K.; Long, G.L.

Thromb. Res. 74, 135-142, 1994

A/Title: Structure of mouse protein S as determined by PCR amplification and DNA sequenc

A/Reference number: S59616; MUID:94302659; PMID:8029814

A/Accession: S59616

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 33-492, 'L', 494-675 <RES>

A/Cross-references: UNIPARC: UP1000016CEPD2; GB: I27439; NID: g487866; PIDN: AAA40006.1; PID

C/Complex: in plasma forms a complex with C4b binding protein

C/Function: a cofactor for activated protein C (EC 3.4.21.69); thrombin cleavage deact

C/Superfamily: Plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom

C/Keywords: beta-hydroxyaspartate; beta-hydroxyaspartic acid; blood coagulation; carbox

F:1-24/Domain: signal sequence #status predicted <Sig>

F:25-41/Domain: propeptide #status predicted <PRO>

F:26-85/Domain: Gla domain homology <GLA>

F:42-675/Product: plasma protein S #status predicted <MAT>

F:121-154/Domain: EGF homology <EG1>

F:161-199/Domain: EGF homology <EG2>

F:205-241/Domain: EGF homology <EG3>

F:247-282/Domain: EGF homology <EG4>

F:315-666/Domain: sex hormone-binding globulin homology <SHB>

F:325-678/Domain: laminin G repeat homology <LGR>

F:47-48,55,57,60,61,66,67,70,73,77/Modified site: gamma-carboxyglutamic acid (Glu) #sta

F:78-63,88-113,121-134,126-143,145-154,161-175,171-184,186-199,205-217,212-226,228-241

F:111-112/Cleavage site: Arg-Ser (thrombin) #status predicted

F:313/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted

F:177,219,258/Modified site: erythro-beta-hydroxyaspartate (Asn) #status predicted

F:499,509/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 39.5%; Score 1452; DB 1; Length 675;

Best Local Similarity 43.0%; Pred. No. 4.8e-94; Matches 291; Conservative 120; Mismatches 225; Indels 40; Gaps 15;

QY 21 LILAACALALPLAREAQPLRP-----RQRAFOVFEAKQGLERECEVEELCSR 72  
 DB 10 VLLA---CALVLPVSE-TNPLSKERASQVVLVAKRRANLTFERTMKNLEKECELECNK 65  
 QY 73 EEAREVFENDPETDYFYPYLDICINKY--GSPYTKNSG-----FATCVQNLPDQCTPNP 124  
 DB 66 EEAREVFENNPERDYFYPYLDICINKY--GSPYTKNSG-----FATCVQNLPDQCTPNP 125  
 QY 125 CDRKGTQACODLMGNFCLCKAKMGRLCDKVDNEC---SQENGGCLQICHNKGSGFHS 181



Db 126 CNEGYLACODGQAFTCEKPGMGQDRQYDVNECKDPNVNNGSGQICDNTPGSYHCS 185  
 QY 182 CHSGFELSDGRTCODIDECA-DSEACGEARCKNLPGSYSLCDEGFAYSQEKACRDVD 240  
 Db 186 CKRGFAMLPNKCKDKDECLAKPSVCTAVCKNIPGDFECCPDGRIYDPSKSCQVD 245  
 QY 241 ECLQGRCEQYCVNPSGYSYCHCDGRGGLKLSQDMDCEDILPCVPFSVAKSVKSLYLGRM 300  
 Db 246 ECEENMCAQLCVNPPGYSYCYCDGKGFKLADQDKSGEGIPVCLSLDLDKNYELLYLAEQ 305  
 QY 301 FSGTPVIRLRFKRLQPLRLVAEPFRTPDEGILLFPGGHODSTWYLAIPAGLEIQLR 360  
 Db 306 FAGV-VLYLFRPLDITRFSAEPFRFYDESGIILYAESLDHSNMLLIALRDGKIEVOFK 364  
 QY 361 YNGVRATSSGPIVNHGMQOTISVEELARLVKNRDVAMKIAVAGDLPOPEGLYHIN 420  
 Db 365 NEFTQITTTGGNVINNGIMNMVSVLEEDDSVSIKIAKEAVANNIKLSLEFPDGFIDTK 424  
 QY 421 LTVGGIIPFH-EKDLVOPINRLDGCNRSMNWLNGEDTTIOETVKVNTRMQCFSTERGSP 479  
 Db 425 IYFAGLPRKVESALIKRINPRLDGICRGNMLMKQALGAKELIEGKQNKICFLNVEKGSY 484  
 QY 480 YPSSGFAFYSLDYMRTPLDVGTESTWEVEVAHIRPAADTGVLPALMAPDLRAVPISVAL 539  
 Db 485 YPSSGIAQFSIDYN---NVTNAEGMQMNTLINIRPSTGTGVMALVSGD--TVFPALSL 538  
 QY 540 VDHSTFKKLKKOLVLAVEHTALALME-IKVCGQGEHVVTVSL-RDEGATLEVDGTRGOS 597  
 Db 539 VDSRSG---TSQDILVFEVSNVVARLEVASLCSQDSQOLCNVRNG--LELMTPIRKD 592  
 QY 598 EVSAAQLQERLAVLERHLSPVLTFPAGLDPDVPTASAPVTAIFYGCGTLEVNRLDLDE 657  
 Db 593 VIVSKDLQRLALVLDKMKRTVATYLGIPDISFSAIPVNAFVSGCMENVINQVQDLDE 652  
 QY 658 AAKHSDITRAHSCPPV 673  
 Db 653 AISKHNDIRAHSCPSV 668

## RESULT 10

KXRTS

Plasma protein S precursor - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 04-Oct-1995 #sequence\_revision 26-Jan-1996 #text\_change 09-Jul-2004

C/Accession: J04180

R.Yasuda, F.; Hayashi, T.; Tanitame, K.; Nishioka, J.; Suzuki, K.

J. Biochem. 117, 374-383, 1995

A/Title: Molecular cloning and functional characterization of rat plasma protein S.

A/Reference number: J04180; MUID:95332263; PMID:7608128

A/Accession: J04180

A/Molecule type: mRNA

A/Residues: 1-675 &lt;YAS&gt;

A/Cross-references: UNIPROT:P53813; UNIPARC:UP100001333EB; GB:S78744; NID:G1041903; PIDN

C/Comment: This protein is a vitamin K-dependent plasma glycoprotein that has an anticoag

activation of coagulation factors Va and VIII. This protein also binds to factor Va and

C/Suprafamily: Plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom

C/Keywords: beta-hydroxyaspartate; beta-hydroxyaspartic acid; blood coagulation; carbox

F.1-24/Domain: signal sequence #status predicted &lt;S1G&gt;

F.25-41/Domain: propeptide #status predicted &lt;PRO&gt;

F.26-85/Domain: Gla domain homology &lt;GLA&gt;

F.2-675/Product: plasma protein S #status predicted &lt;MAT&gt;

F.121-154/Domain: EGF homology &lt;EG1&gt;

F.161-199/Domain: EGF homology &lt;EG2&gt;

F.205-241/Domain: EGF homology &lt;EG3&gt;

F.247-282/Domain: EGF homology &lt;EG4&gt;

F.315-666/Domain: sex hormone-binding globulin homology &lt;SHB&gt;

F.325-478/Domain: laminin G repeat homology &lt;LGR&gt;

F.57-48,55,57,60,61,66,67,70,73,77/Modified site: gamma-carboxyglutamic acid (Glu) #stat

F.58-63,88-113,121-134,126-143,145-154,161-175,171-184,186-199,205-217,212-226,228-241,2

F.111-112/Cleave site: Arg-Ser (thrombin) #status predicted

F.136/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted

F.177,219,258/Modified site: erythro-beta-hydroxyaspartate (Asn) #status predicted

F.499,509/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 39.4%; Score 1448; DB 1; Length 675;

Best Local Similarity 42.8%; Pred. No. 9.3e-94;

Matches 289; Conservative 124; Mismatches 223; Indels 40; Gaps 15;

QY 21 LLLAAECALAAALPAREATQFLRP-----RORARFOVEEAKOGHLECEVEELCSR 72  
 Db 10 VLLA---CLALVLPNSE-TNFLSKERASQVLYRRKRANTLLEETKGNLEKECEELCNK 65  
 QY 73 EBAEVEENDEPETYFPYRYLDCINKY-----GSPYTKNS--GFATCVONLPDQCTPNP 124  
 Db 66 EBAEVEENNPEDTYFPYRYLDCINKY-----GSPYTKNS--GFATCVONLPDQCTPNP 125  
 QY 125 CDKRGTAQCODLMGNFCLCKAAGRLCKDVNEC---SQENGGCLQICHNKGFSHCS 181  
 Db 126 CNEGYLSCDGGGAFCICPKPMQDCKCFDINECDPNNINGGCSQOTDNPFGSYHCS 185  
 QY 182 CHSGFELSDGRTCODIDECA-DSEACGEARCKNLPGSYSLCDEGFAYSQEKACRDVD 240  
 Db 186 CKRGFAMLPNKCKDKDECLAKPSVCTAVCKNIPGDFECCPDGRIYDPSKSCQVD 245  
 QY 241 ECLQGRCEQYCVNPSGYSYCHCDGRGGLKLSQDMDCEDILPCVPFSVAKSVKSLYLGRM 300  
 Db 246 ECEENMCAQLCVNPPGYSYCYCDGKGFKLADQDKSGEGIPVCLSLDLDKNYELLYLAEQ 305  
 QY 301 FSGTPVIRLRFKRLQPLRLVAEPFRTPDEGILLFPGGHODSTWYLAIPAGLEIQLR 360  
 Db 306 FAGV-VLYLFRPLDITRFSAEPFRFYDESGIILYAESLDHSNMLLIALRDGKIEVOFK 364  
 QY 361 YNGVRATSSGPIVNHGMQOTISVEELARLVKNRDVAMKIAVAGDLPOPEGLYHIN 420  
 Db 365 NEFTQITTTGGNVINNGIMNMVSVLEEDDSVSIKIAKEAVANNIKLSLEFPDGFIDTK 424  
 QY 421 LTVGGIIPFH-EKDLVOPINRLDGCNRSMNWLNGEDTTIOETVKVNTRMQCFSTERGSP 479  
 Db 425 IYFAGLPRKVESALIKRINPRLDGICRGNMLMKQALGAKELIEGKQNKICFLNVEKGSY 484  
 QY 480 YPSSGFAFYSLDYMRTPLDVGTESTWEVEVAHIRPAADTGVLPALMAPDLRAVPISVAL 539  
 Db 485 YPSSGIAQFSIDYN---NVTNAEGMQMNTLINIRPSTGTGVMALVSGD--TVFPALSL 538  
 QY 540 VDHSTFKKLKKOLVLAVEHTALALME-IKVCGQGEHVVTVSL-RDEGATLEVDGTRGOS 597  
 Db 539 VDSRSG---TSQDILVFEVSNVVARLEVASLCSQDSQOLCNVRNG--LELMTPIRKD 592  
 QY 598 EVSAAQLQERLAVLERHLSPVLTFPAGLDPDVPTASAPVTAIFYGCGTLEVNRLDLDE 657  
 Db 593 VIVSKDLQRLALVLDKMKRTVATYLGIPDISFSAIPVNAFVSGCMENVINQVQDLDE 652  
 QY 658 AAKHSDITRAHSCPPV 673  
 Db 653 AISKHNDIRAHSCPSV 668

## RESULT 11

protein S - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004

C/Accession: I59618

R.Jamson, C.S.; McDowell, S.A.; Marlar, R.A.; Degen, S.J.F.

Thromb. Res. 78, 407-419, 1995

A/Title: Developmental expression of protein C and protein S in the rat.

A/Reference number: I59618; MUID:95389408; PMID:7660357

A/Accession: I59618

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-346 &lt;RES&gt;

A/Cross-references: UNIPROT:Q62628; UNIPARC:UP1000006B601; EMBL:U06230; NID:G497116; PIF

C/Suprafamily: Plasma protein S; EGF homology; Gla domain homology; laminin G repeat

F.1-337/Domain: sex hormone-binding globulin homology &lt;SHB&gt;

F.1-149/Domain: laminin G repeat homology (fragment) &lt;LGR&gt;

Query Match 16.3%; Score 600; DB 2; Length 346;  
 Best Local Similarity 37.5%; Pred. No. 1.3e-34;  
 Matches 133; Conservative 71; Mismatches 129; Indels 22; Gaps 8;

QY 322 EFDFFPTPEGILLFAGGHQSDTWIYLAIRAGRLLEIQRNGVGRVTSQGVPIINQMOT 381  
 DB 4 ETSCHGFSEBSL-----DHSNMILLIAREBKIEVQFNPFSQTQTTGGVNIINGMIWM 56

QY 382 ISVEELARNLVTKNRDAVMKTAVAGDLFQPERGLYHMLTYGGIPFH-EKLVQPINR 440  
 DB 57 VSVSEELSDSVSIKIKAEAVMNINKLSLFKPTDGLDTIYFAGAPRKVESALIKPINR 116

QY 441 LDGCRSMWMLNGEDDTTQETKVNTRMOCFSVTERGSPYPSGFAFYSDIWRFTLDG 500  
 DB 117 LDGCTRGMWMLKQAGLGAKEIVEGKONKICFLTVEKSTYPSGSLAKQSFIDN---NVT 172

QY 501 TESTVEVEVAHIRPADTGVLPALMAPDLRAVPLSVALVDYHSTKGLKKQVLVAVENT 560  
 DB 173 NAEQDQINTLNIIRPTGTGVMLALVSGD--TVPFALSLVDSGSG---TSQDILVFEVS 227

QY 561 ALALME-IVCGQGEHVTVSL-RDGEATLEVDGTRGSEVSAALQOEKLAVERHLRSP 618  
 DB 228 VAHAEIATLCSEPSQLKCNINRNG---LEIMTPVRKQVIYSKDLQRDLATIDTKMGT 284

QY 619 VLTFAAGLPDVPVTSAPVAFYRGCGWTELEVRRLDLEAAVYKSHDITAHSCPV 673  
 DB 285 VAVYLGVDIPDSFATPVNAFISGCMENVINGQLDDEAISKANDIRAHSCPSV 339

RESULT 12  
 578040  
 fibulin, splice form C precursor - mouse  
 M:Alternate names: Basement-membrane protein BM-90  
 C:Species: Mus musculus (house mouse)  
 C>Date: 24-Jul-1998 #sequence, revision 24-Jul-1998 #text\_change 09-Jul-2004  
 C:Accession: S78040; S78560; S36440  
 R:Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.  
 Eur. J. Biochem. 215, 733-740, 1993  
 A:Title: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dependent  
 A:Reference number: S34968; MUID:93358897; PMID:8354280  
 A:Accession: S78040  
 A:Molecule type: mRNA  
 A:Residues: 1-685 <PAM>  
 A:Cross-references: UNIPROT:Q08879; UNIPARC:UPI0000176527; EMBL:X70854  
 R:Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.  
 submitted to the EMBL Data Library, January 1993  
 A:Description: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dep  
 A:Reference number: S36440  
 A:Accession: S78560  
 A:Molecule type: mRNA  
 A:Residues: 1-39, 'P', '41-685 <CHU>  
 A:Cross-references: UNIPARC:UPI000002A96F; EMBL:X70854  
 C:Genetics:  
 A:introns: 568/3  
 C:Superfamily: fibulin-1; EGF homology  
 C:Keywords: alternative splicing; basement membrane; calcium binding; extracellular matr  
 F:1-29/Domain: signal sequence #status predicted <Sig>  
 F:30-685/Product: fibulin, splice form C #status predicted <MAT>  
 F:98,537,541/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.9%; Score 362; DB 2; Length 685;  
 Best Local Similarity 38.2%; Pred. No. 1.5e-17;  
 Matches 84; Conservative 24; Mismatches 68; Indels 44; Gaps 12;

QY 95 CINKGSPYTKNSGFATCYQNL-----DOCTP--NECDKRGTOAQO 134  
 DB 327 CINTBGS-----YTCQKNVPCNGRGYHLNEBGRVCVDVDECAPAPFCG-KG-HHCL 376

QY 135 DLMGNFPLCLKAGW-----GRLCDKDVNECSQENG-CLOICINKKGSFHCSHSGFELS 189  
 DB 377 NSPGSRFCCKAKGFYDGSIRTC-VDINCCQRYPRGLCHKCENTPGSFHCSGSAFRLS 435

QY 190 SDGRTQDIDBCAUSAEAGRCRKNLPGSYSCLCDGFAYSQGE-KACRDVDECLQGR-- 246  
 DB 436 VDRSCDEVDNECLNPGSQE--CANVYGYCCYCRGRYQLSDVDVDEIDECALPTGG 493

QY 247 --CEOVCVNSPGSYTCHCDGRGLKLSQDMTCEIILFCV 284  
 DB 494 HICSYRCINIPGSFQSCPS-SGYRLAPGRNCODIDECV 532

RESULT 13  
 S34968  
 fibulin, splice form D precursor - mouse  
 M:Alternate names: Basement-membrane protein BM-90; calcium-binding protein BM-90  
 C:Species: Mus musculus (house mouse)  
 C>Date: 10-Dec-1993 #sequence, revision 10-Nov-1995 #text\_change 09-Jul-2004  
 C:Accession: S34968; S36441; S13814  
 R:Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.  
 Eur. J. Biochem. 215, 733-740, 1993  
 A:Title: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dependent  
 A:Reference number: S34968; MUID:93358897; PMID:8354280  
 A:Accession: S34968  
 A:Molecule type: mRNA  
 A:Residues: 1-705 <PAM>  
 A:Cross-references: UNIPROT:Q08879; UNIPARC:UPI000017651E  
 R:Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.  
 submitted to the EMBL Data Library, January 1993  
 A:Description: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dep  
 A:Reference number: S36440  
 A:Accession: S36441  
 A:Molecule type: mRNA  
 A:Residues: 1-39, 'P', '41-705 <PAM>  
 A:Cross-references: UNIPARC:UPI0000028FD1; EMBL:X70854; NID:g396820; PIDN:CAA50207.1; PI  
 A:Experimental source: cell-line F9 teratocarcinoma  
 R:Kluge, M.; Mann, K.; Dziadek, M.; Timpl, R.  
 Eur. J. Biochem. 193, 651-659, 1990  
 A:Title: Characterization of a novel calcium-binding 90-kDa glycoprotein (BM-90) shared  
 A:Reference number: S13814; MUID:91065369; PMID:2249686  
 A:Accession: S13814  
 A:Molecule type: protein  
 A:Residues: 28,31-49, 'X', '51-53; 'XX', '110-117;231-240, 'X', '242-243;339-362, 'S', '364-387;434-  
 A:Cross-references: UNIPARC:UPI000011EBB0; UNIPARC:UPI000017651F; UNIPARC:UPI0000176520,  
 525; UNIPARC:UPI0000176526  
 C:Superfamily: fibulin-1; EGF homology  
 C:Keywords: alternative splicing; basement membrane; calcium binding; extracellular matr  
 F:1-29/Domain: signal sequence #status predicted <Sig>  
 F:30-705/Product: fibulin, splice form D #status predicted <MAT>  
 F:98,537,541/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.9%; Score 362; DB 2; Length 705;  
 Best Local Similarity 38.2%; Pred. No. 1.5e-17;  
 Matches 84; Conservative 24; Mismatches 68; Indels 44; Gaps 12;

QY 95 CINKGSPYTKNSGFATCYQNL-----DOCTP--NPCRKGTOAQO 134  
 DB 327 CINTBGS-----YTCQKNVPCNGRGYHLNEBGRVCVDVDECAPAPFCG-KG-HHCL 376

QY 135 DLMGNFPLCLKAGW-----GRLCDKDVNECSQENG-CLOICINKKGSFHCSHSGFELS 189  
 DB 377 NSPGSRFCCKAKGFYDGSIRTC-VDINCCQRYPRGLCHKCENTPGSFHCSGSAFRLS 435

QY 190 SDGRTQDIDBCAUSAEAGRCRKNLPGSYSCLCDGFAYSQGE-KACRDVDECLQGR-- 246  
 DB 436 VDRSCDEVDNECLNPGSQE--CANVYGYCCYCRGRYQLSDVDVDEIDECALPTGG 493

QY 247 --CEOVCVNSPGSYTCHCDGRGLKLSQDMTCEIILFCV 284  
 DB 494 HICSYRCINIPGSFQSCPS-SGYRLAPGRNCODIDECV 532

RESULT 14  
 A47221  
 fibritin 1 precursor - human (fragment)  
 C:Species: Homo sapiens (man)



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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 29, 2006, 11:07:36 ; Search time 303 Seconds  
(without alignments)  
2094.260 Million cell updates/sec

Title: US-10-671-054-1  
Perfect score: 3675  
Sequence: 1 MAPSLSPGPAALRRAPQLLL.....AHSCPVEPAADYKDDDDK 686

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3628	98.7	678	2	061MNI_HUMAN
2	3596.5	97.9	721	1	GAS6_HUMAN
3	2993	81.4	674	1	GAS6_RAT
4	2989	81.3	674	2	061RL1_RAT
5	2965	80.7	674	1	GAS6_MOUSE
6	2322	63.2	671	2	Q2MJP6_NOTY1
7	2293.5	62.4	669	2	Q6DPA5_XENLA
8	2286	62.2	668	2	Q6PAE0_XENLA
9	1802	49.0	626	2	Q4SHY2_TETNG
10	1755	47.8	648	2	Q7T3H4_BRARE
11	1543	42.0	676	1	PROS_HUMAN
12	1516	41.3	649	1	PROS_MACMU
13	1516	41.3	650	2	Q16519_HUMAN
14	1514	41.2	650	2	Q9NSD0_HUMAN
15	1479	40.0	675	1	PROS_BOVIN
16	1470.5	40.0	648	2	Q29094_PIG
17	1457.5	39.7	646	1	PROS_RABIT
18	1452	39.5	675	1	PROS_MOUSE
19	1452	39.5	675	1	PROS_MOUSE
20	1448	39.4	675	1	PROS_RAT
21	891	24.2	729	2	Q4SHY3_TETNG
22	634.5	17.3	129	2	Q6SBL2_HUMAN
23	600	16.3	346	2	Q62628_RAT
24	376	10.2	907	2	Q68EF9_MOUSE
25	374.5	10.2	2884	2	Q4SHN1_TETNG
26	366.5	10.0	941	2	Q5AYP0_DICDI
27	366	10.0	1277	2	Q7PPC0_ANOXA
28	363	9.9	705	1	FBNL1_MOUSE
29	363	9.9	705	1	FBNL1_MOUSE
30	359	9.8	1577	2	Q9V889_DROME
31	358.5	9.8	992	2	Q8C9Q4_MOUSE

32	358.5	9.8	997	2	Q9JUS0_MOUSE	Q9JUS0_MOUSE
33	358	9.7	1018	2	Q6NZL8_MOUSE	Q6NZL8_MOUSE
34	357.5	9.7	961	2	Q9EOC6_MOUSE	Q9EOC6_MOUSE
35	357	9.7	708	2	P87363_CHICK	P87363_CHICK
36	356.5	9.7	477	2	Q5XJ74_BRARE	Q5XJ74_BRARE
37	356.5	9.7	1021	2	Q3UGU1_MOUSE	Q3UGU1_MOUSE
38	356.5	9.7	1666	1	LTPP4_MOUSE	LTPP4_MOUSE
39	356	9.7	469	2	Q5BLE3_BRARE	Q5BLE3_BRARE
40	354.5	9.6	1587	2	Q00508_HUMAN	Q00508_HUMAN
41	353.5	9.6	509	2	Q4SUJ7_TETNG	Q4SUJ7_TETNG
42	353.5	9.6	1557	2	Q75412_HUMAN	Q75412_HUMAN
43	353.5	9.6	1624	2	Q75413_HUMAN	Q75413_HUMAN
44	353	9.6	3857	2	Q88840_MOUSE	Q88840_MOUSE
45	352	9.6	1365	2	Q75N88_HUMAN	Q75N88_HUMAN

## ALIGNMENTS

RESULT 1  
ID 061MNI\_HUMAN PRELIMINARY; PRT; 678 AA.  
AC 061MNI;  
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.  
DT 10-MAY-2005, sequence version 1.  
DI 07-MAR-2006, entry version 10.  
DE Growth arrest-specific 6.  
GN Name=GAS6; ORFNames=RP11-199F6.6-001;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15108283; DOI=10.1002/humu.20025;  
RA Munoz X., Sumoy L., Ramirez-Lorca R., Villar J., de Frutos P.G.,  
RA Sala N.;  
RT "Human vitamin K-dependent GAS6: gene structure, allelic variation,  
RT and association with stroke.";  
RL Hum. Mutat. 23:506-512(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Matthews L.;  
RP Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
CC - MISCLEANNEDUS: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NonDerivs license

EMBL: BK001240; DA01155.1; -; Genomic DNA.  
EMBL: BX072579; CAH71174.1; -; Genomic DNA.  
SRR: 061MNI, 261-678.  
DR Ensembl: ENSG00000183087; Homo sapiens.  
DR GO: GO:0005576; C:extracellular region; IEA.  
DR GO: GO:0005509; F:calcium ion binding; IEA.  
DR InterPro: IPR000152; Asx\_hydroxyl\_S.  
DR InterPro: IPR001320; ConA\_like\_subgrp.  
DR InterPro: IPR006210; EGF.  
DR InterPro: IPR000742; EGF\_3.  
DR InterPro: IPR001881; EGF\_Ca\_bd.  
DR InterPro: IPR013091; EGF\_Ca\_bd\_2.  
DR InterPro: IPR006209; EGF-like.  
DR InterPro: IPR013032; EGF-like\_reg.  
DR InterPro: IPR002383; GLA\_blood.  
DR InterPro: IPR001791; Laminin-G.  
DR InterPro: IPR012680; Laminin-G\_2.  
DR InterPro: IPR000294; Vitk\_dep\_GLA.  
DR Pfam: PF00008; EGF; 2.  
DR Pfam: PF07645; EGF\_CA; 2.  
DR Pfam: PF00594; GLA; 1.  
DR Pfam: PF02210; Laminin\_G\_2; 2.



RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.B.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [5]  
 RP NCLECTIDE SEQUENCE OF 1-85.  
 RA Marce A.O., Hillmann A., McRedmond J.P., Fitzgerald D.J.;  
 RL Submitted (Oct-2002) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP RECEPTOR INTERACTION.  
 RX PubMed=7854420; DOI=10.1038/373623a0;  
 RA Varnum B.C., Young C., Elliott G., Garcia A., Bartley T.D.,  
 RA Fridell Y.W., Hunt R.W., Trail G., Clogston C., Toso R.J.,  
 RA Yameghata D., Bennett L., Sylber M., Merewether L.A., Tseng A.,  
 RA Escobar E., Liu E.T., Yaman H.K.;  
 RT "X1 receptor tyrosine kinase stimulated by the vitamin K-dependent  
 RT protein encoded by growth-arrest-specific gene 6.";  
 RL Nature 373:623-626(1995).  
 RN [7]  
 RP RECEPTOR INTERACTION.  
 RX PubMed=7867073; DOI=10.1016/0092-8674(95)90520-0;  
 RA Sitt T.N., Conn G., Gore M., Lai C., Bruno J., Radziejewski C.,  
 RA Mattsson K., Fisher J., Gies D.R., Jones P.F., Maslakowski P.,  
 RA Ryan T.E., Tobies N.J., Chen D.H., DiStefano P.S., Long G.L.,  
 RA Basilio C., Goldfarb M.P., Lemke G., Gales D.J., Yancopoulos G.D.;  
 RT "The anticosagulation factor protein S and its relative, Gas6, are  
 RT ligands for the Tyro 3/Axl family of receptor tyrosine kinases.";  
 RL Cell 80:661-670(1995).  
 RN [8]  
 RP ALTERNATIVE SPLICING (ISOROM 1), AND TISSUE SPECIFICITY.  
 RX PubMed=9326368; DOI=10.1016/S0014-5793(97)01094-6;  
 RA Marcandalli P., Goetisa M., Varnum B., Goruppi S., Schneider C.;  
 RT "Identification and tissue expression of a splice variant for the  
 RT growth arrest-specific gene gas6.";  
 RL FEBS Lett. 415:56-58(1997).  
 RN [9]  
 RP RECEPTOR INTERACTION.  
 RX PubMed=939948; DOI=10.1074/jbc.271.47.30022;  
 RA Nagata K., Ohachi K., Nakano T., Arita H., Zong C., Hanafusa H.,  
 RA Mizuno K.;  
 RT "Identification of the product of growth arrest-specific gene 6 as a  
 RT common ligand for Axl, Sky, and Met receptor tyrosine kinases.";  
 RL J. Biol. Chem. 271:30022-30027(1996).  
 RN [10]  
 RP RECEPTOR INTERACTION, SUBCELLULAR LOCATION, AND PROCESSING.  
 RX PubMed=9326369; DOI=10.1016/S0014-5793(97)01093-4;  
 RA Goruppi S., Yamane H., Marcandalli P., Garcia A., Clogston C.,  
 RA Goetisa M., Varnum B., Schneider C.;  
 RT "The product of a gas6 splice variant allows the release of the domain  
 RT responsible for Axl tyrosine kinase receptor activation.";  
 RL FEBS Lett. 415:59-63(1997).  
 RN [11]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 261-721 (ISOFORM 2), AND  
 RP MUTAGENESIS OF PHE-530; LEU-663 AND TYR-703.  
 RX PubMed=8621659; DOI=10.1074/jbc.271.16.9785;  
 RA Mark M.R., Chen J., Hammonds R.G., Sadtick M., Godowski P.J.;  
 RT "Characterization of Gas6, a member of the superfamily of G domain-  
 RT containing proteins, as a ligand for Rea and Axl.";  
 RL J. Biol. Chem. 271:9785-9789(1996).  
 CC CC -|- FUNCTION: Ligand for tyrosine-protein kinase receptors AXL, TYRO3  
 CC and MER whose signaling is implicated in cell growth and survival,  
 CC cell adhesion and cell migration. Plays a role in thrombosis by  
 CC amplifying platelet aggregation and secretion in response to known  
 CC agonists (By similarity).  
 CC -|- SUBUNIT: Monomer (Probable).  
 CC -|- SUBCELLULAR LOCATION: secreted protein.  
 CC -|- ALTERNATIVE PRODUCTS:  
 CC Name=1; Synonyms=gas6v;  
 CC

CC CC IsoId=014393-1; Sequence=Displayed;  
 CC CC Name=2;  
 CC CC IsoId=014393-2; Sequence=VSP\_010494;  
 CC CC Name=3;  
 CC CC IsoId=014393-3; Sequence=VSP\_010492, VSP\_010493, VSP\_010494;  
 CC CC Note=No experimental confirmation available;  
 CC CC -|- TISSUE SPECIFICITY: Plasma. Isoform 1 and isoform 2 are widely  
 CC expressed. Isoform 1 is the predominant form in spleen.  
 CC CC -|- PPM: Isoform 1 is proteolytically processed after secretion to  
 CC yield a N-terminal 36 kDa protein and a C-terminal 50 kDa protein  
 CC including the laminin G-like domains which activates AXL.  
 CC CC -|- PPM: Gamma-carboxyglutamate residues are formed by vitamin K  
 CC dependent carboxylation. These residues are essential for the  
 CC binding of calcium (By similarity).  
 CC CC -|- SIMILARITY: Contains 4 EGF-like domains.  
 CC CC -|- SIMILARITY: Contains 1 Gia (gamma-carboxy-glutamate) domain.  
 CC CC -|- SIMILARITY: Contains 2 laminin G-like domains.  
 CC CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC CC Distributed under the Creative Commons Attribution-NoDerivs license  
 CC CC -----  
 CC EMBL: U13720; AA58494.1; -; mRNA.  
 CC DR EMBL: AY256843; AA084057.1; -; Genomic DNA.  
 CC DR EMBL: AY256830; AA084057.1; JOINED; Genomic DNA.  
 CC DR EMBL: AY256831; AA084057.1; JOINED; Genomic DNA.  
 CC DR EMBL: AY256832; AA084057.1; JOINED; Genomic DNA.  
 CC DR EMBL: AY256833; AA084057.1; JOINED; Genomic DNA.  
 CC DR EMBL: AY256834; AA084057.1; JOINED; Genomic DNA.  
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 CC DR EMBL: AY256836; AA084057.1; JOINED; Genomic DNA.  
 CC DR EMBL: AY256837; AA084057.1; JOINED; Genomic DNA.  
 CC DR EMBL: AY256838; AA084057.1; JOINED; Genomic DNA.  
 CC DR EMBL: AY256839; AA084057.1; JOINED; Genomic DNA.  
 CC DR EMBL: AY256840; AA084057.1; JOINED; Genomic DNA.  
 CC DR EMBL: AY256841; AA084057.1; JOINED; Genomic DNA.  
 CC DR EMBL: AY256842; AA084057.1; JOINED; Genomic DNA.  
 CC DR EMBL: AY256533; BAC86580.1; -; mRNA.  
 CC DR EMBL: BC039884; AA039884.1; -; mRNA.  
 CC DR EMBL: AY170372; AA041859.1; -; Genomic DNA.  
 CC DR PIR: B48089; B48089.  
 CC DR PDB: 1H30; X-ray; A=322-721.  
 CC DR GO: 0008283; P: cell proliferation; TAS.  
 CC DR GO: 0007165; P: signal transduction; TAS.  
 CC DR InterPro: IPR000152; Asx\_hydroxyl\_S.  
 CC DR InterPro: IPR013320; Conn\_like\_subgrp.  
 CC  
 CC Query Match 97.9%; Score 3596.5; DB 1; Length 721;  
 CC Best Local Similarity 94.0%; Pred. No. 6, 2e-248;  
 CC Matches 678; Conservative 0; Mismatches 0; Indels 43; Gaps 1;  
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 CC 1 MAPSPSPGPAALRRAPQULLLLLAACALALIPAREALQFLPRPRRAFOVFEAKKH 60  
 CC 1 MAPSPSPGPAALRRAPQULLLLLAACALALIPAREALQFLPRPRRAFOVFEAKKH 60  
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 CC 61 LRECEVEELCSREAREVEENDEPETYFYPRYDCTINKGSPPTKNSGFATCVQNLPDCC 120  
 CC 61 LRECEVEELCSREAREVEENDEPETYFYPRYDCTINKGSPPTKNSGFATCVQNLPDCC 120  
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 CC 181 SCHSGFEISSDRTQDIDECADSEACGEGARCKNIPGSYCLCDSEFAVSSQEKARVD 240  
 CC 241 ECIQRCQOVCVNPSPSYTCCHCDGRGGLKLSQDMDTCE----- 278

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Db      241  |||||
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QY      279  -----DILCPVPSVAKSVKSLYLGMSFGSTPIRLRPFKRLQPT 317
Db      301  GAQGRSEGHIPDRRGPRPMQDILCPVPSVAKSVKSLYLGMSFGSTPIRLRPFKRLQPT 360
QY      318  RLVASFDPFPDEGLLFPAGGHODSTWLVLLRAGRLELQRYNGVGVVTSSGPVING 377
Db      361  RLVAFDFPFPDEGLLFPAGGHODSTWLVLLRAGRLELQRYNGVGVVTSSGPVING 420
QY      378  NMQTTISVEELANLVIKVRDAVMKIAVAGDLFOPERGLYHNLTVGGIPFEKDLVQPI 437
Db      421  NMQTTISVEELANLVIKVRDAVMKIAVAGDLFOPERGLYHNLTVGGIPFEKDLVQPI 480
QY      438  NPLRDCGRKSNMNLNGEDTTIOETVYKONTRMOCFSYTERGSPYSGSPFYSLDYRTP 497
Db      481  NPLRDCGRKSNMNLNGEDTTIOETVYKONTRMOCFSYTERGSPYSGSPFYSLDYRTP 540
QY      498  DVGSTSTVEVVAHVRPAADGVLPALMAPDLRAVPLSVALVDYHSTKKLKKOLVVLAV 557
Db      541  DVGSTSTVEVVAHVRPAADGVLPALMAPDLRAVPLSVALVDYHSTKKLKKOLVVLAV 600
QY      558  EHTALALMEIKYCDGGEHVTVSLRDGEATLEVDGTRGQSEVSAQLQERLAVLERHLS 617
Db      601  EHTALALMEIKYCDGGEHVTVSLRDGEATLEVDGTRGQSEVSAQLQERLAVLERHLS 660
QY      618  PVLTRAGLIPDVPTSAPYATYRGCMTLEVNRLDLDEBAVAKSDITAHSCPPVEPA 677
Db      661  PVLTRAGLIPDVPTSAPYATYRGCMTLEVNRLDLDEBAVAKSDITAHSCPPVEPA 720
QY      678  A 678
Db      721  A 721

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RT      common ligand for AxL, Sky, and Mer receptor tyrosine kinases."
RL      J. Biol. Chem. 271:30022-30027(1996).
RN      [4]
RP      GAMMA-CARBOXYGLUTAMIC ACIDS.
RA      Pubmed=9163328;
RX      Nakano T., Kawamoto K., Kishino J., Nomura K., Higashino K., Arita H.;
RT      "Requirement of gamma-carboxyglutamic acid residues for the biological
RT      activity of Gas6: contribution of endogenous Gas6 to the proliferation
RT      of vascular smooth muscle cells."
RL      Biochem. J. 323:387-392(1997).
CC      -I- FUNCTION: Ligand for tyrosine-protein kinase receptors AxL, TYRO3
CC      and Mer whose signaling is implicated in cell growth and survival,
CC      cell adhesion and cell migration. Plays a role in thrombosis by
CC      amplifying platelet aggregation and secretion in response to known
CC      agonists (By similarity).
CC      -I- SUBUNIT: Monomer (By similarity).
CC      -I- SUBCELLULAR LOCATION: Secreted protein.
CC      -I- TISSUE SPECIFICITY: Plasma.
CC      -I- PTM: Gamma-carboxyglutamate residues are formed by vitamin K
CC      dependent carboxylation. These residues are essential for the
CC      binding of calcium (Probable).
CC      -I- SIMILARITY: Contains 4 EGF-like domains.
CC      -I- SIMILARITY: Contains 1 Gla (gamma-carboxy-glutamate) domain.
CC      -I- SIMILARITY: Contains 2 laminin G-like domains.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NonCommercial License
CC      -----
DR      EMBL; D42148; BAA07719.1; -; mRNA.
DR      PIR; I55476; I55476.
DR      HSSP; P00740; ICFH.
DR      SMR; O63772; 258-674.
DR      Ensembl; ENSRNOG0000018233; Rattus norvegicus.
DR      RGD; 61913; Gas6.
DR      InterPro; IPR000152; Asx_hydroxyl_S.
DR      InterPro; IPR013320; Cona_like_subgrp.
DR      InterPro; IPR006210; EGF.
DR      InterPro; IPR000742; EGF_3.
DR      InterPro; IPR001881; EGF_Ca_bd.
DR      InterPro; IPR013091; EGF_Ca_bd_2.
DR      InterPro; IPR006209; EGF_like.
DR      InterPro; IPR013032; EGF_like_reg.
DR      InterPro; IPR002383; GLA_blood.
DR      InterPro; IPR001791; Laminin_G.
DR      InterPro; IPR012680; Laminin_G_2.
DR      InterPro; IPR000294; VICK_dep_GLA.
DR      Pfam; PF00008; EGF_1.
DR      Pfam; PF07645; EGF_CA_2.
DR      Pfam; PF00594; GLA_1.
DR      Pfam; PF02210; Laminin_G_2; 2.
DR      PRINTS; PR00001; GLABLOOD.
DR      SMART; SM00181; EGF_4.
DR      SMART; SM00179; EGF_CA_3.
DR      SMART; SM00069; GLA_1.
DR      SMART; SM00282; LamG_2.
DR      PROSITE; PS00010; ASX_HYDROXYL; 4.
DR      PROSITE; PS00022; EGF_1; 1.
DR      PROSITE; PS01186; EGF_2; 3.
DR      PROSITE; PS00026; EGF_3; 4.
DR      PROSITE; PS01187; EGF_CA_3.
DR      PROSITE; PS00011; GLA_1; 1.
DR      PROSITE; PS50998; GLA_2; 1.
DR      PROSITE; PS50025; LAM_G_DOMAIN; 2.
KW      Calcium; EGF-like domain; Gamma-carboxyglutamic acid; Glycoprotein;
KW      Growth regulation; Metal-binding; Repeat; Signal.
FT      SIGNAL 1 27
FT      CHAIN 28 674
FT      DOMAIN 50 91
FT      DOMAIN 113 151
FT      DOMAIN 153 193
FT      DOMAIN 194 234
FT      DOMAIN 235 275

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Query Match	81.4%	Score 2993	DB 1	Length 674
Best Local Similarity	82.9%	Pred. No. 7.3e-205		
Matches 558	Conservative 40	Mismatches 71	Indels 4	Gaps 3

RESULT 4	
Q6IRL1_RAT	
ID	Q6IRL1_RAT
PRELIMINARY;	PRT; 674 AA.

DT	05-JUL.-2004,	integrated into UniProtKB/TrEMBL.
DT	05-JUL.-2004,	sequence version 1.
DT	07-FEB.-2006,	entry version 12.
DT	05-JUL.-2004,	

GN Name=Gaag;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Chirostoma; Clivosa; Rodentia; Sciurimorphi;

CC Muroidea; Muridae; Murinae; Rattus.  
OX NCBI\_TaxId=10116;  
RN [1]  
RP NUCLEOTIDE SEQUENCE

RC 11550=Lnng;  
RX MEDLINE=22388257; Pubmed=12477932; DOI=10.1073/pnas.242603899;  
RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Krausner R.D., Collins F.S., Wäner L., Shamen C.M., Schlier G.D.

KA Albrechts, F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Ra Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
Rosenberg M.P., Ussan L.D., Lombardi S., Cantrich F., Fange C.,  
Ra Rana S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Rosa S.A., Bosak S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
Richards S.,

RA Fahney J., Helton E., Kettlemann M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Fahney J., Helton E., Kettlemann M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,  
Schmerch A., Schein J.E., Jones S.U.M., Marra M.A.,  
"Generation and initial analysis of more than 15,000 full-length human

RL Proc. Natl. Acad. Sci. U.S.A. 99:16889-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.

RA Strausberg R.†  
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
CC  
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CC Distributed under the Creative Commons Attribution-NonDerivs license  
CC  
EMBL: BC070881; AAH70881.1; -, mRNA.  
HSSD BC073735.1; HPO  
DR

DR SMR; 061RL1; 258-674.  
DR Ensembl; ENSRNOG00000018233; *Rattus norvegicus*.  
DR GO; GO:0005576; C:extracellular region; IEA.  
DR CC; CC:0000509; F:calcium ion binding; IEA.

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DR InterPro: IPR000742; EGF_3.
DR InterPro: IPR006210; EGF.
DR InterPro: IPR013320; ConA_like_subgrp.
DR InterPro: IPR001352; Asx_hydroxyl_5.
DR InterPro: IPR000320; ConA_like_subgrp.

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DR InterPro: EGF\_Ca<sup>2+</sup>\_bd\_2.  
DR InterPro: IPR013091; EGF-like.  
DR InterPro: IPR006209; EGF-like.  
DR InterPro: IPR013032; EGF-like reg.  
DR InterPro: IPR013033; EGF-like reg.

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DR      interPro; lam_csd; laminin_G-  
DR      interPro; IPR01791; laminin_G-  
DR      interPro; IPR012680; laminin_G_2.
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CC Distributed under the Creative Commons Attribution-NoDerivs license  
CC  
  
DR EMBL; BC070881; AAH70881.1; -, mRNA.  
DR HSSB; P00736; IAPQ.  
DR SMK; Q6IRLL1\_258-674.  
DR Ensemble; ENSRNOG00000018233; Ratius norvegicus.  
DR GO; GO:0005576; C:extracellular region; IEA.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR InterPro; IPRO00152; Asx hydroxyl S.  
DR InterPro; IPRO13320; ConA\_like\_subgrp.  
DR InterPro; IPRO06210; EGF.  
DR InterPro; IPRO00742; EGF\_3.  
DR InterPro; IPRO01881; EGF\_Ca\_bd.  
DR InterPro; IPRO13091; EGF\_Ca\_bd\_2.  
DR InterPro; IPRO06209; EGF\_like\_  
DR InterPro; IPRO13032; EGF\_like\_reg.  
DR InterPro; IPRO02383; GLA\_blood.  
DR InterPro; IPRO01791; laminin G.  
DR InterPro; IPRO12680; laminin G\_2.

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DR InterPro; IP000294; Vitec_deg_GLA.
DR Pfam; PF00008; EGF_1.
DR Pfam; PF07645; EGF_CA_2.
DR Pfam; PF00594; Gla_1.
DR Pfam; PF02210; Laminin_G_2.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF_4.
DR SMART; SM00179; EGF_CA_3.
DR SMART; SM0069; GLA_1.
DR SMART; SM00282; LamG_2.
DR PROSITE; PS00010; ASK_HYDROXYL_4.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS00026; EGF_3; 4.
DR PROSITE; PS01187; EGF_CA_3.
DR PROSITE; PS00011; GLA_1; UNKNOWN_1.
DR PROSITE; PS00998; GLA_2; 1.
DR PROSITE; PS00025; LAM_G_DOMAIN; 2.
DR SEQUENCE 674 AA; 74672 MW; CC9A5EBD04480AE7 CRC64;

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Query Match      81.3%; Score 2989; DB 2; Length 674;
Best Local Similarity 82.8%; Pred. No. 1.4e-204;
Matches 557; Conservative 40; Mismatches 72; Indels 4; Gaps 3;

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7 PGP-AALRRAPOLLILLALLAECALALPAREATQFLRPRORARFQVFEAKQGHLEKRC 65
5 PEPALALGTA--ILLILLASSESHYTLARAREAQFLRRORARAYQVFEAKQGHLEKRC 62
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63 VEEVSKERAREVFENDPETDYFYPRYOCMKRYGPRBKPNFATCVKNLPDQCTPNRC 122
126 DRKGTAQCDLDMGNFPCCLKAGWGRCLCKDVNVEGSGQENGCCLOICHNKGSPHSCSG 185
123 DRKGITOLCDLDMGNFPCCLKAGWGRCLCKDVNVEGSGQENGCCLOICHNKGSPHSCSG 182
186 FEISDRTGRTODIDECADSEACGEARCKNLPGSYCLCEGFAVSSQEKACRDVDECLG 245
183 FSLQSNKSCQDIDEDTSDTCGDANCKNLPGSYCLCEGFAVSSQEKACRDVDECLG 242
246 RCEQCVNVPSTGTTCHCDGRGGLKLSQMDMTCEDIIICVPPSYAKSVKSLYLGKMSGTP 305
243 RCEQCVNVPSTGTTCHCDGRGGLKLSQMDMTCEDIIICVPPSYAKSVKSLYLGKMSGTP 302
306 VIRLRKRLQPTFLVAFEPRTFDPBGILLFAGGHDSFWIVATLAFGRLEQLRLNGVG 365
303 VIRLRKRLQPTFLVAFEPRTFDPBGILLFAGGHDSFWIVATLAFGRLEQLRLNGVG 362
366 RVTSAGPVINHGMQOTISVEELARNLVIKVRDANVKIAYAGDLFQPERGLYHLNLTVG 425
363 RITSSGPTINHGMQOTISVEELARNLVIKVRDANVKIAYAGDLFQPERGLYHLNLTVG 422
426 IPHEKDLVQPINRDLDCGKRSNNMLNGEPTTIOEIVKVNTRQCSYTERGSGFFGNGP 485
423 IPHEKDLVQPINRDLDCGKRSNNMLNGEPTTIOEIVKVNTRQCSYTERGSGFFGNGP 482
486 AAFSLDYMTPLDVGESESTVEVVAHIRPAADTGVFLPMAADLPAVPLSVALLVYHST 545
483 AAFSLDYMTPLDVGESESTVEVVAHIRPAADTGVFLPMAADLPAVPLSVALLVYHST 541
546 KKLKQQLVLAVENTALALMEIKVCQGEHVVTVSLRDGEATLLEVDGTRQSEVSAQQL 605
542 KKLKQQLVLAVENTALALMEIKVCQGEHVVTVSLRDGEATLLEVDGTRQSEVSAQQL 601
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602 ERLAVLERHRSVVLFPAGGLPVPVTSAAVYAFYRGCMTLLENRRLLDDEALYKSDI 661
666 TASHCPVEPAA 678
662 TSHSCPVEAVTA 674

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RESULT 5
GAS6 MOUSE STANDARD: PRT: 674 AA.
AC Q61592; Q99K57;
DT 07-JUN-2004, integrated into UniProtKB/Swiss-Prot.
DT 07-JUN-2004, sequence version 2.
DE 07-MAR-2006, entry version 45.
DE Growth-arrest-specific protein 6 precursor (GAS-6).
GN Name=Gas6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=93330291; PubMed=8336730;
RA Manfioletti G., Brancolini C., Avanzi G., Schneider C.,
RT "The protein encoded by a growth arrest-specific gene (gas6) is a new
RT member of the vitamin K-dependent proteins related to protein S, a
RT negative coregulator in the blood coagulation cascade.";
RL Mol. Cell. Biol. 13:4976-4985(1993).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Burow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaefer T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosa S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalls D.E.,
RA Schermer A., Schein J.E., Jones S.J.M., Maita M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP FUNCTION.
RX PubMed=11175853; DOI=10.1038/84667;
RA Angelillo-Scherer A., de Frutos P., Aparicio C., Melis E., Savi P.,
RA Lupu F., Arnout J., Dewerchin M., Hoylaerts M., Herbert J., Collen D.,
RA Dahlback B., Carmeliet P.;
RT "Deficiency or inhibition of Gas6 causes platelet dysfunction and
RT protects mice against thrombosis.";
RL Nat. Med. 7:215-221(2001).
CC -1- FUNCTION: Ligand for tyrosine-protein kinase receptors AXL, TYRO3
CC and MER whose signaling is implicated in cell growth and survival,
CC cell adhesion and cell migration (By similarity). Plays a role in
CC thrombosis by amplifying platelet aggregation and secretion in
CC response to known agonists.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted protein (By similarity).
CC -1- PTM: Gamma-carboxyglutamate residues are formed by vitamin K
CC dependent carboxylation. These residues are essential for the
CC binding of calcium (By similarity).
CC -1- MISCELLANEOUS: GAS6 deficient mice show protection against
CC thrombosis, but no spontaneous bleeding.
CC -1- SIMILARITY: Contains 4 EGF-like domains.
CC -1- SIMILARITY: Contains 1 Gla (gamma-carboxy-glutamate) domain.
CC -1- SIMILARITY: Contains 2 laminin G-like domains.
CC
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CC

```



RT "The new ortholog of growth arrest-specific 6 (Ngas6) is implicated  
 RT in stress response during newt forelimb regeneration."  
 RL Dev. Dyn. 0:0-0(2006).

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 CC

DR EMBL: DQ324381; ABC5062.1; -; mRNA.  
 DR SEQUENCE 671 AA; 74727 MW; 9D860B80336BAD64 CRC64;

Query Match 63.2%; Score 2322; DB 2; Length 671;  
 Best Local Similarity 64.0%; Pred. No. 6.2e-157;  
 Matches 427; Conservative 89; Mismatches 147; Indels 4; Gaps 4;

QY 10 AALRRAPOLLLLLLAECALAL-LPAREATFLPRORARQVPEAKOGLERECEE 68  
 DB 4 AALALGAILFLTLAADPAQGTIVPAKASQFLSRQRANQIPEETKQGLERECEE 63  
 QY 69 LCSREAREVFENDETEYFYRYLDCINKKSPYTKNGSPATQVONLPDOCTPNDCK 128  
 DB 64 RCSRREARVFENDETEYFYRYLDCINKKSPYTKNGSPATQVONLPDOCTPNDCK 123  
 QY 129 GTQACODLMGNFPCCKAGMGRLCDKDVNCSQENGGLQICHNKPSFHCSCSGFEL 188  
 DB 124 GSTSCEDQKGDYFCHCKLGMIGKCKDADKDECFVANNNGCNOICLNKPSYHSCSGVAL 183  
 QY 189 SSDGRTCODIDECADSEA-CGEARCKNLPGSYCLCDEGPAVSSQEKACRDVDECIQGR 247  
 DB 184 QANNRICEDIDCKDSPTICGTAQCGRNHISYSCHCKDKGYKADCAVDDECDKPC 243  
 QY 248 EGVCNVSPSYTCHCDRGGLKLSQMDCEPILPVPPSVKSVSKYLGMFSGTPY 307  
 DB 244 EGTCVNTGSGYCHCDRGGLKLSQMDCEPILPVPPSVKSVSKYLGMFSGTPY 303  
 QY 308 RLRFKRLQPTRLVAEPDFPTPEGILLPAGGHODSTWIVLALRAGRLQLRYNGVGRV 367  
 DB 304 WRFRKQPTRLVAEPDFPTPEGILLPAGGHODSTWIVLALRAGRLQLRYNGVGRV 363  
 QY 368 TSSGPIVINGMWTISVEELARNLVIKNRDAVMKIAVAGDLFQPERGLYHLNLYGSLP 427  
 DB 364 TSSGPIVINGMWTISVEELARNLVIKNRDAVMKIAVAGDLFQPERGLYHLNLYGSLP 423  
 QY 428 FHEKDLVQFINRLDGCMSNMNLNEDPTIOFTVYVNRMOCFSTEEGSPGSGPAP 487  
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 QY 488 YSLDVYKRTPLDVGTSESTWEVVAHTRPADTGVLFALNAPDRAVPLSAVALDVHSTK 547  
 DB 484 FNIQITASSGEADKMTVALTAETRAPVDITGLAL-VNDNNVPLSLIDHSSYK 542  
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 QY 608 LAVLEHNLASPTLTGGLPDPVNTSAPRTAFRGCTLEVENRLLDDEAKHSDITA 667  
 DB 602 LKLMHNLORGVTYLGGLPDEVTSTPVAFYHGCMTIKMNEKPLDLALYKSDITS 661  
 QY 668 HSCPPVE 674  
 DB 662 HSCPPVD 668

RESULT 7

Q6BPAS\_XENLA PRELIMINARY; PRT; 669 AA.  
 AC O6BPAS; 16-AUG-2004, integrated into UniProtKB/TrEMBL.  
 DT 16-AUG-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 13.  
 DE Gas6-prov protein.  
 GN Name=ga6-prov;  
 OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
 OC Xenopodinae; Xenopus; Xenopus.  
 OK NCBI\_TaxID=8355;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Oocytes;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
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 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosch S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Clifton S.W.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Oocytes;  
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RA Richardson P.,  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 RT initiative."  
 RL Dev. Dyn. 225:384-391(2002).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Oocytes;  
 RA Klein S., Gerhardt D.S.,  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
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 CC

DR EMBL: BC076835; AAH76835.1; -; mRNA.  
 DR GO: GO:0005576; C:extracellular region; IEA.  
 DR GO: GO:0005509; F:calcium ion binding; IEA.  
 DR InterPro: IPR000152; Cons\_hydroxyl\_S.  
 DR InterPro: IPR013320; Cons\_like\_subgrp.  
 DR InterPro: IPR006210; EGF.  
 DR InterPro: IPR000742; EGF\_3.  
 DR InterPro: IPR001881; EGF\_Ca\_bd.  
 DR InterPro: IPR013091; EGF\_Ca\_bd\_2.  
 DR InterPro: IPR006209; EGF\_like\_reg.  
 DR InterPro: IPR013032; EGF\_like\_reg.  
 DR InterPro: IPR002383; GLA\_blood.  
 DR InterPro: IPR012680; laminin\_G\_2.  
 DR InterPro: IPR000294; Vitk\_deg\_GLA.  
 DR Pfam: PF00008; EGF\_1.  
 DR Pfam: PF07645; EGF\_CA\_3.  
 DR Pfam: PF00594; GLA\_1.  
 DR Pfam: PF02210; laminin\_G\_2\_1.  
 DR PRINTS: PRO0001; GLABLOOD.  
 DR SMART: SM00181; EGF\_4.  
 DR SMART: SM00179; EGF\_CA\_3.  
 DR SMART: SM00069; GLA\_1.  
 DR SMART: SM00282; LamG\_2.  
 DR PROSITE: PS00010; ASX\_HYDROXYL\_3.  
 DR PROSITE: PS00022; EGF\_1; 1.  
 DR PROSITE: PS01186; EGF\_2; 3.

DR PROSITE; PS50026; EGF\_3; 4.  
 DR PROSITE; PS01187; EGF\_CA; 2.  
 DR PROSITE; PS00011; GLA\_1; UNKNOWN\_1.  
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 DR PROSITE; PS50025; LAM\_G\_DOMAIN; 1.  
 SQ SEQUENCE 669 AA; 7523 MW; ABDELEB362540F643 CRC64;  
 Query Match 62.4%; Score 2293.5; DB 2; Length 669;  
 Best Local Similarity 61.9%; Pred. No. 676-155;  
 Matches 413; Conservative 105; Mismatches 144; Indels 5; Gaps 5;  
 QY 9 PAIRPAPQILLIAECALALLIPAREATQIPRPRRAFPVFEAKQGHLEECVEE 68  
 Bb 4 PSALTATWLVTLIAEPLHSTIILSAMDAQIPRQRORRANOFEETKQGHLEECVEE 63  
 QY 69 LCSSEARREVENDEPNDYFPRYLDCINXGSPYTKNSGATVCQNIPDCTNPPCPRK 128  
 Bb 64 QCSSEARREVENDEPNDYFPRYLDCINXGSPYTKNSGATVCQNIPDCTNPPCPRK 122  
 QY 129 GTQACODLGNFPCICRAGMGRLCDKDVNESCOENGCLQICNNKPGSFHCSGHPFL 188  
 Bb 123 GSHCTDLHGFCHCKRPGWTGKTCSDRDINCATENGCNHCINIKRGTHQCLCRSGRL 182  
 QY 189 SSDGRTQDIDECADS-DAGEAPACKNLPGSYSLCDGFAVSSQEKACRDVDECLQRC 247  
 Bb 183 HTNNKLCIDIDECAESPNICGTAQCKNVLSTYVCLCEGGRYRDESTKSCQIDCEKGRG 242  
 QY 248 EYCVNNSPGSYTCHGCDRGGLKLSODMTCEDILPCVPFSAKSVKSLYGRMSSGPVI 307  
 Bb 243 EYCVNNSPGSYTCHGCDRGGLKLSODMTCEDILPCVPFSAKSVKSLYGRMSSGPVI 302  
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 Bb 303 RLRFKRLQPTRLVAEPFRTFDPREGILLFAGGHODSTWIVLALRAGLEQLRNGVGRV 362  
 QY 368 TSSGPIVNHGMQOTISVEELARNLVIKVNDVAKKIAVAGDLFQPERGLYHLNLTVGIP 427  
 Bb 363 TSSGPIVNHGMQOTISVEELARNLVIKVNDVAKKIAVAGDLFQPERGLYHLNLTVGIP 422  
 QY 428 FHEKDLVQIPNPLDGMBSMNLNGEDTIOEVKKNITNOCSTVERSGFYGSFAF 487  
 Bb 423 FHEKDLVQIPNPLDGMBSMNLNGEDTIOEVKKNITNOCSTVERSGFYGSFAF 482  
 QY 488 YSLDYMTPLDVGTSTWEEVVAHIRPADTGVLFALMAIPDLRAVELSVALVDYHSTKK 547  
 Bb 483 FHLIDY-TYPSKETETAMRWVNAQINPATDTGVLFALVSKDM-VVPLSLALIDYHSSAK 540  
 QY 548 LKKQVLVLAVENTLALAMEIKVCDGQEHVTVSLRDEATLEVDGTRGQSEVSAALOER 607  
 Bb 541 IKRQPLILSIENIVSRIEVQCD-SEHIVEISASINDLFLSPDGTIGQKELPESQWRTT 599  
 QY 608 LALLENHRLRSPVLTFAGGLPDVPTVSPVAFRGCMTLEVNRLDLDEAKYHSITA 667  
 Bb 600 LHLNHLGKGVQTVYGGLPDVAVTATPFAFGHGTWKIKQKPLDLDDAVYKNDITS 659  
 QY 668 HSCPVE 674  
 Bb 660 HSCPTIK 666

RESULT 8  
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 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
 DT 05-JUL-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 12.  
 DE MG668463 protein.  
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 GN Xenopus laevis (African clawed frog).  
 OS Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
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 OC Xenopodinae; Xenopus; Xenopus.

OX NCBI\_TaxID=8355;  
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 RC TISSUE=Liver;  
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Dackiwko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,  
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallus D.E.,  
 RA Scherren A., Schein J.B., Jones S.U.M., Maira M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RA Richardson P.;  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 RT initiative.";  
 RL Dev. Dyn. 225:384-391(2002).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Liver;  
 RA Klein S., Strausberg R.,  
 RL Submitted (Oct-2003) to the EMBL/GenBank/DBJ databases.  
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 CC Distributed under the Creative Commons Attribution-NonDerivative license  
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 CC EMBL: BC060355; AAH60355.1; -; mRNA.  
 DR HSSP; P00743; 1APO.  
 DR GO; GO:0005576; C:extracellular region; IEA.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR InterPro; IPR0010152; Axx\_hydroxyl\_S.  
 DR InterPro; IPR013320; ConA\_like\_subgrp.  
 DR InterPro; IPR006210; EGF.  
 DR InterPro; IPR000742; EGF\_3.  
 DR InterPro; IPR001881; EGF\_Ca\_bd.  
 DR InterPro; IPR013091; EGF\_Ca\_bd\_2.  
 DR InterPro; IPR006209; EGF\_like.  
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 DR InterPro; IPR001791; Laminin\_G.  
 DR InterPro; IPR012680; Laminin\_G\_2.  
 DR InterPro; IPR000294; Vltk\_dep\_Gla.  
 DR Pfam; PF00008; EGF; 1.  
 DR Pfam; PF07645; EGF\_CA; 3.  
 DR Pfam; PF00584; Gla\_1.  
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 DR SMART; SM00179; EGF\_CA; 3.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00282; Lamg; 2.  
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 DR PROSITE; PS01186; EGF\_2; 3.  
 DR PROSITE; PS50026; EGF\_3; 4.  
 DR PROSITE; PS01187; EGF\_CA; 2.

DR PROSITE: PS00011; GLA\_1: UNKNOWN\_1.  
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 77 EYFENDPETYFYPPYLDICINXGSGYTTKNSGFATCVQMLPQCPCNPDCDRKGTQACDL 136  
 71 EYFENNPPETFFYFKYIECNRRY-RHLNKKDSLTTCTHNIPOCCSAPCYRSGSLHCLD 129  
 137 MGNFPLCKAGMGRGLCDQVNECSQENGCLQICHNKPGSFHCSGSELSDDGTQO 196  
 130 HGFPCCHKRGMTGKSGCTDINECATENNGNSQICNKGCTHQCICSSGYRLHANNKLCI 189  
 197 DIDECAQS-EACGEARCKNLPGSYSLCDEGFAYSSQERACRDVDECLQGRCEQVCNSP 255  
 190 DIDECAESFNICGTACQCKNVRSYVCLCEDGYRYDELTKSCDVDECKEGRCEQTCVNSP 249  
 256 GSYTCHCDGRGGLKLSQMDTCEDLPCVFPVAKSVKSLVYGRMSTGPVRLRFRKRLQ 315  
 250 GSYTCHCDGRGGLKLSQMDTCEDLPCVFPVAKSVKSLVYGRMSTGPVRLRFRKRLQ 309  
 316 PTRLVAEPFRTFDEGILLFAGGHDSITWIVLAFAGRLLEQLRYNGVRYTSSGPV 375  
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 376 HGMQOTISVEELARNLVKNDVAVKIAVAGDLFQPERGLTHLNTVGGIPHEKDLVQ 435  
 370 HGMQOTISVEELARNLVKNDVAVKIAVAGDLFQPERGLTHLNTVGGIPHEKDLVQ 429  
 436 PINPRLDGCGRSMNMTNGEDDTIOETVKNTRMOCSEVBERGSFYFGSGPAPFLMYMT 495  
 430 LINPRLDGCGRSMNMTNGEDDTIOETVKNTRMOCSEVBERGSFYFGSGPAPFLMYMT 488  
 496 PLDVGESTWEVEVVAHIRPAADTVGLFALMAPDLRAVPLSVLVYHSTKLLKQDLVYL 555  
 489 PKKETBEANMRVEFPAQINPARDTVGLFALVSKDM-AVPLSLALIDYHSAKIKRQFLIL 547  
 556 AVETHALAMEIKVCCGQHVTVTSLRDGEATLEVDTGSGQSVSAQLOERLAVLERH 615  
 548 SVEENVVSRIEVQVCD-REHIVEISASINDVLISFGDTGLKELPDSQOMQLLLINDHL 606  
 616 RSPVLTFAAGLPVPVPTSAVPTAFYAGCMTLEVNRLDLDEAAYKHSDTTAHSCPVE 674  
 607 GKGVKTYVGGLPDVAATATPVTAFYHGMCTMKIQNKPLDLDVAVYKANDITSHSCPIK 665

RESULT 9  
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 AC QASHY2; 19-JUL-2005, integrated into UniProtKB/TrEMBL.  
 DT 19-JUL-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 7.  
 DE Chromosome 5 SCAP14581, whole genome shotgun sequence. (Fragment).  
 GN ORFNames=GSTEN00017935001;  
 OS Tetradon nigrovittatus (Green puffer).  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Tetradontoidea; Tetradontidae; Tetradon.  
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 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=15496914; DOI=10.1038/nature03025;  
 Jallion O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,

RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 RA Nicard S., Jaffe D., Fieber S., Lutfalla G., Dessat C., Segreus B.,  
 RA Daesliva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
 RA Antouard V., Jubin C., Caetelli V., Katinka M., Vacherie B.,  
 RA Biemont C., Skalli Z., Catolico L., Poulain J., De Berardinis V.,  
 RA Crnaud C., Duprat S., Broctier P., Coutanceau J.-P., Gouzy J.,  
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,  
 RA Kellis M., Wolff J.-N., Guigo R., Zody M.C., Mesirov J.,  
 RA Landel-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Landel V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
 RA Winkler P., Lander B.S., Weissbach J., Roest Crollius H.,  
 RA "Genome duplication in the teleost fish Tetradon nigrovittatus reveals  
 RT the early vertebrate proto-karyotype.";  
 RL Nature 431:946-957(2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RG Genoscope, Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 CC -----  
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 CC Distributed under the Creative Commons Attribution-NonCommercial License  
 CC -----  
 CC EMBL: CAE01014581; CAP9750.1; -? Genomic DNA.  
 DR GO: GO:0005576; C:extracellular region; IEA.  
 DR GO: GO:0005509; P:calcium ion binding; IEA.  
 DR InterPro: IPR000152; Asx\_hydroxyl\_5.  
 DR InterPro: IPR006210; EGF.  
 DR InterPro: IPR000742; EGF\_3.  
 DR InterPro: IPR001881; EGF\_Ca\_bd.  
 DR InterPro: IPR013032; EGF-like reg.  
 DR InterPro: IPR002383; GLA\_blood.  
 DR InterPro: IPR001791; Laminin G.  
 DR InterPro: IPR000294; Vitk\_dep\_GLA.  
 DR Pfam: PF07645; EGF\_CA; 3.  
 DR Pfam: PF00594; GLA; 1.  
 DR Pfam: PF02210; Laminin G\_2; 2.  
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 DR SMART: SM00181; EGF; 4.  
 DR SMART: SM00179; EGF\_CA; 3.  
 DR SMART: SM00069; GLA; 1.  
 DR SMART: SM00282; LamG; 2.  
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 DR PROSITE: PS50026; EGF\_3; 4.  
 DR PROSITE: PS01187; EGF\_CA; 3.  
 DR PROSITE: PS50998; GLA\_2; 1.  
 DR PROSITE: PS50025; LAM\_G\_DOMAIN; 2.  
 KM Calcium; EGF-like domain.  
 FT NON\_TER 1  
 FT NON\_TER 626  
 SQ SEQUENCE 626 AA; 69527 MW; 2FE5AECDD4068947 CRC64;

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 93 LDCINKGSPYTKNSGFATCVQMLPQCPCNPDCDRKGTQACQMLMGNFPLCKAGMGR 152  
 60 LACVERFPGAERKQDLITCVNHIPOCCSPPCHPGIVRCEBKQDFLCHCTGNAGAR 119  
 153 CDQVNECSQENGCLQICHNKPGSFHCSGSELSDDGTQO-TCODIDECAESACGEAR 211  
 120 CDDVDECGKRGNGCCHRCNNMTGSTRCSGQYEL--HGRTCADVDEKDEVEVGTA 177  
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DB 178 CONNEGVDCLCEGTYVYDNETKSLDVBDECEGTCAEVCINIGSFRCFCGQGRYLS 237
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DB 238 QDLRSCKPLPRPISPKKRSRLYLGMFSGVMVRLRFRPKLPTGSAFEDRTDPE 297
QY 332 GILLFAGHODSTWIVLALRAGRLQLRYNGVGRVITSSGCVINHGMMQTSVEELRNL 391
DB 298 GVVFFAGHILNMSIVLAVHHGKQLQLOKYSISRVITSSGPRINDGCMRKISVEGGRSL 357
QY 392 VIKNRDPAVKIAGLFLPERGVLHNLTVGGIPFHEKDLVOPINPRLDGCMRSNWL 451
DB 358 VIKIDREAVMKIIVISNLFTRKGVHEINLFVGVPPREDDLVQVNPRLDGCKEKWKML 417
QY 452 NGEDTTIOETVKNTRNOCFSVTERGSPFGSGFAFSLDYMRPLDVGVSTEVVA 511
DB 418 AGEDTSLQETIRSDNNQCFSSADPGAVYPGTGALNTSYDELPSLSQ-NLSVRL 476
QY 512 HIRPADTGVLPALMAPDLRAVPLSVLVYHSTFKLKKOLVLAVENTALMEIKVCD 571
DB 477 SLRPTAVGLVLLLVHOD--RVLSTILVYHPTGQWRDYIIVTADDAIVASAPALCD 534
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DB 535 GSGHQVHTVITSGNQTLLLVLDGQSGRRD-----ADVPTELLSGSTYIGLPPVPL 585
QY 632 TSAPTAFYRCMTLEVNRLDLDEAAVGHSDITANSCP 671
DB 586 ASLTVAFAFYSGCMDVILNQPVLDQAVHKNDRISHSCP 625

RESULT 10
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DB 073H4_BRARE
AC 073H4;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 15.
DE Growth arrest specific 6.
GN ORFName=zc63860;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RA and mouse cDNA sequences.";
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;

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RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
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CC
DR EMBL; BC053117; AAH53117.1; -; mRNA.
DR HSSP; Q14393; 1H30.
DR ZFIN; ZDB-GENE-030131-7773; zgc:63860.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx hydroxylase.
DR InterPro; IPR002453; Beta tubulin.
DR InterPro; IPR013320; Cona-like subgrp.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR000742; EGF_3.
DR InterPro; IPR001881; EGF_Ca_bd.
DR InterPro; IPR013091; EGF_Ca_bd_2.
DR InterPro; IPR006209; EGF_like_reg.
DR InterPro; IPR013032; EGF_like_reg.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR001792; Laminin G.
DR InterPro; IPR012680; Laminin G_2.
DR InterPro; IPR000294; Vtk_dep_GLA.
DR Pfam; PF00008; EGF_1.
DR Pfam; PF07645; EGF_CA_3.
DR Pfam; PF00594; GLA_1.
DR Pfam; PF02210; Laminin G_2; 2.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF_4.
DR SMART; SM00179; EGF_CA_2.
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DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS50026; EGF_3; 3.
DR PROSITE; PS01187; EGF_CA_2.
DR PROSITE; PS00011; GLA_1; UNKNOWN_1.
DR PROSITE; PS50998; GLA_2; 1.
DR PROSITE; PS50025; LAM G DOMAIN; 2.
DR PROSITE; PS00228; TUBULIN B AUTOREG; UNKNOWN_1.
SQ SEQUENCE 648 AA; 72626 MW; E2935F42AF21CF64 CRC64;

Query Match 47.8%; Score 1755; DB 2; Length 648;
Best Local Similarity 50.8%; Pred. No. 1.9e-116;
Matches 334; Conservative 103; Mismatches 198; Indels 22; Gaps 9;

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QY 378 MWQTSVEELARNLVYKVRDAVMKIAVAGDLFOFERGLYHNLTVGGVIFPEHKLVDPI 437  
 DB 367 QMHKISVEEGKSLVYIKIDREAVMKIAVNGDLFTLANKMHELNITVGVFPFDDDLGNSV 426  
 QY 438 NPRLDGCRSMNWLNGEDDTTIGETVKNTRMOCFSVTERGSFYPSGFAFSLDYWRTP 497  
 DB 427 NPLRDGCMKMDRWMLTGEDETSIQETIRHNERMOCYANEDHSAFVPGHGFAYFNHSH----- 481  
 QY 488 DVGSTSTVEEVVAHRRPADGCVLPALMAPDLRAVPLSVLALVDVHSTKGLKKQVLAV 557  
 DB 482 --GDNQTLSSVHT--LRAASSMGVLPALVRD--RVFPFISLSLDYHPTGLQMTKHLVSL 535  
 QY 558 EHTALALMEIKVCDCEHVTSLRDGEATLEVDGTRGQSEVSAQLOERLAVLERHLS 617  
 DB 536 GDNVGVSGPVNLSDQTHVNTVMTSGNSBVLVDQAQME-----MMEGVDSL--LTS 588  
 QY 618 PVLTFAGGLPDVPTVSAPTYAFVRCGMLTEVNRLLDLDEAAVKSDITAHSCPPVE 674  
 DB 589 SYSTFGIGIPDVSLVSSPVSAFPTCGMDVRVNGQLLDVDEAQHKNDIRSHSCPLVD 645

RESULT 11  
 PROS\_HUMAN  
 ID PROS\_HUMAN STANDARD; PRT; 676 AA.  
 AC P07225; O15518; Q72715;  
 DT 01-APR-1988, integrated into UniProtKB/Swiss-Prot.  
 DT 01-APR-1988, sequence version 1.  
 DT 07-MAR-2006, entry version 86.  
 DE Vitamin K-dependent protein S precursor.  
 GN Name=PROS1; Synonyms=PROS;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Homo.  
 NCBI\_TaxID=9606;  
 RX NUCLEOTIDE SEQUENCE.  
 RP NUCLEOTIDE SEQUENCE.  
 RA Hoskins J., Notman D.K., Beckmann R.J., Long G.L.;  
 RT "Cloning and characterization of human liver cDNA encoding a protein S  
 RT precursor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:349-353(1987).  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA MEDLINE=87092407; PubMed=3467362;  
 RT "Human protein S cDNA encodes Phe-16 and Tyr 222 in consensus  
 RT sequences for the post-translational processing.";  
 RL FEBS Lett. 222:186-190(1987).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RA MEDLINE=91084444; PubMed=2148110;  
 RX Schmidt D.K., Tatro A.V., Phelps L.G., Tomczak J.A., Long G.L.;  
 RT "Organization of the human protein S genes.";  
 RL Biochemistry 29:7845-7852(1990).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Liver;  
 RA MEDLINE=91084445; PubMed=2148111;  
 RX Ploos van Amstel H.K., Reitsma P.H., der Logt C.P., Bertina R.M.;  
 RT "Intron-exon organization of the active human protein S gene PS alpha  
 RT and its pseudogene PS beta: duplication and silencing during primate  
 RT evolution.";  
 RL Biochemistry 29:7853-7861(1990).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RA Rieder M.J., Garrington D.P., da Ponte S.H., Hastings N.C.,  
 RA Ahearn M.O., Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q.,  
 RA Nickerson D.A.;  
 RT "SeattleSNPs: NHLBI HUG6682 program for genomic applications, UW-  
 RT FHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";  
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.

RN [6]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC TISSUE=Uterus;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Klausner R.L., Reingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Bahay J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [7]  
 RP NUCLEOTIDE SEQUENCE OF 27-676.  
 RX MEDLINE=86313649; PubMed=2944113;  
 RA Lundwall A., Dackowski W., Cohen E., Shaffer W., Mahr A., Dahlback B.,  
 RA Stenflo J., Wydro R.;  
 RT "Isolation and sequence of the cDNA for human protein S, a regulator  
 RT of blood coagulation.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:6716-6720(1986).  
 RN [8]  
 RP CARBOHYDRATE-LINKAGE SITE ASN-530.  
 RX PubMed=16335952; DOI=10.1021/pr0502065;  
 RA Liu T., Qian W.-U., Gritsenko M.A., Camp D.G. II, Monroe M.E.,  
 RA Moore R.J., Smith R.D.;  
 RT "Human plasma N-glycoproteome analysis by immunoaffinity subtraction,  
 RT hydrazide chemistry, and mass spectrometry.";  
 RL J. Proteome Res. 4:2070-2080(2005).  
 RN [9]  
 RP VARIANT HEERLEN PRO-501.  
 RX MEDLINE=90335440; PubMed=2143091;  
 RA Bertina R.M., Ploos van Amstel H.K., van Wijngaarden A., Coenen J.,  
 RA Leenhuis M.P., Deutz-Terlouw P.P., van der Linden I.K., Reitsma P.H.;  
 RT "Heerlen polymorphism of protein S, an immunologic polymorphism due to  
 RT dimorphism of residue 460.";  
 RL Blood 76:538-548(1990).  
 RN [10]  
 RP VARIANT PROS1 DEFICIENCY SER-258.  
 RA Cooper D.N.;  
 RL Unpublished observations (SEP-1993).  
 RN [11]  
 RP VARIANT PROS1 DEFICIENCY TOKUSHIMA GLU-196.  
 RX MEDLINE=94129009; PubMed=8298131;  
 RA Hayashi T., Nishio K., Shigekito T., Saito S., Suzuki K.;  
 RT "Protein S Tokushima: abnormal molecule with a substitution of Glu for  
 RT Lys-155 in the second epidermal growth factor-like domain of protein  
 RT S.";  
 RL Blood 83:663-690(1994).  
 RN [12]  
 RP VARIANTS PROS1 DEFICIENCY CYS-482; CYS-485 AND GLY-561, AND VARIANTS  
 RP PRO-501 AND MET-559.  
 RX MEDLINE=99374922; PubMed=10447256;  
 DOI=10.1002/(SICI)1098-1004(1999)14:1<30::AID-HUMVA>3.3.CO;2-O;  
 RA Espinosa-Parilla Y., Morell M., Souto J.C., Tirado I.,  
 RA Fontcuberta J., Estivill X., Sala N.;  
 RT "Protein S gene analysis reveals the presence of a cosegregating  
 RT mutation in most pedigrees with type I but not type III PS  
 RT deficiency.";  
 RL Hum. Mutat. 14:30-39(1999).  
 CC -!- FUNCTION: Anticoagulant plasma protein; it is a cofactor to  
 CC activated protein C in the degradation of coagulation factors Va



CC and VIIa. It helps to prevent coagulation and stimulating  
 CC fibrinolysis.  
 CC -1- SUBCELLULAR LOCATION: Secreted protein.  
 CC -1- TISSUE SPECIFICITY: Plasma.  
 CC -1- DISEASE: Defects in PROS1 are the cause of protein S deficiency  
 CC (PROS1 deficiency) [MIM:176880]. It is associated with an  
 CC increased risk to develop thrombotic disease (thrombophilia).  
 CC -1- SIMILARITY: Contains 4 EGF-like domains.  
 CC -1- SIMILARITY: Contains 1 Gla (gamma-carboxy-glutamate) domain.  
 CC -1- SIMILARITY: Contains 2 laminin G-like domains.  
 CC -----  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NonDerivative license  
 CC -----  
 DR EMBL: M15036; AAA6479.1; -; mRNA.  
 DR EMBL: Y00692; CAA68687.1; -; mRNA.  
 DR EMBL: Y00692; CAA68687.1; ALT\_SEQ; mRNA.  
 DR EMBL: M57853; AAA60357.1; -; Genomic DNA.  
 DR EMBL: M57840; AAA60357.1; JOINED; Genomic DNA.  
 DR EMBL: M57841; AAA60357.1; JOINED; Genomic DNA.  
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 DR EMBL: M57844; AAA60357.1; JOINED; Genomic DNA.  
 DR EMBL: M57845; AAA60357.1; JOINED; Genomic DNA.  
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 DR EMBL: M57851; AAA60357.1; JOINED; Genomic DNA.  
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 DR EMBL: M36563; AAA60180.1; JOINED; Genomic DNA.  
 DR EMBL: AY308744; AAP45054.1; ALT\_SEQ; Genomic DNA.  
 DR EMBL: BC015801; AAH15801.1; -; mRNA.  
 DR PIR: A35610; KKHUS.  
 DR PDB: 1Z6C; NMR; A=200-286.  
 DR Ensembl: ENSG00000184500; Homo sapiens.  
 DR H-InvDB: HIX022087; -.  
 DR HGNC: HGNC:9456; PROS1.  
 DR MIM: 176880; gene+phenotype.  
 DR Reactome: P07225; -.  
 DR LinkHub: P07225; -.  
 DR GO: GO:0005576; Extracellular region; NNS.  
 DR GO: GO:0004866; Endopeptidase inhibitor activity; TAS.  
 DR GO: GO:0007596; P: blood coagulation; TAS.  
 DR InterPro: IPR000152; Asx\_hydroxyl\_S.  
 DR InterPro: IPR033320; ConA\_like\_subgrp.  
 DR InterPro: IPR006210; EGF.  
 DR InterPro: IPR000742; EGF\_3.  
 DR InterPro: IPR001881; EGF\_Ca\_bd.  
 DR InterPro: IPR013091; EGF\_Ca\_bd\_2.  
 DR InterPro: IPR006209; EGF\_like\_reg.  
 DR InterPro: IPR013032; EGF\_like\_reg.  
 DR InterPro: IPR002383; GLA\_blood.  
 DR InterPro: IPR001791; Laminin\_G.  
 DR InterPro: IPR012679; Laminin\_G\_1.  
 DR InterPro: IPR012680; Laminin\_G\_2.  
 DR InterPro: IPR000294; Vltk\_dep\_GLA.  
 DR Pfam: PF00008; EGF\_2.  
 DR Pfam: PF07645; EGF\_CA\_2.  
 DR Pfam: PF00594; Gla\_1.  
 DR Pfam: PF00054; Laminin\_G\_1; 1.

DR Pfam: PF02210; Laminin\_G\_2; 1.  
 DR PRINTS: PR00001; GLABLOD.  
 DR SMART: SM00181; EGF\_4.  
 DR SMART: SM00179; EGF\_CA; 3.  
 Query Match 42.0%; Score 1543; DB 1; Length 676;  
 Best Local Similarity 44.4%; Pred. No. 2.7e-101;  
 Matches 298; Conservative 127; Mismatches 218; Indels 28; Gaps 14;  
 QY 18 LLLILLAECAALALPAREATQFLRPRORARFVFEBAQGLERECVEELSGREARE 77  
 DB LACILLVLVPSSEANFLSKQOASQVL-VRKRANSLIETKQNLERECIEELCNKEARE 70  
 QY 78 VFENDPDTDYFYPYRLDICIKNY-----GSPYTKNS--GFATCYQLPDQTPPCDRKG 129  
 DB 71 VFENDPDTDYFYPYRLVCLRSFQTGLFTARQSTNAAPDLRSQVNAIPDQSPPLCNEDG 130  
 QY 130 TQACODLMGNFPLCLKAGMGGRLCDKDVNCC---SQENGCLQICHKKPGSFHSCSHGF 186  
 DB 131 YMSCKOKKASFTCTCKRGMGKCEFPINCKDPSNINGCSCQICDTPPGSYHSCXNGF 190  
 QY 187 ELSSDGRFCODIDBCA-DSEACGEARCKNLPGSYSLCDEGFAYVSQEKACRDVDECLQG 245  
 DB 191 VMLSNKDKCDKVDCELSKPSICGTAVCKNIPGDFECCEPGRYNLKSKCEDIDECSEN 250  
 QY 246 RCEQVCVNSPGSYTCHDGRGGLKLSQDMQTCEDILPCVFPFSAKSVKSLYLGMFSGTP 305  
 DB 251 MCAQLCVNYPGGTYCTCYDGKKGFPLADQKSCVSVCLPLNLTKEYELLYLAEQFAGV- 309  
 QY 306 VIRLRFKRLQPTRLVAEFDPRTFDPPEGILLFAGGHQDSTWIVLALRAGRLEQLRYNGVG 365  
 DB 310 VLVKFRPLPISRFSAEPDRTYDSGVILYAESIDHSALLLALRGCKIEVOLKENTHS 369  
 QY 366 RVTSSEGVINHGMMQITISVEELARNLVIKVNRDAVMKIAVAGDLFQPERGLYHLNLTVG 425  
 DB 370 KITTGSGVINNGLMNWSVEELSHSISIKTAKAVMDINKPFLFKENGILLETXYFAG 429  
 QY 426 IPRH-EXDVLQPINPLDQGMBSMNLTNGDPTTIOELVKNYNTMOCQSVTERGSGFGSG 484  
 DB 430 FPKRVSESLIKPINPRIDGCTIRSMNLMKQASGSIKELTQKQNHCKLVTVEKSGSYGSG 489  
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 DB 490 IAPFHDYN---NVSSAEGMHVNTLNTIRPSGTGMALVALVSGN-NTVFPAISLVN--S 542  
 QY 545 TKYLKQQLVLAVENTAL-ALMEIKVC-DQGEHVVTLSLDGATYLEVDGTRQSEVSA 602  
 DB 543 TSE-KSQDILLSEVNTVIYRIQALSLCSDQSH---LEFRVNRNMLELSTPLKIETISHE 598  
 QY 603 QLOERLAVLERHLSRYLTFAGGLPDVPTASAVTYAFYRCMTLEVVNRLLDDEAYKH 662  
 DB 599 DLQRQLAVLDKAKAKAVATYGLPDVPSATPVNAFYNGCMVNINGVQLDDEALSKI 658  
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 DB 659 NDIRAHSCSV 669  
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 AC 028520;  
 DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.  
 DT 01-NOV-1997, sequence version 2.  
 DT 07-MAR-2006, entry version 56.  
 DE Vitamin K-dependent protein S precursor (Fragment).  
 GN Name:PROS1; Synonyms=PROS;  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 OC Cercopithecoidea; Cercopithecinae; Macaca.  
 NCBI\_Taxid=9544;  
 RN [1]

Accession	Protein Name	Gene Name	Protein Description	Gene Description
NP_001131	NUCLEOTIDE SEQUENCE [mRNA].			
RC	TISSUE=Liver;			
RC	MEBLIN=95134217; PubMed=7832752;			
RA	Greengard J.S., Fernandez J.A., Radtke K.P., Griffin J.H.;			
RT	"Identification of candidate residues for interaction of protein S with C6b binding protein and activated protein C";			
RL	Biochem. J. 305:397-403(1995).			
CC	-1- FOLDCTION: Anticoagulant plasma protein; it is a cofactor to activated protein C in the degradation of coagulation factors Va and VIIa. It helps to prevent coagulation and stimulating fibrinolysis.			
CC	-1- SUBCELLULAR LOCATION: Secreted protein.			
CC	-1- TISSUE SPECIFICITY: Plasma.			
CC	-1- SIMILARITY: Contains 4 EGF-like domains.			
CC	-1- SIMILARITY: Contains 1 Gla (gamma-carboxy-glutamate) domain.			
CC	-1- SIMILARITY: Contains 2 laminin G-like domains.			
CC	Copyrighted by the UniProt Consortium, see <a href="http://www.uniprot.org/terms">http://www.uniprot.org/terms</a>			
CC	Distributed under the Creative Commons Attribution-NoDerivs License			
CC	EMBL, L31380; AAAV0376.1; ALT_INIT; mRNA.			
DR	HSSP, P00740; 1CFH.			
DR	SMR, Q28520; 173-259.			
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DR	InterPro, IPR013320; ConA_like_subgrp.			
DR	InterPro, IPR006210; EGF_.			
DR	InterPro, IPR000742; EGF_3.			
DR	InterPro, IPR001881; EGF_Ca bd.			
DR	InterPro, IPR013091; EGF_Ca bd_2.			
DR	InterPro, IPR006209; EGF_like.			
DR	InterPro, IPR013032; EGF_like_reg.			
DR	InterPro, IPR002383; GLA blood.			
DR	InterPro, IPR001791; laminin G.			
DR	InterPro, IPR012680; laminin G_2.			
DR	InterPro, IPR000294; VitK_dep_GLA.			
DR	Pfam, PF00008; EGF_1.			
DR	Pfam, PF07645; EGF_CA_3.			
DR	Pfam, PF00594; GLA_1.			
DR	Pfam, PF00054; laminin_G_1; 1.			
DR	Pfam, PF02210; laminin_G_2; 2.			
DR	PRINTS: PR00001; GLABLOOD.			
DR	SMART, SM00181; EGF_4.			
DR	SMART, SM00179; EGF_CA_3.			
DR	SMART, SM00069; GLA_1.			
DR	SMART, SM00282; LamG_1.			
DR	PROSITE, PS00010; ASX_HYDROXYL; 4.			
DR	PROSITE, PS00022; EGF_1; 1.			
DR	PROSITE, PS01186; EGF_2; 3.			
DR	PROSITE, PS00026; EGF_3; 4.			
DR	PROSITE, PS01187; EGF_CA_3.			
DR	PROSITE, PS00011; GLA_1; 1.			
DR	PROSITE, PS00998; GLA_2; 1.			
DR	PROSITE, PS00025; LAM_G_DOMAIN; 2.			
KW	Blood coagulation; Calcium; EGF-like domain;			
KW	Gamma-carboxyglutamic acid; Glycoprotein; Hydroxylation; Repeat;			
KW	Zymogen.			
FT	PROPEP	<1	14	By similarity. /FPIID=PRO_0000022121.
FT	CHAIN	15	649	Vitamin K-dependent protein S. /FPIID=PRO_0000022122.
FT	DOMAIN	15	60	Gla.
FT	DOMAIN	90	128	EGF-like 1.
FT	DOMAIN	130	173	EGF-like 2; calcium-binding (Potential).
FT	DOMAIN	174	215	EGF-like 3; calcium-binding (Potential).
FT	DOMAIN	216	256	EGF-like 4; calcium-binding (Potential).
FT	DOMAIN	272	448	Laminin G-like 1.
FT	DOMAIN	457	639	Laminin G-like 2.
FT	REGION	61	89	Thrombin-sensitive.
FT	MOD_RES	20	20	4-carboxyglutamate (By similarity).
FT	MOD_RES	21	21	4-carboxyglutamate (By similarity).
FT	MOD_RES	28	28	4-carboxyglutamate (By similarity).
FT	MOD_RES	30	30	4-carboxyglutamate (By similarity).
FT	MOD_RES	33	33	4-carboxyglutamate (By similarity).

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					40	Gaps
FT MOD_RSS	34	34	4-carboxyglutamate	(By similarity)		
FT MOD_RSS	39	39	4-carboxyglutamate	(By similarity)		
FT MOD_RSS	40	40	4-carboxyglutamate	(By similarity)		
FT MOD_RSS	43	43	4-carboxyglutamate	(By similarity)		
FT MOD_RSS	46	46	4-carboxyglutamate	(By similarity)		
FT MOD_RSS	50	50	4-carboxyglutamate	(By similarity)		
FT MOD_RSS	109	109	3-hydroxyaspartate	(By similarity)		
FT CARBOHYD	472	472	N-linked (GlcNAc . .)	(Potential)		
FT CARBOHYD	482	482	N-linked (GlcNAc . .)	(Potential)		
FT CARBOHYD	503	503	N-linked (GlcNAc . .)	(Potential)		
FT DISULFID	31	36	By similarity.			
FT DISULFID	94	107	By similarity.			
FT DISULFID	99	116	By similarity.			
FT DISULFID	118	127	By similarity.			
FT DISULFID	134	148	By similarity.			
FT DISULFID	144	157	By similarity.			
FT DISULFID	159	172	By similarity.			
FT DISULFID	178	190	By similarity.			
FT DISULFID	185	199	By similarity.			
FT DISULFID	201	214	By similarity.			
FT DISULFID	220	229	By similarity.			
FT DISULFID	225	238	By similarity.			
FT DISULFID	240	255	By similarity.			
FT DISULFID	422	448	By similarity.			
FT DISULFID	612	639	By similarity.			
FT NON_TER	1	1				
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					40	Gaps
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3	QOASQVL-VRRKRANSMLEETKQGLERCELECNKEAREVEVNDPDTFFPKYLYVC	61				
96	INKYSGPTTKNSGPRAT-----CVQNLPPDCTNPCCRKCTQACODLMGNPF	141				
62	LRSF-----OSGFTARQSTDAVPDLRSCVNALPDQCSPLPCNEDGYMSCKDKASFT	115				
142	CLCKRAGMGRLCDKQVNEC-----SOENGSGCLQICHNKPSCFHCSCHSFELSDDGRTCDI	198				
116	CTCKRGMGRCERPEINCKQPSNINNGSCQICONTPESHYSCSKSGFVMLSNKKDCQDV	175				
199	DECA-DSEACGEARCKNLPGSYSCLCDGFAVSSOEKACRDVDECLQGRCEQVQVYNSGQS	257				
176	DECSLKPMNCGYAVCKNIPGDPECCPEGGRYMLKSKSCBVDSESMWCAQLCVNYBGG	235				
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236	YTCYCDGKGKFLADQKSCSAVSYCLPLNIDTKYELLYLAEQFAGV-VLYLKRPLPEIS	294				
318	RLVAEFDRPTPEEGILLFAGGHQDSTWIVLALRAGRLELQRLRYNGVGRVTSGGPVINH	377				
295	RPSAFDRRTYDSQVILYABEIDHSANLILLALRGKKEIYVQKNHTSKITTGDDIINN	354				
378	MMQTSIVELAEALNIVIKYNRDAVMKIAVAGDLPQERGLYHNLTVGGIPFH-EXDLYQ	436				
355	LMNWYSVEELHESISIKLAKAEMDINKRPLFKPEENGLETKVYFAFPRKVESELIKP	414				
437	INPRLDGCMRSMNMLNGEDDTIQEIVXKNTRQCSVTERGSEFYFGSGAPFLSYNMRTP	496				
415	INPRLDGCTRSMNMLKQASGKKEIIQEKQNHKCLVTEKSGSYFGSGAEHHIDY----	470				
497	LDVGTEST-WBEVYVAHTRPADDTGVLFALMAPDRLAPVLSVALVDYSTKKLQKQVLV	555				
471	NWNGSNABSMHINVTINLRPSYGTGVMALVSN-NYTPFAVSLVD--STSP-KSDIYI	525				
556	AVEHTAL-ALMEIKYCDQGEHVVTYSLRDEATLEVDGTGROSQVSAQQLQERLAVLEBH	614				
526	SVENTVIYRIQLSLSCSYGRS--HLEFRVNRNLEILFPLKETITSQELQTLAILDRA	583				
615	LRSPLVTRFGGLPDVPTASRPTAYARGCMTELVNRRLILDEBAVYKSHDITAHSGPPV	673				

Db 584 MKGKATYIGLDPVPFSATPVNAFYNGCMENVINGVLDLDEAISKNDIRAHSCPSV 642

```

RESULT 13
ID 016519 HUMAN PRELIMINARY; PRT; 650 AA.
AC 016519;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 29.
DE Protein S precursor (Fragment).
GN Name=PROS1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
R1 NUCLEOTIDE SEQUENCE.
RA Lundwall A., Dackowski W., Cohen E., Shaffer M., Mahr A., Dahlback B.,
RA Stenflo J., Wydro R.;
RT "Isolation and sequence of the cDNA for human protein S, a regulator
RT of blood coagulation."
RL Proc. Natl. Acad. Sci. U.S.A. 83:6716-6720(1986).
CC -1- FUNCTION: Anticoagulant plasma protein; it is a cofactor to
CC and vitra. It helps to prevent coagulation and stimulating
CC fibrinolysis (by similarity).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivative license
CC -----
EMBL: M4338; AAA60181.1; -.
HSSP: P00740; 1CFH.
DR SRR; Q16519; 174-260.
DR Ensembl; ENSG00000184500; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR013320; ConA_like_subgrp.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR000742; EGF_3.
DR InterPro; IPR001881; EGF_Ca_bd.
DR InterPro; IPR013091; EGF_Ca_bd_2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR013032; EGF_like_reg.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR012679; Laminin_G_1.
DR InterPro; IPR012680; Laminin_G_2.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF07645; EGF_CA_1.
DR Pfam; PF00594; GLA_1.
DR Pfam; PF00054; Laminin_G_1; 1.
DR Pfam; PF02210; Laminin_G_2; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF_4.
DR SMART; SM00179; EGF_CA_3.
DR SMART; SM00069; GLA_1.
DR SMART; SM00282; LamG_2.
DR PROSITE; PS00010; ASX_HYDROXYL_3.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS00026; EGF_3; 4.
DR PROSITE; PS01187; EGF_CA_2.
DR PROSITE; PS00011; GLA_1; UNKNOWN_1.
DR PROSITE; PS00998; GLA_2; 1.
DR PROSITE; PS50025; LAM_G_DOMAIN; 2.
DR CATH; EGF-like domain; Signal.
FT SIGNAL <1 15 Potential.

```

```

FT CHAIN 16 650 protein S.
FT NON TER 1 1
SQ SEQUENCE 650 AA; 72462 MW; 9A8C044C503BF474 CRC64;
Query Match 41.3%; Score 1516; DB 2; Length 650;
Best Local Similarity 44.4%; Pred. No. 2.2e-99;
Matches 291; Conservative 127; Mismatches 210; Indels 28; Gaps 14;
QY 33 LPRAEATQFLPRPRRRAQVFEAKQGLRECEYELCSREAEVENDDETYFYRY 92
DB 1 LSPKQASQVL-VRRRRANSLLEETKQGNLECEIECNKEAREVENDDETYFYRY 59
QY 93 LDCINKY-----GSPYTKNS--GFATCVQNLPGCTPNDPDRGTQACODLMNPFCLC 144
DB 60 LVCLRSQTGLFTRARSTNAYPDLRSCVNAIPQCSPFLPCNENGYNSCKGKASFTCTC 119
QY 145 KAAGGRLCDKDVNEC---SQENGCLQICHNKGSFHCSGSELSDDRTCODIDEC 201
DB 120 KPGWQGEKCEFDINECKDPNINNGCSQICDNTPGSYHCSCKNGFVLSNKKCKDQVDEC 179
QY 202 A-DSEAGGEARCKRLPGSYGCLDEGFAYSQEACADVDECLGRCEQCVNSPGSYTC 260
DB 180 SLKPSICGTAVCKNIILDEFECEBEGRYNLSKSCEDIDECSENMCAQLCVNYPGGHTC 239
QY 261 HCDGRGGLKLSQMDTCEDILPCVPSVAKSVSILYGMFSGTPVRLRPFKRLQPTRLV 320
DB 240 YCDGKGFKLADQKSCSEVSVCLPLNLDTRKYLLEYLAQFAGV-VLYLFRLEISRFS 298
QY 321 AEFDFRTPEEGILFAGGHQDSTWIVLALRAGRLLEQLRYNGRVTSSGPPVNHGMQ 380
DB 299 AEFDFRTYDEGVILVABSYHSAMILLARGKIEVQLKNEHTSKITGGDVINNGLM 358
QY 381 TIVSEELARLVKVNDAVMKIAVAGDLFQPERGLYHNLTVGGIPFH-EKDLVQPI 439
DB 359 MVSVEELHSHISIKIKEAAMDINKPGPLFKPNGLLETXYVAPGFRKYESELIKINP 418
QY 440 RLDCGRSNWMLNGEDTTOETVKNVTRMQCFSTVTRGSRFSGFAYSLDWMRPLDV 499
DB 419 RLDCGRSNWMLNGEDTTOETVKNVTRMQCFSTVTRGSRFSGFAYSLDWMRPLDV 474
QY 500 GTESTVEVEVAHIRPADTGVLALAPDLRAVPLSVLVYDHSSTKLKKQLVLAVER 559
DB 475 SSAEGWHVNTLNIRSTGTGVMALVSGN-NVPRFVSLVD--STSE-KSDIILSVEN 530
QY 560 TAL-ALMEIKVC-DGGEHVYVSLRDEATLEVDTGRGSEVSAALOERLAVLERHRS 617
DB 531 TVIYRIQALSLCSDDQSH--LEFRVNRNMLELSTPLKLETISHEDLQRLAVLDKAKA 587
QY 618 PVLTFAGGLPDVPVTSAPVTAFFRGCMTELVNRRLLDLDEAAVKHSDITHSCSPV 673
DB 588 KQATYIGLDPVPFSATPVNAFYNGCMENVINGVLDLDEAISKNDIRAHSCPSV 643

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RESULT 14
ID 09NSD0 HUMAN PRELIMINARY; PRT; 650 AA.
AC 09NSD0;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE Protein S precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
R1 NUCLEOTIDE SEQUENCE.
RA Wydro R., Cohen E., Dackowski W., Stenflo J., Lundwall A.,
RA Dahlback B.;
RL Submitted (FEB-1992) to the EMBL/Genbank/DBJ databases.

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 29, 2006, 11:03:41 ; Search time 198 Seconds  
(without alignments)  
1584.093 Million cell updates/sec

Title: US-10-671-054-1

Perfect score: 3675  
Sequence: 1 MAPSLSPGPAALRRAPQLTL.....AHSCPVEPAADYKDDDDK 686

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq\_8:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*
- 9: geneseqp2005s:\*
- 10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3675	100.0	686	8	Adm40823 Human Gas
2	3628	98.7	678	2	AAR99414 Human gas
3	3628	98.7	678	2	AAM46463 Human gas
4	3628	98.7	678	2	AAV29794 Human gro
5	3628	98.7	678	3	AAV57383 Amino aci
6	3628	98.7	678	8	AdL83231 Human PRO
7	3628	98.7	678	8	Adm40825 Human Gas
8	3628	98.7	678	8	Adm60275 Human Gas
9	3628	98.7	678	8	AdT91779 Human GAS
10	3628	98.7	678	9	AdV91450 Human gro
11	3628	98.7	678	10	AE887023 Human che
12	3628	98.7	678	7	AdD48757 Human pro
13	3146	85.6	624	8	AD067207 Novel hum
14	2955.5	80.4	673	2	AAW46462 Murine gr
15	2955.5	80.4	673	2	AAV29793 Murine gr
16	2955.5	80.4	673	3	AAAB3459 Human PRO
17	2955.5	80.4	673	3	AAV57382 Amino aci
18	2955.5	80.4	673	5	AB884840 Human PRO
19	2955.5	80.4	673	5	AB884840 Human PRO
20	2955.5	80.4	673	7	AD010337 Human ang
21	2955.5	80.4	673	7	AD011297 Human sec
22	2955.5	80.4	673	7	AD057090 Human sec
23	2955.5	80.4	673	8	AdE41298 Human sec

#### ALIGNMENTS

24	2955.5	80.4	673	8	ADH43481	Adh43481 Human PRO
25	2955.5	80.4	673	8	ADK82826	Adk82826 Human PRO
26	2931	79.8	703	8	ABO84420	ABO84420 Mouse can
27	2622	71.3	518	8	ABO84421	ABO84421 Human can
28	1547.5	42.1	676	8	ADP24054	ADP24054 PRO polyP
29	1547.5	42.1	676	8	ADT91805	Adt91805 Human GAS
30	1547.5	42.1	676	9	ADZ14050	Adz14050 Human pro
31	1543	42.0	676	2	AAW46464	AAW46464 Human pro
32	1543	42.0	676	2	AAV29795	AAV29795 Human pro
33	1543	42.0	676	3	AAV57384	AAV57384 Amino aci
34	1543	42.0	676	7	AD046140	AD046140 Human PRO
35	1543	42.0	676	7	AD062065	AD062065 Human PRO
36	1532	41.7	650	8	AD017650	Ad017650 Human sof
37	1516	41.3	650	1	AA081137	AA081137 Human pro
38	1516	41.3	650	7	ADD48900	Add48900 Human pro
39	1515.5	41.2	676	1	AA070083	AA070083 Human rec
40	1511.5	41.1	635	2	AA072350	AA072350 Mature hu
41	1510.5	41.1	635	2	AA031875	AA031875 Vitamin K
42	1479	40.2	675	1	AA081136	AA081136 Bovine Pr
43	1448	39.4	675	7	ADD48898	Add48898 Rat Prote
44	1437.5	39.1	675	2	AA070728	AA070728 Human pro
45	1297	35.3	227	9	ADV91465	Adv91465 Human gro

RESULT 1  
ID ADM40823 standard; protein; 686 AA.  
XX  
AC ADM40823;  
XX  
DT 01-JUL-2004 (first entry)  
XX  
DE Human Gas6 protein with a C-terminal epitope tag SEQ ID NO:1.  
XX  
KW growth arrest specific gene 6; Gas6; epitope tag; variant Gas6;  
KW anti-apoptotic; Gas6 inhibitor; Gas6-dependent receptor phosphorylation;  
KW receptor internalisation; cell proliferation; cell apoptosis prevention;  
KW signalling molecule; cell marker; human.  
XX  
OS Homo sapiens.  
XX  
PN W02004029209-A2.  
XX  
PD 08-APR-2004.  
XX  
PF 24-SEP-2003; 2003MO-US030330.  
XX  
PR 24-SEP-2002; 2002US-0413157P.  
XX  
(GEN2 ) CENTOCOR INC.  
XX  
Yang J, Chen C, Hu B, Andrade-Gordon P, Jordan R;  
WPI; 2004-316097/29.  
XX  
New epitope-tagged Growth Arrest Specific Gene 6 (Gas6) proteins for  
PT manufacturing medicines or for identifying inhibitors of Gas6 and its  
PT receptors.  
XX  
PS Claim 2; SEQ ID NO 1; 28pp; English.  
XX  
XX The present invention describes an isolated growth arrest specific gene 6  
CC (Gas6) polypeptide, or its variant, with an epitope tag fused at the C-  
CC terminus. The epitope tag comprises a Flag sequence of 8 amino acids (SEQ  
CC ID NO:2, ADM40824), or a polypeptide sequence. The variant Gas6  
CC polypeptide has 75% identity to native human Gas6 protein. Also  
CC described: (1) a recombinant DNA molecule encoding the amino acid  
CC sequence of the polypeptide described above; (2) a vector comprising the  
CC above nucleic acid; (3) a host cell comprising the vector, where the host  
CC cell is of mammalian origin; and (4) a composition comprising the

CC polypeptide and a pharmaceutical carrier. Gas6 has anti-apoptotic activity. The composition is useful for manufacturing medicines or for identifying inhibitors of Gas6 and its receptors. The Gas6 polypeptide CC may also be used for Gas6-dependent receptor phosphorylation, receptor CC internalisation, cell proliferation, prevention of cell apoptosis, or CC induction of signaling molecules or cell markers. The present sequence CC represents the human Gas6 protein with an epitope tag fused at the C-terminus, from the present invention.

XX  
SQ Sequence 686 AA;

Query Match 100.0%; Score 3675; DB 8; Length 686;  
Best Local Similarity 100.0%; Pred. No. 7,1e-248;  
Matches 686; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MAPSISPGPALRRAPQILLILLALAEALALPAREATQFLRPRORAFQVFEAKQGH 60
DB 1 MAPSISPGPALRRAPQILLILLALAEALALPAREATQFLRPRORAFQVFEAKQGH 60
QY 61 LERECVEELCSRBEAREVEFENDPETYFPRYLDCINKGSPYTKNSGFATCVQNLPDQC 120
DB 61 LERECVEELCSRBEAREVEFENDPETYFPRYLDCINKGSPYTKNSGFATCVQNLPDQC 120
QY 121 TPNPCDRKGTQACQDLMGNFCLCKAGMGRLCDKDVNCSQENGCLQICHNKPSSFFHC 180
DB 121 TPNPCDRKGTQACQDLMGNFCLCKAGMGRLCDKDVNCSQENGCLQICHNKPSSFFHC 180
QY 181 SCHSGFEISSDRTCCDIDECADSEAGCARCKNLPGSYCLCDEGFAYSSQEKACRDV 240
DB 181 SCHSGFEISSDRTCCDIDECADSEAGCARCKNLPGSYCLCDEGFAYSSQEKACRDV 240
QY 241 ECLQRCCEQVCVNSPSSYTCCHDGRGLKLSQDMDCEDILPCVPSVAKSVKSLYLGM 300
DB 241 ECLQRCCEQVCVNSPSSYTCCHDGRGLKLSQDMDCEDILPCVPSVAKSVKSLYLGM 300
QY 301 FSGTPVIRLRFKRLQPTRLVAEFDFRTPDEGILLFAGGHODSTWIVLALRAGRLQLQR 360
DB 301 FSGTPVIRLRFKRLQPTRLVAEFDFRTPDEGILLFAGGHODSTWIVLALRAGRLQLQR 360
QY 361 YNGVGRVTS SGPVINGMMQTTISVEELARNLVTKNRDAVMKIAVAGDLFQPERGLYHNL 420
DB 361 YNGVGRVTS SGPVINGMMQTTISVEELARNLVTKNRDAVMKIAVAGDLFQPERGLYHNL 420
QY 421 LTVGGIPRHEKDLVQFINRLDGCMSNMNLNGEDTTIETVKNTRMOCFSTTERGSFY 480
DB 421 LTVGGIPRHEKDLVQFINRLDGCMSNMNLNGEDTTIETVKNTRMOCFSTTERGSFY 480
QY 481 PGSGFAFYSILDVWRTPLDVGTSTWEVEVAHIRPAADTGVLFALWAPDLRAVPLSVALY 540
DB 481 PGSGFAFYSILDVWRTPLDVGTSTWEVEVAHIRPAADTGVLFALWAPDLRAVPLSVALY 540
QY 541 DVHSTKTKLKKQVLVAVENTALAMEIKYCDGSEHVVVYSLRGEATLEVDGTRGSEVS 600
DB 541 DVHSTKTKLKKQVLVAVENTALAMEIKYCDGSEHVVVYSLRGEATLEVDGTRGSEVS 600
QY 601 AAQLOERLAVLEHRHSPVLTFAAGLPDVVTSAPVTAFAFGCMTLEVNRRLLDLEAAY 660
DB 601 AAQLOERLAVLEHRHSPVLTFAAGLPDVVTSAPVTAFAFGCMTLEVNRRLLDLEAAY 660
QY 661 KHSIDITAHSCPPVPAADYKDDDDK 686
DB 661 KHSIDITAHSCPPVPAADYKDDDDK 686

RESULT 2
AA99414
ID AA99414 standard; protein; 678 AA.
XX
AC AA99414;
XX
XX 04-DEC-1996 (first entry)
DT
XX Human gas6 protein, an S protein homologue and axl receptor ligand.

```

XX Axl receptor ligand; human protein S homologue; growth factor;  
KW myeloid cell proliferation; myeloid malignancy; regulation; prevention;  
KW recombinant production.

XX Homo sapiens.

XX US5538861-A.

XX 23-JUL-1996.

XX 29-JUL-1994; 94US-00282141.

XX 29-JUL-1994; 94US-00282141.

XX (AMGE-) AMGEN INC.

XX (SCHN/) SCHNEIDER C.

XX Manfioletti G, Varnum BC, Schneider C, Avanzi G, Brancolini C;

XX MPI: 1996-353825/35.

XX N-PSDB; AAT41544.

XX Claim 1; Col 19-22; 36pp; English.

XX AA99414 is the gas6 protein (from the growth arrest specific gene number

CC 6). The gas6 protein has homology to human protein S which functions as a

CC cofactor in a protease cascade that regulates coagulation. Gas6

CC expression, as with gas1 and gas2, is associated with cell growth arrest

CC which suggests a possible role of gas6 in the regulation of cell growth.

CC In fact the gas6 protein is an axl receptor (axlr) ligand and a growth

CC factor for any cells expressing axlr e.g. bone marrow, spleen, thymus,

CC ovary, heart, intestine and lung cells. The axl receptor is involved in

CC myeloid cell proliferation and myeloid malignancies, so gas6 may regulate

CC growth of such cells

XX  
SQ Sequence 678 AA;

Query Match 98.7%; Score 3628; DB 2; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.3e-244;  
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MAPSISPGPALRRAPQILLILLALAEALALPAREATQFLRPRORAFQVFEAKQGH 60
DB 1 MAPSISPGPALRRAPQILLILLALAEALALPAREATQFLRPRORAFQVFEAKQGH 60
QY 61 LERECVEELCSRBEAREVEFENDPETYFPRYLDCINKGSPYTKNSGFATCVQNLPDQC 120
DB 61 LERECVEELCSRBEAREVEFENDPETYFPRYLDCINKGSPYTKNSGFATCVQNLPDQC 120
QY 121 TPNPCDRKGTQACQDLMGNFCLCKAGMGRLCDKDVNCSQENGCLQICHNKPSSFFHC 180
DB 121 TPNPCDRKGTQACQDLMGNFCLCKAGMGRLCDKDVNCSQENGCLQICHNKPSSFFHC 180
QY 181 SCHSGFEISSDRTCCDIDECADSEAGCARCKNLPGSYCLCDEGFAYSSQEKACRDV 240
DB 181 SCHSGFEISSDRTCCDIDECADSEAGCARCKNLPGSYCLCDEGFAYSSQEKACRDV 240
QY 241 ECLQRCCEQVCVNSPSSYTCCHDGRGLKLSQDMDCEDILPCVPSVAKSVKSLYLGM 300
DB 241 ECLQRCCEQVCVNSPSSYTCCHDGRGLKLSQDMDCEDILPCVPSVAKSVKSLYLGM 300
QY 301 FSGTPVIRLRFKRLQPTRLVAEFDFRTPDEGILLFAGGHODSTWIVLALRAGRLQLQR 360
DB 301 FSGTPVIRLRFKRLQPTRLVAEFDFRTPDEGILLFAGGHODSTWIVLALRAGRLQLQR 360
QY 361 YNGVGRVTS SGPVINGMMQTTISVEELARNLVTKNRDAVMKIAVAGDLFQPERGLYHNL 420
DB 361 YNGVGRVTS SGPVINGMMQTTISVEELARNLVTKNRDAVMKIAVAGDLFQPERGLYHNL 420

```



Qy 421 LTVGIPFHEKDLVOPINRLDGCMSWMNLNGEDTTIOETVKVNTRMQCFSTYERGSFY 480  
 Db 421 LTVGIPFHEKDLVOPINRLDGCMSWMNLNGEDTTIOETVKVNTRMQCFSTYERGSFY 480  
 Qy 481 PGSGFAFYSLDYKRTPLDVGTSTWVEVVAHIRPADTGVLPALMADPLRAVPLSVALV 540  
 Db 481 PGSGFAFYSLDYKRTPLDVGTSTWVEVVAHIRPADTGVLPALMADPLRAVPLSVALV 540  
 Qy 541 DYHSTKKLKKQVLVAEHTALALMEIKVCDGQEHVVVSLRDGEATLEVDGTGQSEVS 600  
 Db 541 DYHSTKKLKKQVLVAEHTALALMEIKVCDGQEHVVVSLRDGEATLEVDGTGQSEVS 600  
 Qy 601 AAQOERLAVLERHLSRSPVLTFAAGLPDVPTSAFVTAFAFGCMTELVNRRLLDLDEAAY 660  
 Db 601 AAQOERLAVLERHLSRSPVLTFAAGLPDVPTSAFVTAFAFGCMTELVNRRLLDLDEAAY 660  
 Qy 661 KHSIDTAHSCPPVEPAAA 678  
 Db 661 KHSIDTAHSCPPVEPAAA 678

RESULT 3

AAW46463 ID AAW46463 standard; protein; 678 AA.

AAW46463 AC AAW46463;

DT 15-MAY-1998 (first entry)

DE Human growth arrest specific-gene 6 (gas6) protein.

KM Growth arrest specific-gene 6; gas6; Rsa; Axl; receptor; mitogenic agent;  
 KM receptor tyrosine kinase; regulation; protease cascade; insulin;  
 KM growth regulation; serum-free culture medium; human; Schwann cell;  
 KM receptor activator; erbB receptor; heregulin; cAMP level; proliferation;  
 KM treatment; nervous system injury.  
 XX Homo sapiens.

FM Key Location/Qualifiers  
 FT Domain 49..89  
 FT Domain /note="A domain of gas6"

FT Domain 90..117  
 FT Domain /note="B domain of gas6 comprising a thrombin sensitive loop"

FT Domain 118..278  
 FT Domain /note="C domain of gas6, contains 4 epidermal growth factor-like repeats"

FT Domain 279..678  
 FT Domain /note="D domain of gas6, homologous to steroid binding hormone"

FT Domain 314..471  
 FT Domain /note="G domain 1"

FT Domain 503..671  
 FT Domain /note="G domain 2"

US5714385-A.

03-FEB-1998.

10-MAY-1995; 95US-00435434.

10-MAY-1995; 95US-00435434.

(GETH ) GENENTECH INC.

Chen J, Mather JP, Li R;

WPI; 1998-129864/12.

PT Medium for culturing human Schwann cells - is serum-free and contains Rse  
 PT receptor activator and other mitogens.  
 XX

PS Disclosure; Fig 2; 51pp; English.  
 CC The present sequence represents a human growth arrest specific-gene 6  
 CC (gas6) protein which is able to activate the Rse and Axl receptor. Rse is  
 CC a receptor tyrosine kinase that is preferentially expressed in the adult  
 CC brain. Gas6 is a vitamin K dependent protein which may play a role in the  
 CC regulation of a protease cascade relevant in growth regulation. The  
 CC protein is used in a serum-free culture medium for culturing human  
 CC Schwann cells, which does not support fibroblast growth. Gas6 functions  
 CC as a mitogenic agent which is a Rse/Axl receptor activator. A second  
 CC mitogenic agent e.g. insulin or an erbB receptor activator such as  
 CC heregulin, is also required to raise cAMP levels and enhance survival or  
 CC proliferation of human Schwann cells. The culture medium additionally  
 CC comprises a molecule or composition that provides Fe ions to the Schwann  
 CC cells, vitamin E, a protease inhibitor, and progesterone. The Schwann  
 CC cells can be used to treat patients with nervous system injuries  
 CC  
 SQ Sequence 678 AA;

Query Match 98.7%; Score 3628; DB 2; Length 678;  
 Best Local Similarity 100.0%; Pred. No. 1,3e-244;  
 Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAPSLSPGPAALRRAPOLLILLALAECAALALPAREATOPLRPRORAPQVFEAKQGH 60  
 Db 1 MAPSLSPGPAALRRAPOLLILLALAECAALALPAREATOPLRPRORAPQVFEAKQGH 60  
 Qy 61 LERECVELCSREBARFVENDPETYFPRYILDICINKYSPYTKNSGFATCVGNLPDQC 120  
 Db 61 LERECVELCSREBARFVENDPETYFPRYILDICINKYSPYTKNSGFATCVGNLPDQC 120  
 Qy 121 TPMPDCKKQAOQODLMGNFCLCKAGWGRLCDKVNESQENGGCLQICHNKGSGFHC 180  
 Db 121 TPMPDCKKQAOQODLMGNFCLCKAGWGRLCDKVNESQENGGCLQICHNKGSGFHC 180  
 Qy 181 SCHSGFELSSDGRTCODIDECADSEACGAEKCNKLPSYSCLCEGFAYSQEAACDVP 240  
 Db 181 SCHSGFELSSDGRTCODIDECADSEACGAEKCNKLPSYSCLCEGFAYSQEAACDVP 240  
 Qy 241 ECLQGRCEQVCVNSPGSYTCHDGRGLKLSQDMTCEILLPCVPFSVAKSVSLYGRM 300  
 Db 241 ECLQGRCEQVCVNSPGSYTCHDGRGLKLSQDMTCEILLPCVPFSVAKSVSLYGRM 300  
 Qy 301 FSGTPVRLRLEFKLOPRLVAEEDFRFPDEGILLFAGGHQDSWTIVLARAQLLEQLR 360  
 Db 301 FSGTPVRLRLEFKLOPRLVAEEDFRFPDEGILLFAGGHQDSWTIVLARAQLLEQLR 360  
 Qy 361 YNGVGRVTSQGVINHGMMOTISVEELARLVKVRDAVMKIAVAGDLFQPERGLYHLN 420  
 Db 361 YNGVGRVTSQGVINHGMMOTISVEELARLVKVRDAVMKIAVAGDLFQPERGLYHLN 420  
 Qy 421 LTVGIPFHEKDLVOPINRLDGCMSWMNLNGEDTTIOETVKVNTRMQCFSTYERGSFY 480  
 Db 421 LTVGIPFHEKDLVOPINRLDGCMSWMNLNGEDTTIOETVKVNTRMQCFSTYERGSFY 480  
 Qy 481 PGSGFAFYSLDYKRTPLDVGTSTWVEVVAHIRPADTGVLPALMADPLRAVPLSVALV 540  
 Db 481 PGSGFAFYSLDYKRTPLDVGTSTWVEVVAHIRPADTGVLPALMADPLRAVPLSVALV 540  
 Qy 541 DYHSTKKLKKQVLVAEHTALALMEIKVCDGQEHVVVSLRDGEATLEVDGTGQSEVS 600  
 Db 541 DYHSTKKLKKQVLVAEHTALALMEIKVCDGQEHVVVSLRDGEATLEVDGTGQSEVS 600  
 Qy 601 AAQOERLAVLERHLSRSPVLTFAAGLPDVPTSAFVTAFAFGCMTELVNRRLLDLDEAAY 660  
 Db 601 AAQOERLAVLERHLSRSPVLTFAAGLPDVPTSAFVTAFAFGCMTELVNRRLLDLDEAAY 660  
 Qy 661 KHSIDTAHSCPPVEPAAA 678  
 Db 661 KHSIDTAHSCPPVEPAAA 678

RESULT 4

AAV29794  
 ID AAV29794 standard; protein; 678 AA.  
 XX  
 AC AAV29794;  
 XX  
 DT 15-NOV-1999 (first entry)  
 XX  
 DE Human growth arrest-specific gene 6 protein.  
 XX  
 KM Rse receptor protein tyrosine kinase; Rse ligand; Rse- $\beta$ ; gas6;  
 KM growth arrest-specific gene 6; proliferation; differentiation;  
 KM glial cell; Schwann cell; fusion protein.  
 XX  
 OS Homo sapiens.  
 XX  
 PM US5955420-A.  
 XX  
 PD 21-SEP-1999.  
 XX  
 PF 10-MAY-1995; 95US-00438864.  
 XX  
 PR 10-MAR-1995; 95US-00402253.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 PI Mark MR, Mather JP, Li R, Chen J, Hammonds RG, Godowski PJ;  
 XX WPI; 1999-539585/45.  
 DR  
 XX  
 PT Activation of the Rse receptor on a cell, useful for promoting cell  
 PT proliferation and differentiation.  
 XX  
 PS Disclosure; Fig 2; 48pp; English.  
 XX  
 CC A method has been developed for activating the Rse receptor on a cell.  
 CC The method comprises exposing the receptor to the exogenous growth arrest  
 CC -specific gene 6 (gas6) polypeptide. The method is useful for enhancing  
 CC cell proliferation and cell differentiation. The present sequence  
 CC represents human gas6 given in the present invention  
 XX  
 SQ Sequence 678 AA;  
 Query Match 98.7%; Score 3628; DB 2; Length 678;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-244;  
 Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAPSLSPGPAALRRAPQQLLLLLAALALPAREATQFLPRQRARQVREAKQGH 60  
 DB 1 MAPSLSPGPAALRRAPQQLLLLLAALALPAREATQFLPRQRARQVREAKQGH 60  
 QY 61 LERECVEELCSREAREVFENDEPETYFYPRYLDCINKKSPYTKNSGFATCVQNLPDQC 120  
 DB 61 LERECVEELCSREAREVFENDEPETYFYPRYLDCINKKSPYTKNSGFATCVQNLPDQC 120  
 QY 121 TPNPCDRKGTQACQDLMGNFCLCKAGWGRLCDKDVNECSQENGGCLQICHNKPSPFHC 180  
 DB 121 TPNPCDRKGTQACQDLMGNFCLCKAGWGRLCDKDVNECSQENGGCLQICHNKPSPFHC 180  
 QY 181 SCHSGEELSSDGTCCDIDECADSEACGEARCKNLPGSYCLDDEGFAYSSQEKACRDVD 240  
 DB 181 SCHSGEELSSDGTCCDIDECADSEACGEARCKNLPGSYCLDDEGFAYSSQEKACRDVD 240  
 QY 241 ECLQGCCEQVCNVPSTYCHCGRGGLKLSQDMDCEDLLPCVPSPVAKSVSLYIGRM 300  
 DB 241 ECLQGCCEQVCNVPSTYCHCGRGGLKLSQDMDCEDLLPCVPSPVAKSVSLYIGRM 300  
 QY 301 FSGTPVIRLRFKRLQPTRLVAEPDFRTFDEGILLFAGHQDSWTIVLALRAQLRLQLR 360  
 DB 301 FSGTPVIRLRFKRLQPTRLVAEPDFRTFDEGILLFAGHQDSWTIVLALRAQLRLQLR 360  
 QY 361 YNGVGVTSSTGPIYINNGMOTISVEELARNLVIKVRDAVMKIAVAGDLFQPERGLYHLN 420  
 DB 361 YNGVGVTSSTGPIYINNGMOTISVEELARNLVIKVRDAVMKIAVAGDLFQPERGLYHLN 420

QY 421 LTVGGIPFHEKDLVQPINRPLDGCNRSMNMLNGEDTTIOETVKVNTRMQCFSTYTERGSFY 480  
 DB 421 LTVGGIPFHEKDLVQPINRPLDGCNRSMNMLNGEDTTIOETVKVNTRMQCFSTYTERGSFY 480  
 QY 481 PGSGFAFYSLDYMRTPLDVGTESTWEVEVAHIRPADTGVLPALMAPDLRAVPLSLVALY 540  
 DB 481 PGSGFAFYSLDYMRTPLDVGTESTWEVEVAHIRPADTGVLPALMAPDLRAVPLSLVALY 540  
 QY 541 DYHSTKQLKKOLVLAVENTALAMEIKVCDQGEHVTVSLRDGEATLEVDGTRGQSEVS 600  
 DB 541 DYHSTKQLKKOLVLAVENTALAMEIKVCDQGEHVTVSLRDGEATLEVDGTRGQSEVS 600  
 QY 601 AAQLOERLAVLBRHLRSPVLTFAGGLPDVPTVSAPVTAFYRCMTLEVNRLDLDDEAAY 660  
 DB 601 AAQLOERLAVLBRHLRSPVLTFAGGLPDVPTVSAPVTAFYRCMTLEVNRLDLDDEAAY 660  
 QY 661 KHSIDITAHSCPVEPAA 678  
 DB 661 KHSIDITAHSCPVEPAA 678  
 RESULT 5  
 ID AAV57383  
 XX AAV57383 standard; protein; 678 AA.  
 AC AAV57383;  
 XX  
 DT 19-JUN-2000 (first entry)  
 XX  
 DE Amino acid sequence of human gas6 (h gas6) protein.  
 XX  
 KM Nervous system; Schwann cell; mitogen; Res/Axl receptor activator;  
 KM central nervous system; peripheral nervous system; injury; trauma;  
 KM nutritional deficiency; systemic disease; toxin; demyelination; gas6;  
 KM protein S.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6033660-A.  
 XX  
 PD 07-MAR-2000.  
 XX  
 PF 10-MAY-1995; 95US-00438862.  
 XX  
 PR 10-MAY-1995; 95US-00438862.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 PI Mather JP, Chen J, Li R;  
 XX  
 DR WPI; 2000-246046/21.  
 XX  
 PT Repairing nervous system injuries in mammals, by administering human  
 PT Schwann cells that have been propagated in medium supplemented with  
 PT mitogens.  
 XX  
 PS Disclosure; Fig 2; 52pp; English.  
 XX  
 CC The invention relates to a method for treating nervous system injuries in  
 CC mammals by administering human Schwann cells (SC) that have been cultured  
 CC in serum-free medium. The serum-free medium is a nutrient solution  
 CC supplemented with two mitogens, one of which, is a Res/Axl receptor  
 CC activator, to increase survival and proliferation of SC. The method is  
 CC used to treat (or prevent) central or peripheral nervous system injury,  
 CC e.g. traumatic, ischemic, malignant, infectious or degenerative lesions,  
 CC or lesions associated with nutritional deficiencies, systemic disease,  
 CC toxins or demyelination. Culturing cells in the specified medium allows  
 CC proliferation of adult SC for use in autologous transplants. The present  
 CC sequence represents a human gas6 (h gas6) protein, having 44% sequence  
 CC identity to human protein S. Gas6 is demonstrated to be a potent growth/  
 CC survival factor for SCs in defined serum-free culture

SQ Sequence 678 AA:  
 Query Match 98.7%; Score 3628; DB 3; Length 678;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-244;  
 Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAPSLSPGPAALRRAPOLLILLILAAECALALIPAREATQFLPRORRAFOVFEEAKQGH 60  
 DB 1 MAPSLSPGPAALRRAPOLLILLILAAECALALIPAREATQFLPRORRAFOVFEEAKQGH 60  
 QY 61 LERECVEELCSREAREVEFENDPETDYFPRYLDICINKGSPYTKNSGFATCVONLPDQC 120  
 DB 61 LERECVEELCSREAREVEFENDPETDYFPRYLDICINKGSPYTKNSGFATCVONLPDQC 120  
 QY 121 TPNPCDRKGTQACODLMGNFPCICKAGMGRLCDKDVNECSQENGGCLQICHNKPSPFHC 180  
 DB 121 TPNPCDRKGTQACODLMGNFPCICKAGMGRLCDKDVNECSQENGGCLQICHNKPSPFHC 180  
 QY 181 SCHSGFELSSDGRTCODIDECADSEACGEARCKNLPGSYSCLCDEGFAYSSQEKACRDVD 240  
 DB 181 SCHSGFELSSDGRTCODIDECADSEACGEARCKNLPGSYSCLCDEGFAYSSQEKACRDVD 240  
 QY 241 ECLQGRCEQVCVNSPGSYTCHCDGRGGLKLSQDMTCEDILPCVPFSVAKSVKSLYLGRM 300  
 DB 241 ECLQGRCEQVCVNSPGSYTCHCDGRGGLKLSQDMTCEDILPCVPFSVAKSVKSLYLGRM 300  
 QY 301 FSGTPVIRLRFRKLOPRLVAEPFRTPDEGILLFAGGHODSTWIVLALRAGRLLEQLR 360  
 DB 301 FSGTPVIRLRFRKLOPRLVAEPFRTPDEGILLFAGGHODSTWIVLALRAGRLLEQLR 360  
 QY 361 YNGVGRVTSGGPIVINGMOTISVEELARNLVIKNRDAVMKIAVAGDLFOBERGLYHLN 420  
 DB 361 YNGVGRVTSGGPIVINGMOTISVEELARNLVIKNRDAVMKIAVAGDLFOBERGLYHLN 420  
 QY 421 LTVGGIPFHEKDLVQPINRLDGCMSNMWLNGBEDTTIGETVKNVTRMOCFSYTERGSFY 480  
 DB 421 LTVGGIPFHEKDLVQPINRLDGCMSNMWLNGBEDTTIGETVKNVTRMOCFSYTERGSFY 480  
 QY 481 PGGGFAFYSLDVNRTPLDVGTSTWEVVAHTRPADTVLPALAMPDLRAVPLSALV 540  
 DB 481 PGGGFAFYSLDVNRTPLDVGTSTWEVVAHTRPADTVLPALAMPDLRAVPLSALV 540  
 QY 541 DYHSTKKLKKQLVLAVENTALALMEIKVCDGQEHVTVSLRQGEATLEVDTGRGQSEVS 600  
 DB 541 DYHSTKKLKKQLVLAVENTALALMEIKVCDGQEHVTVSLRQGEATLEVDTGRGQSEVS 600  
 QY 601 AAQLOERLAVLEHRLSPVLTFAGGLPDVPTSAFVTAFFRGCMTELEVNRLDLDEAY 660  
 DB 601 AAQLOERLAVLEHRLSPVLTFAGGLPDVPTSAFVTAFFRGCMTELEVNRLDLDEAY 660  
 QY 661 KHSDDTAHSCRPVEPAA 678  
 DB 661 KHSDDTAHSCRPVEPAA 678  
 RESULT 6  
 ADL83231  
 ID ADL83231 standard; protein; 678 AA.  
 XX ADL83231;  
 AC ADL83231;  
 XX 17-JUN-2004 (first entry)  
 DT 17-JUN-2004 (first entry)  
 XX Human PRO12613, SEQ ID 433.  
 DE Human PRO12613, SEQ ID 433.  
 KW Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;  
 KW Antiallergic; Muscular; Neuroprotective; Nephrotoxic; Antiinflammatory;  
 KW Gene Therapy; PRO; B cell related disorder; cancer;  
 KW Immune-mediated inflammatory disease; human.  
 OS Homo sapiens.  
 XX  
 PN WO2004024097-A2.

XX 25-MAR-2004.  
 PD 15-SEP-2003; 2003WO-US029097.  
 XX 16-SEP-2002; 2002US-0411392P.  
 PR (GETH ) GENENTECH INC.  
 XX Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;  
 PI Wu TJ;  
 DR WPI: 2004-3329389/30.  
 PS N-PSDB; ADL83230.  
 PT New PRO polypeptide, useful for diagnosing and treating a B cell related  
 PT disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune  
 PT mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.  
 PS Claim 10; Fig 433; 695DP; English.  
 CC The present invention relates to PRO proteins and their coding sequences.  
 CC The PRO proteins are useful for diagnosing and treating a B cell related  
 CC disorder, e.g. X-linked infantile hypogammaglobulinemia, polycystic  
 CC antigen unresponsiveness, selective IgA deficiency, selective IgM  
 CC deficiency, selective deficiency of IgG subclasses, immunodeficiency with  
 CC hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's  
 CC lymphoma, intermediate lymphoma, follicular lymphoma, type II  
 CC hypereosinophilia, rheumatoid arthritis, autoimmune mediated hemolytic  
 CC anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or  
 CC ankylosing spondylitis. The PRO proteins are also useful for preparing a  
 CC medicament for treating a condition that is responsive to the PRO  
 CC protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO  
 CC coding sequences are useful as hybridization probes in chromosome and  
 CC gene mapping, in preparing PRO proteins, or in generating transgenic  
 CC animals or knockout animals, which in turn are useful in the development  
 CC and screening of therapeutically useful reagents.  
 SQ Sequence 678 AA:  
 Query Match 98.7%; Score 3628; DB 8; Length 678;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-244;  
 Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAPSLSPGPAALRRAPOLLILLILAAECALALIPAREATQFLPRORRAFOVFEEAKQGH 60  
 DB 1 MAPSLSPGPAALRRAPOLLILLILAAECALALIPAREATQFLPRORRAFOVFEEAKQGH 60  
 QY 61 LERECVEELCSREAREVEFENDPETDYFPRYLDICINKGSPYTKNSGFATCVONLPDQC 120  
 DB 61 LERECVEELCSREAREVEFENDPETDYFPRYLDICINKGSPYTKNSGFATCVONLPDQC 120  
 QY 121 TPNPCDRKGTQACODLMGNFPCICKAGMGRLCDKDVNECSQENGGCLQICHNKPSPFHC 180  
 DB 121 TPNPCDRKGTQACODLMGNFPCICKAGMGRLCDKDVNECSQENGGCLQICHNKPSPFHC 180  
 QY 181 SCHSGFELSSDGRTCODIDECADSEACGEARCKNLPGSYSCLCDEGFAYSSQEKACRDVD 240  
 DB 181 SCHSGFELSSDGRTCODIDECADSEACGEARCKNLPGSYSCLCDEGFAYSSQEKACRDVD 240  
 QY 241 ECLQGRCEQVCVNSPGSYTCHCDGRGGLKLSQDMTCEDILPCVPFSVAKSVKSLYLGRM 300  
 DB 241 ECLQGRCEQVCVNSPGSYTCHCDGRGGLKLSQDMTCEDILPCVPFSVAKSVKSLYLGRM 300  
 QY 301 FSGTPVIRLRFRKLOPRLVAEPFRTPDEGILLFAGGHODSTWIVLALRAGRLLEQLR 360  
 DB 301 FSGTPVIRLRFRKLOPRLVAEPFRTPDEGILLFAGGHODSTWIVLALRAGRLLEQLR 360  
 QY 361 YNGVGRVTSGGPIVINGMOTISVEELARNLVIKNRDAVMKIAVAGDLFOBERGLYHLN 420  
 DB 361 YNGVGRVTSGGPIVINGMOTISVEELARNLVIKNRDAVMKIAVAGDLFOBERGLYHLN 420  
 QY 421 LTVGGIPFHEKDLVQPINRLDGCMSNMWLNGBEDTTIGETVKNVTRMOCFSYTERGSFY 480

DB 421 LTVGGIPFHEKDLVOPINPRLDGCKRSMWMLNGEDTTIOETVKVNTRMQCFSTERGSPY 480  
QY 481 PGSGFAFSLDYMRPLDVGTSTWEEVVAHIRPADTGVLPALMAPDLRAVPLSVLV 540  
DB 481 PGSGFAFSLDYMRPLDVGTSTWEEVVAHIRPADTGVLPALMAPDLRAVPLSVLV 540  
QY 541 DYHSTKCLKKQVLVAVENTALAMEIKVCDGQEHVTVSLRDGEATLEVDGTRGSEVS 600  
DB 541 DYHSTKCLKKQVLVAVENTALAMEIKVCDGQEHVTVSLRDGEATLEVDGTRGSEVS 600  
QY 601 AAQLOERLAVLERHLRSPVLTFAGGLPDVPTVSAPVTAFYRCGMLTVNRLLDDEAAY 660  
DB 601 AAQLOERLAVLERHLRSPVLTFAGGLPDVPTVSAPVTAFYRCGMLTVNRLLDDEAAY 660  
QY 661 KHSDDITAHSCPVEPAA 678  
DB 661 KHSDDITAHSCPVEPAA 678  
RESULT 7  
ADM40825  
ID ADM40825 standard; protein; 678 AA.  
AC ADM40825;  
XX  
DT 01-JUL-2004 (first entry)  
XX  
DE Human Gas6 protein SEQ ID NO:3.  
XX  
KW growth arrest specific gene 6; Gas6; epitope tag; variant phospho;  
KW anti-apoptotic; Gas6 inhibitor; Gas6-dependent receptor phosphorylation;  
KW receptor internalisation; cell proliferation; cell apoptosis prevention;  
KW signaling molecule; cell marker; human.  
XX  
OS Homo sapiens.  
XX  
PN WO2004029209-A2.  
XX  
PD 08-APR-2004.  
XX  
PF 24-SEP-2003; 2003WO-US030330.  
XX  
PR 24-SEP-2002; 2002US-0413157P.  
XX  
PA (CENZ ) CENTOCOR INC.  
XX  
PI Yang J, Chen C, Hu B, Andrade-Gordon P, Jordan R;  
XX  
DR WPI; 2004-316097/29.  
XX  
PT New epitope-tagged Growth Arrest Specific Gene 6 (Gas6) proteins for  
PT manufacturing medicines or for identifying inhibitors of Gas6 and its  
PT receptors.  
XX  
PS Disclosure; SEQ ID NO 3; 28pp; English.  
XX  
CC The present invention describes an isolated growth arrest specific gene 6  
CC (Gas6) polypeptide, or its variant, with an epitope tag fused at the C-  
CC terminus. The epitope tag comprises a Flag sequence of 8 amino acids (SEQ  
CC ID NO:2, ADM40824), or a polypeptide sequence. The variant Gas6  
CC polypeptide has 75% identity to native human Gas6 protein. Also  
CC described: (1) a recombinant DNA molecule encoding the amino acid  
CC sequence of the polypeptide described above; (2) a vector comprising the  
CC above nucleic acid; (3) a host cell comprising the vector, where the host  
CC cell is of mammalian origin; and (4) a composition comprising the  
CC polypeptide and a pharmaceutical carrier. Gas6 has anti-apoptotic  
CC activity. The composition is useful for manufacturing medicines or for  
CC identifying inhibitors of Gas6 and its receptors. The Gas6 polypeptide  
CC may also be used for Gas6-dependent receptor phosphorylation, receptor  
CC internalisation, cell proliferation, prevention of cell apoptosis, or  
CC induction of signaling molecules or cell markers. The present sequence  
CC represents the human Gas6 protein from the present invention.

XX  
SQ Sequence 678 AA;  
Query Match 98.7%; Score 3628; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.3e-244;  
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAPSLPGPALRRAPOLLILLALLAECAALALPAREATQFLRPRORRAFOVEEAKQKH 60  
DB 1 MAPSLPGPALRRAPOLLILLALLAECAALALPAREATQFLRPRORRAFOVEEAKQKH 60  
QY 61 IERSCVEELCSREAREVENDPETDYPRYLDCINKYGSPTTQNSGPATCVQNI.PDOC 120  
DB 61 IERSCVEELCSREAREVENDPETDYPRYLDCINKYGSPTTQNSGPATCVQNI.PDOC 120  
QY 121 TPNPCDRKGTQACQDLMGNFCLCKAGWGGRICDDVNECSQENGGCLOICHNKQGSFHC 180  
DB 121 TPNPCDRKGTQACQDLMGNFCLCKAGWGGRICDDVNECSQENGGCLOICHNKQGSFHC 180  
QY 181 SCHSGFELSSDRTQDIDECADSEACGEARCKNLPGSYSCLCDEGFAYSQEKACRDVD 240  
DB 181 SCHSGFELSSDRTQDIDECADSEACGEARCKNLPGSYSCLCDEGFAYSQEKACRDVD 240  
QY 241 ECLQGRCEQVCVNSPGSYTCHCDGRGGLKLSQMDTCEDILPCVPPSVAKSYKSLYLGM 300  
DB 241 ECLQGRCEQVCVNSPGSYTCHCDGRGGLKLSQMDTCEDILPCVPPSVAKSYKSLYLGM 300  
QY 301 FSGTPIVIRLRFRKRLQPTRLVAEFDPRTDPBEGILLPAGGHODSTWLVIALRAGRLEQLR 360  
DB 301 FSGTPIVIRLRFRKRLQPTRLVAEFDPRTDPBEGILLPAGGHODSTWLVIALRAGRLEQLR 360  
QY 361 YNGVGRVITSSGPGVINHGMMQTISVEELANLVIKNRRDAVMKIAVAGDLFOBERGLYHNL 420  
DB 361 YNGVGRVITSSGPGVINHGMMQTISVEELANLVIKNRRDAVMKIAVAGDLFOBERGLYHNL 420  
QY 421 LTVGGIPFHEKDLVOPINPRLDGCKRSMWMLNGEDTTIOETVKVNTRMQCFSTERGSPY 480  
DB 421 LTVGGIPFHEKDLVOPINPRLDGCKRSMWMLNGEDTTIOETVKVNTRMQCFSTERGSPY 480  
QY 481 PGSGFAFSLDYMRPLDVGTSTWEEVVAHIRPADTGVLPALMAPDLRAVPLSVLV 540  
DB 481 PGSGFAFSLDYMRPLDVGTSTWEEVVAHIRPADTGVLPALMAPDLRAVPLSVLV 540  
QY 541 DYHSTKCLKKQVLVAVENTALAMEIKVCDGQEHVTVSLRDGEATLEVDGTRGSEVS 600  
DB 541 DYHSTKCLKKQVLVAVENTALAMEIKVCDGQEHVTVSLRDGEATLEVDGTRGSEVS 600  
QY 601 AAQLOERLAVLERHLRSPVLTFAGGLPDVPTVSAPVTAFYRCGMLTVNRLLDDEAAY 660  
DB 601 AAQLOERLAVLERHLRSPVLTFAGGLPDVPTVSAPVTAFYRCGMLTVNRLLDDEAAY 660  
QY 661 KHSDDITAHSCPVEPAA 678  
DB 661 KHSDDITAHSCPVEPAA 678  
RESULT 8  
ADN60275  
ID ADN60275 standard; protein; 678 AA.  
AC ADN60275;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Human growth arrest-specific 6 (GAS6) protein.  
XX  
KW angiogenesis modulator; tumorigenesis modulator; angiogenesis; Axl;  
KW tubulin cofactor D; transglutaminase 2; cytosine deaminase;  
KW peptidase M41; paraplegin; CD13 aminopeptidase; PKP-1; zip kinase; Gas6;  
KW Srm160; non-muscle myosin heavy chain; calmodulin 2; symporter;  
KW semaphorin; zinc finger helixase; plexin-A2; deoxycytidylate deaminase;  
KW sugar transporter; tumorigenesis; antiangiogenic; cytoskeletal;  
KW cerebroprotective; vasotrophic; antiinfectility; cardiac;

KM antibody therapy; antisense therapy; RNA interference therapy;  
 KM RNAi therapy; cancer; stroke; infertility; heart disease; human.  
 OS Homo sapiens.  
 XX  
 PN WO2004039955-A2.  
 XX  
 PD 13-MAY-2004.  
 XX  
 PF 29-OCT-2003; 2003WO-US034281.  
 XX  
 PR 29-OCT-2002; 2002US-0421989P.  
 PR 17-OCT-2003; 2003US-0512251P.  
 XX  
 PA (RIGE-) RIGEL PHARM INC.  
 PI Lorens JB, Atchison RE, Friera A, Holland S;  
 XX WPI; 2004-376181/35.  
 DR N-PSDB; ADN60274.  
 XX  
 PT Identifying a compound that modulates angiogenesis or tumorigenesis,  
 PT useful in diagnosing and treating angiogenesis, cancer, stroke,  
 PT infertility and heart disease, comprises contacting the compound with  
 PT angiogenesis polypeptide.  
 XX  
 PS Disclosure; Page 65; 105pp; English.  
 XX  
 CC The present invention describes a method for identifying a compound that  
 CC modulates angiogenesis or tumorigenesis. The method comprises: (a)  
 CC contacting the compound with angiogenesis polypeptide, e.g. Ax1, tubulin  
 CC cofactor D, transglutaminase 2, cytosine deaminase, peptidase M41  
 CC (paraplegin), CD13 aminopeptidase, PPK-1, zip kinase, Gas6, Srm160, non-  
 CC muscle myosin heavy chain, calmodulin 2, novel symporter, novel  
 CC semaphorin, novel zinc finger helixase (FLJ22611), plexin-A2,  
 CC deoxycytidylate deaminase or novel sugar transporter; (b) determining the  
 CC functional effector of the compound upon the angiogenesis polypeptide or  
 CC the physical effect of the compound upon the target polypeptide or  
 CC fragment or inactive variant; and (c) determining the chemical or  
 CC phenotypic effect of the compound upon a cell comprising the target  
 CC polypeptide or its fragment or inactive variant, thus identifying a  
 CC compound that modulates cell cycle arrest. Also described is a method of  
 CC modulating angiogenesis in a subject. The angiogenesis or tumorigenesis  
 CC modulating compound has antiangiogenic, cytostatic, cerebroprotective,  
 CC vasotropic, antifertility and cardiac activities, and can be used in  
 CC antibody, antisense and RNA interference (RNAi) therapies. The method is  
 CC useful in identifying a compound that modulates angiogenesis. The methods  
 CC and compounds or compositions are useful in diagnosing and treating  
 CC angiogenesis, cancer, stroke, infertility and heart disease. The present  
 CC sequence represents a human growth arrest-specific 6 (GAS6) protein,  
 CC which is used in the exemplification of the present invention.  
 XX  
 XX Sequence 678 AA:  
 Query Match 98.7%; Score 3628; DB 8; Length 678;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-244;  
 Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 ECLQRCGEYCVNPSGSYTCHCDGRGGLKLSQDMDCEDILPCVPFSVAKSVKSLYLGRM 300  
 DB 241 ECLQRCGEYCVNPSGSYTCHCDGRGGLKLSQDMDCEDILPCVPFSVAKSVKSLYLGRM 300  
 QY 301 FSGTPVIRLRFKRLQPTRLVAEPDFRTFDEGILLFAGHQDSTWIVLALRAGLELQLR 360  
 DB 301 FSGTPVIRLRFKRLQPTRLVAEPDFRTFDEGILLFAGHQDSTWIVLALRAGLELQLR 360  
 QY 361 YNGVGRYTSAGPYVNHGMQOTISVEELARNLVVKWMDAVKIAVAQDLFQPEGLYHLN 420  
 DB 361 YNGVGRYTSAGPYVNHGMQOTISVEELARNLVVKWMDAVKIAVAQDLFQPEGLYHLN 420  
 QY 421 LTVGGIPFHEKDLVQPINPLDGMRSMMNLNGEDTTIOETVKNTSMOCQSVTERSGFY 480  
 DB 421 LTVGGIPFHEKDLVQPINPLDGMRSMMNLNGEDTTIOETVKNTSMOCQSVTERSGFY 480  
 QY 481 PGSGFAFYSLDYWRTPLDVGTSTWEVVAHIRPAADTVLPALMAPDLRAVPLSVALV 540  
 DB 481 PGSGFAFYSLDYWRTPLDVGTSTWEVVAHIRPAADTVLPALMAPDLRAVPLSVALV 540  
 QY 541 DYHSTKKLKKQVYVLAVERHALMEIKVCDGQEHVTVSLRDGEATLEVDTGRGSEVS 600  
 DB 541 DYHSTKKLKKQVYVLAVERHALMEIKVCDGQEHVTVSLRDGEATLEVDTGRGSEVS 600  
 QY 601 AAQLOERLAVLERHLSPLVTFAGGLPDVPVTSAPVAFYRGCMTLEVNRLLDLDEAY 660  
 DB 601 AAQLOERLAVLERHLSPLVTFAGGLPDVPVTSAPVAFYRGCMTLEVNRLLDLDEAY 660  
 QY 661 KHSIDITAHSCPPVEPAAA 678  
 DB 661 KHSIDITAHSCPPVEPAAA 678

RESULT 9  
 ADT91779  
 ID ADT91779 standard; protein; 678 AA.  
 XX  
 AC ADT91779;  
 DT 13-JAN-2005 (first entry)  
 XX  
 DE Human GAS6 polypeptide #1.  
 XX  
 KM Human; GAS6; osteoarthritis; OA; receptor tyrosine kinase; antiarthritic;  
 KM osteopathic.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO2004092735-A2.  
 XX  
 PD 28-OCT-2004.  
 XX  
 PF 16-APR-2004; 2004WO-EP004052.  
 XX  
 PR 18-APR-2003; 2003US-0463935P.  
 XX  
 PA (NOVS ) NOVARTIS AG.  
 PA (NOVS ) NOVARTIS PHARMA GMBH.  
 PI Daouti S, Kumar CS, Latario BJ;  
 XX  
 DR WPI; 2004-758393/74.  
 DR N-PSDB; ADT91780.  
 XX  
 PT Identifying a compound for treating osteoarthritis (OA) comprises  
 PT contacting a test compound to a reaction mixture that comprises a  
 PT polypeptide member of the TYRO3 subfamily of receptor tyrosine kinases  
 PT and a ligand to the polypeptide.  
 XX  
 PS Claim 6; SEQ ID NO 3; 101pp; English.  
 PS  
 CC The invention relates to a method of identifying a compound for treating

osteoarthritis (OA) comprising contacting a test compound to a reaction mixture that comprises a polypeptide member of the TNF $\alpha$  subfamily of receptor tyrosine kinases and a ligand to the polypeptide, where the reaction mixture conditions permit binding of the polypeptide to the ligand to form a binding complex, detecting levels of formation of the binding complex in the reaction mixture in the presence of the test compound, and comparing the level of the binding complex formed in the presence of the test compound to the level of binding complex formed in the absence of the test compound, where a decrease in the level of the binding complex formed in the presence of the test compound indicates that the test compound may be used to treat OA. The invention also relates to a method for treating, preventing or ameliorating OA and a method of identifying an individual having OA, comprising detecting a TNF $\alpha$  polypeptide in a biological sample derived from the individual and comparing the level of the TNF $\alpha$  polypeptide in the individual to levels of the TNF $\alpha$  polypeptide in individuals not having OA, where elevated levels of the TNF $\alpha$  polypeptide in the biological sample derived from the individual indicates that the individual has OA. The method is useful for the development of drugs for treating osteoarthritis. This sequence represents a human Gas6 polypeptide of the invention.

Sequence 678 AA;

Query Match 98.7%; Score 3628; DB 8; Length 678;

Best Local Similarity 100.0%; Pred. No. 1.3e-244; Indels 0; Gaps 0; Matches 678; Conservative 0; Mismatches 0;

1 MAPSLSPGPAALRRAPQLLLLLLAECALALLPAREATQFLRPRORRAFOVEEAKQGH 60  
 1 MAPSLSPGPAALRRAPQLLLLLLAECALALLPAREATQFLRPRORRAFOVEEAKQGH 60  
 61 LERECVEELCSREAREVFNDEPETYFPYRIYDCINKKSGPTTKSGFATCYONLPDCC 120  
 61 LERECVEELCSREAREVFNDEPETYFPYRIYDCINKKSGPTTKSGFATCYONLPDCC 120  
 121 TNPDCDRKGTQACODLMGNFCLCKAGMGARLCKDKVNECSQENGSCLOICNNKPSGFC 180  
 121 TNPDCDRKGTQACODLMGNFCLCKAGMGARLCKDKVNECSQENGSCLOICNNKPSGFC 180  
 181 SCHSGFELSSDRTCCDIDECADSEACGAEARCKNLPGSYSCLCDEGFAVSSQKACRDV 240  
 181 SCHSGFELSSDRTCCDIDECADSEACGAEARCKNLPGSYSCLCDEGFAVSSQKACRDV 240  
 241 ECLQGRCEQVNCSSSYTCHCDGRGLTISQMDTCEDILPCVPPSVKSVSLYIGM 300  
 241 ECLQGRCEQVNCSSSYTCHCDGRGLTISQMDTCEDILPCVPPSVKSVSLYIGM 300  
 301 FSGTPYIRLRFRKRLQPTRLVAEFDFTPEEGILLFAGGHODSTWIVALLRAGRLQLQR 360  
 301 FSGTPYIRLRFRKRLQPTRLVAEFDFTPEEGILLFAGGHODSTWIVALLRAGRLQLQR 360  
 361 YNGVGVTSSGPIVNHGMQTTISVEELARNLVIKNRDAVMKIAVAGDLFQPERGILYHNL 420  
 361 YNGVGVTSSGPIVNHGMQTTISVEELARNLVIKNRDAVMKIAVAGDLFQPERGILYHNL 420  
 421 LTVGGIPRFEKDLVQPINPLDGMKSMNLNEDDTTIGTVKNTRMQGFSTERSGF 480  
 421 LTVGGIPRFEKDLVQPINPLDGMKSMNLNEDDTTIGTVKNTRMQGFSTERSGF 480  
 481 PGSGFAFYSLDVNRTPLDVGTSTWEVEVAHTRPADTGVLPALNAPDLRAVPLSVALV 540  
 481 PGSGFAFYSLDVNRTPLDVGTSTWEVEVAHTRPADTGVLPALNAPDLRAVPLSVALV 540  
 541 DYHSTKKLKKQVLVAERTALALMEIKVCDGGEHVVTSLRGCEATLEVDGTRGSGSEVS 600  
 541 DYHSTKKLKKQVLVAERTALALMEIKVCDGGEHVVTSLRGCEATLEVDGTRGSGSEVS 600  
 601 AAOLORLAVLREHLSPVLTFAAGLPDVPTSAVTAFAFGCMTELVNRRLLDLDEAAY 660  
 601 AAOLORLAVLREHLSPVLTFAAGLPDVPTSAVTAFAFGCMTELVNRRLLDLDEAAY 660  
 661 KHSIDTAHSCPVEPAAA 678  
 661 KHSIDTAHSCPVEPAAA 678

DB 661 KHSIDTAHSCPVEPAAA 678

RESULT 10

ADV91450

ID ADV91450 standard; protein; 678 AA.

ADV91450;

10-MAR-2005 (first entry)

Human growth arrest specific gene 6 (Gas6) polypeptide.

Growth arrest specific gene 6; Gas6; cardiovascular disease; cancer;

atherosclerosis; sepsis; glomerulosclerosis; diabetes;

rheumatoid arthritis; HIV infection; osteoarthritis; osteoporosis;

multiple sclerosis; cardiovascular-gen.; antineutrotic; antiarthritis;

anti-HIV; cytotoxic; neuroprotective; thrombolytic; cardiac;

cerebroprotective; vasotropic; antiarteriosclerotic; antibacterial;

immunosuppressive; nephrotropic; antidiabetic; osteopathic;

antibody production.

Homo sapiens.

WO2004108748-A2.

24-SEP-2003; 2003WO-US029909.

24-SEP-2002; 2002US-0413250P.

(CENZ) CENTOCOR INC.

Yang J, Heavner G, Jordan R, Sweet RW;

WPI; 2005-031655/03.

Novel human growth arrest specific polypeptide-6, useful for generating

antibodies against growth arrest specific polypeptide-6, and for treating

cardiovascular, rheumatoid arthritis, HIV infection, leukemia, multiple

sclerosis.

Example 2; SEQ ID NO 1; 107pp; English.

The invention relates to an isolated human growth arrest specific gene 6

(Gas6) polypeptide. The invention also relates to a recombinant DNA

molecule encoding the polypeptide, an antibody or antigen binding

fragment capable of binding to the polypeptide and a labeled antibody

generated against Gas6. The Gas6 polypeptide is useful for generating

antibodies against Gas6, which involves immunization with the polypeptide

or screening recombinant antibodies with the polypeptide. The antibodies

are useful for detecting Gas6 polypeptide in a sample suspected of

containing Gas6. Compositions containing the polypeptide are useful for

preventing or treating cardiovascular diseases resulting from a

dysfunction in a mammal. The compositions are also useful for treating

cancer, atherosclerosis, sepsis, glomerulosclerosis, diabetes, rheumatoid

arthritis, HIV infection, osteoarthritis, osteoporosis and multiple

sclerosis. This sequence represents the human Gas6 polypeptide of the

invention.

Sequence 678 AA;

Query Match 98.7%; Score 3628; DB 9; Length 678;

Best Local Similarity 100.0%; Pred. No. 1.3e-244; Indels 0; Gaps 0;

Matches 678; Conservative 0; Mismatches 0;

1 MAPSLSPGPAALRRAPQLLLLLLAECALALLPAREATQFLRPRORRAFOVEEAKQGH 60  
 1 MAPSLSPGPAALRRAPQLLLLLLAECALALLPAREATQFLRPRORRAFOVEEAKQGH 60  
 61 LERECVEELCSREAREVFNDEPETYFPYRIYDCINKKSGPTTKSGFATCYONLPDCC 120  
 61 LERECVEELCSREAREVFNDEPETYFPYRIYDCINKKSGPTTKSGFATCYONLPDCC 120

Db 61 LERECVELCSREAREVEFENDPETDYFPRYLDCINKSGSPYTKNSGFATCVONLPDQC 120  
 QY 121 TPNPCDRKGTQACODLMGNFFCLCKAGWGRLCDKDVNECSQENGGCLQICHNPGSFHC 180  
 Db 121 TPNPCDRKGTQACODLMGNFFCLCKAGWGRLCDKDVNECSQENGGCLQICHNPGSFHC 180  
 QY 181 SCHSGFELSSDGRTCODIDECADSEACGEARCKNLPGSYSLCDEGFAYSSQEKACRDVD 240  
 Db 181 SCHSGFELSSDGRTCODIDECADSEACGEARCKNLPGSYSLCDEGFAYSSQEKACRDVD 240  
 QY 241 ECLQGRCEQYCVNSPGSYTCHCDGRGGLKLSQDMTDCEDILPCVPFSAKSVKSLYIGRM 300  
 Db 241 ECLQGRCEQYCVNSPGSYTCHCDGRGGLKLSQDMTDCEDILPCVPFSAKSVKSLYIGRM 300  
 QY 301 FSGTPIRLRFRKLOPTRLVAEFPDPTDEGILLFAGGHQDSTWIVLALRAGRLBLQLR 360  
 Db 301 FSGTPIRLRFRKLOPTRLVAEFPDPTDEGILLFAGGHQDSTWIVLALRAGRLBLQLR 360  
 QY 361 YNGVGRVTSAGPVINHGMMQTIISVEELARNLVIKNRDAVMKIAVAGDLFQPERGLYHLN 420  
 Db 361 YNGVGRVTSAGPVINHGMMQTIISVEELARNLVIKNRDAVMKIAVAGDLFQPERGLYHLN 420  
 QY 421 LTVGGIIPFHEKDLVQPINRPLDGCMSNMNLNGEDTTIOETVKNVTMOCFSYTERGSFY 480  
 Db 421 LTVGGIIPFHEKDLVQPINRPLDGCMSNMNLNGEDTTIOETVKNVTMOCFSYTERGSFY 480  
 QY 481 PGSGFAFYSLDYMRTPLDVGSTWEEVVAHIRPAADTGVLPALMAPDLRAVPLSVALV 540  
 Db 481 PGSGFAFYSLDYMRTPLDVGSTWEEVVAHIRPAADTGVLPALMAPDLRAVPLSVALV 540  
 QY 541 DYHSTKKLKKQVLVAVEHTALAMEIKVCDGQEHVTVSLRGEATLEVDGTRGQSEVS 600  
 Db 541 DYHSTKKLKKQVLVAVEHTALAMEIKVCDGQEHVTVSLRGEATLEVDGTRGQSEVS 600  
 QY 601 AAQLOERLAVLBERHLSPVLTFAAGLPDVYTSAPVTAFFRGCMTELVNRRLDLDBAAY 660  
 Db 601 AAQLOERLAVLBERHLSPVLTFAAGLPDVYTSAPVTAFFRGCMTELVNRRLDLDBAAY 660  
 QY 661 KHSDDITAHSCPVEPAAA 678  
 Db 661 KHSDDITAHSCPVEPAAA 678

RESULT 11  
 AEE87023  
 ID AEE87023 standard; protein; 678 AA.  
 AC AEE87023;  
 DT 23-FEB-2006 (first entry)  
 DE Human chemotherapy response-related protein Segid107.  
 KW Chemotherapy; cancer; cytostatic; gene therapy; pharmaceutical;  
 KW breast tumor; diagnostic; prognosis.  
 OS Homo sapiens.  
 PN MO2005119260-A2.  
 PD 15-DEC-2005.  
 PF 30-MAY-2005; 2005MO-EP005787.  
 PR 03-JUN-2004; 2004EP-00013107.  
 PA (FARB) BAYER HEALTHCARE AG.  
 PI Munnes M;  
 DR MPI: 2006-047692/05.  
 DR N-PSDB; AEE86958.  
 XX

PT Investigating response to anti-cancer chemotherapy comprises determining  
 PT the expression level of gene(s) of interest in a biopsy sample.  
 XX  
 PS Disclosure; SEQ ID NO 107; 248bp; English.  
 XX  
 CC This invention relates to a novel method of investigating response to  
 CC anti-cancer chemotherapy. The method comprises determining, in a biopsy  
 CC sample taken from a neoplastic lesion after the onset of a chemotherapy  
 CC schedule, the expression level of up to 65 genes included in the  
 CC specification. The invention may be useful for the development of  
 CC compounds with a cytostatic activity whilst the disclosed sequences may  
 CC prove useful for gene therapy. The method is useful for investigating  
 CC response to anti-cancer chemotherapy. The method, composition, and kit  
 CC are useful for predicting, diagnosing, prognosing, preventing, and  
 CC treating malignant neoplasia and breast cancer. The present sequence is  
 CC that of the protein encoded by a human gene related to the response to  
 CC cancer chemotherapy. The gene was claimed for use in the method of the  
 CC invention.  
 CC  
 XX  
 SO Sequence 678 AA:

Query Match 98.7%; Score 3628; DB 10; Length 678;  
 Best Local Similarity 100.0%; Pred. No. 1,3e-244;  
 Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPSLSPGPAALRAPOLLILLALBACALAAALPAREATQFLRRORARQVFEAKQGH 60  
 Db 1 MAPSLSPGPAALRAPOLLILLALBACALAAALPAREATQFLRRORARQVFEAKQGH 60  
 QY 61 LERECVELCSREAREVEFENDPETDYFPRYLDCINKSGSPYTKNSGFATCVONLPDQC 120  
 Db 61 LERECVELCSREAREVEFENDPETDYFPRYLDCINKSGSPYTKNSGFATCVONLPDQC 120  
 QY 121 TPNPCDRKGTQACODLMGNFFCLCKAGWGRLCDKDVNECSQENGGCLQICHNPGSFHC 180  
 Db 121 TPNPCDRKGTQACODLMGNFFCLCKAGWGRLCDKDVNECSQENGGCLQICHNPGSFHC 180  
 QY 181 SCHSGFELSSDGRTCODIDECADSEACGEARCKNLPGSYSLCDEGFAYSSQEKACRDVD 240  
 Db 181 SCHSGFELSSDGRTCODIDECADSEACGEARCKNLPGSYSLCDEGFAYSSQEKACRDVD 240  
 QY 241 ECLQGRCEQYCVNSPGSYTCHCDGRGGLKLSQDMTDCEDILPCVPFSAKSVKSLYIGRM 300  
 Db 241 ECLQGRCEQYCVNSPGSYTCHCDGRGGLKLSQDMTDCEDILPCVPFSAKSVKSLYIGRM 300  
 QY 301 FSGTPIRLRFRKLOPTRLVAEFPDPTDEGILLFAGGHQDSTWIVLALRAGRLBLQLR 360  
 Db 301 FSGTPIRLRFRKLOPTRLVAEFPDPTDEGILLFAGGHQDSTWIVLALRAGRLBLQLR 360  
 QY 361 YNGVGRVTSAGPVINHGMMQTIISVEELARNLVIKNRDAVMKIAVAGDLFQPERGLYHLN 420  
 Db 361 YNGVGRVTSAGPVINHGMMQTIISVEELARNLVIKNRDAVMKIAVAGDLFQPERGLYHLN 420  
 QY 421 LTVGGIIPFHEKDLVQPINRPLDGCMSNMNLNGEDTTIOETVKNVTMOCFSYTERGSFY 480  
 Db 421 LTVGGIIPFHEKDLVQPINRPLDGCMSNMNLNGEDTTIOETVKNVTMOCFSYTERGSFY 480  
 QY 481 PGSGFAFYSLDYMRTPLDVGSTWEEVVAHIRPAADTGVLPALMAPDLRAVPLSVALV 540  
 Db 481 PGSGFAFYSLDYMRTPLDVGSTWEEVVAHIRPAADTGVLPALMAPDLRAVPLSVALV 540  
 QY 541 DYHSTKKLKKQVLVAVEHTALAMEIKVCDGQEHVTVSLRGEATLEVDGTRGQSEVS 600  
 Db 541 DYHSTKKLKKQVLVAVEHTALAMEIKVCDGQEHVTVSLRGEATLEVDGTRGQSEVS 600  
 QY 601 AAQLOERLAVLBERHLSPVLTFAAGLPDVYTSAPVTAFFRGCMTELVNRRLDLDBAAY 660  
 Db 601 AAQLOERLAVLBERHLSPVLTFAAGLPDVYTSAPVTAFFRGCMTELVNRRLDLDBAAY 660  
 QY 661 KHSDDITAHSCPVEPAAA 678  
 Db 661 KHSDDITAHSCPVEPAAA 678

RESULT 12  
ADD48757  
ID ADD48757 standard; protein; 679 AA.  
XX  
AC ADD48757;  
XX  
DT 02-DEC-2004 (revised)  
DT 29-JAN-2004 (first entry)  
XX  
DE Human Protein L13720, SEQ ID NO 14467.  
XX  
KW Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SN1; Chung.  
XX  
OS Homo sapiens.  
OS Unidentified.  
XX  
PN WO2003016475-A2.  
XX  
PD 27-FEB-2003.  
XX  
PE 14-AUG-2002; 2002WO-US025765.  
XX  
PR 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-033347P.  
XX  
PA (GENO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX  
PI Woolf C, D'urso D, Befort K, Costigan M;  
XX  
DR MPI; 2003-268312/26.  
XX  
GENSENK; L13720.  
XX  
PT New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
PS Example 1; Page; 1017p; English.  
XX  
XX The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SN1)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (described in Table 3  
CC of the specification) which is differentially expressed during pain.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 679 AA;  
XX

Query Match

98.7%; Score 3628; DB 7; Length 679;

Best Local Similarity 100.0%; Pred. No. 1,3e-244;  
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPSLSPGPAALRRAPOLLILLILAAECALAAALPAREATQFRRPORAFOVFEKKQKH 60  
DB 1 MAPSLSPGPAALRRAPOLLILLILAAECALAAALPAREATQFRRPORAFOVFEKKQKH 60  
QY 61 LERECVEELCSREAREVFENDPETDYFYPRYLDCINKYSGPYTKNSGFATCVNLPDQC 120  
DB 61 LERECVEELCSREAREVFENDPETDYFYPRYLDCINKYSGPYTKNSGFATCVNLPDQC 120  
QY 121 TPNPCDRKGTQACODLMGNFCLCAWNGRILCDXDVNCSOENGGCLOICHNKKGSPFC 180  
DB 121 TPNPCDRKGTQACODLMGNFCLCAWNGRILCDXDVNCSOENGGCLOICHNKKGSPFC 180  
QY 181 SCHSGFELSSDRTQODIDECDASACGEARKCNLPGSYSCLCDGFAYSOEXACRDVD 240  
DB 181 SCHSGFELSSDRTQODIDECDASACGEARKCNLPGSYSCLCDGFAYSOEXACRDVD 240  
QY 241 ECLGRCBQVCVNSPGSYTCHCDGRGGLKLSQDMOTCEDILPCVPFSAKSVKSLYLGRM 300  
DB 241 ECLGRCBQVCVNSPGSYTCHCDGRGGLKLSQDMOTCEDILPCVPFSAKSVKSLYLGRM 300  
QY 301 FSGTPVIRLRFRRLOPTRLVAEFDRFTDPBGILLFAGGHODSTWIVLALRAGRLEQLR 360  
DB 301 FSGTPVIRLRFRRLOPTRLVAEFDRFTDPBGILLFAGGHODSTWIVLALRAGRLEQLR 360  
QY 361 YNGVGRVYSSGPVINVHGMQVTSVEELARNIVYKXNRDVMKIAVAGDLFOBERGLYHLN 420  
DB 361 YNGVGRVYSSGPVINVHGMQVTSVEELARNIVYKXNRDVMKIAVAGDLFOBERGLYHLN 420  
QY 421 LTVGGIPFHEKDLVOPINPRLDGCMRSNMWNLGEBDTTIOETVKVNTRMQCFSTERGSPY 480  
DB 421 LTVGGIPFHEKDLVOPINPRLDGCMRSNMWNLGEBDTTIOETVKVNTRMQCFSTERGSPY 480  
QY 481 PGSGPAFYSLDYMRTPLDVGSTWEEVVAHIRPAADTGVFALMAAPLRAVPLSVALY 540  
DB 481 PGSGPAFYSLDYMRTPLDVGSTWEEVVAHIRPAADTGVFALMAAPLRAVPLSVALY 540  
QY 541 DYHSTKKLKKOLVLAVENTALAMEIKVCDQOEHVTVSLRDGEATLEVDGTRGSEVS 600  
DB 541 DYHSTKKLKKOLVLAVENTALAMEIKVCDQOEHVTVSLRDGEATLEVDGTRGSEVS 600  
QY 601 AAQOLERLAVLEBRLRSPLYTFAGGLPDVPTSAPTYAFYRCMTLENNRLLDDEAY 660  
DB 601 AAQOLERLAVLEBRLRSPLYTFAGGLPDVPTSAPTYAFYRCMTLENNRLLDDEAY 660  
QY 661 KHSIDITAHSCPVEPAA 678  
DB 661 KHSIDITAHSCPVEPAA 678

## RESULT 13

ADQ67207  
ID ADQ67207 standard; protein; 624 AA.XX  
AC ADQ67207;  
XXDT 07-OCT-2004 (first entry)  
XXDE Novel human protein sequence #2180.  
XXKW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;  
XXKW gene therapy; diagnostic marker; morbid state; osteoporosis;  
XXKW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;  
XXOS Homo sapiens.  
XXPN EP1440981-A2.  
XXPD 28-JUL-2004.  
XX



PF 21-JAN-2004; 2004EP-00001196.  
 XX  
 XX 21-JAN-2003; 2003JP-00102206.  
 PR 09-MAY-2003; 2003JP-00131392.  
 XX  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 PI Isegaal T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
 PI Yamamoto J, Iseono Y, Nagai K, Irie R;  
 XX WPI; 2004-53376/52.  
 DR N-PSDB; AD065019.  
 XX  
 PT Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,  
 PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.  
 XX  
 PS Claim 1; SEQ ID NO 4366; 2449bp; English.  
 XX  
 XX The invention relates to 2495 novel polynucleotides (I) and their encoded  
 CC polypeptides, sequences hybridizing to these nucleotides, sequences  
 CC encoding partial polypeptides and sequences having 70% or 90% identity to  
 CC the nucleotide and protein sequences. The nucleotides and polypeptides  
 CC are useful as diagnostic markers or therapeutic target for the diseases  
 CC or morbid states. They are also useful for treating osteoporosis,  
 CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,  
 CC dementia and various cancers. This sequence corresponds to a protein  
 CC sequence of the invention.  
 XX  
 XX Sequence 624 AA;  
 SQ  
 Query Match 85.6%; Score 3146; DB 8; Length 624;  
 Best Local Similarity 99.8%; Pred. No. 5.5e-211;  
 Matches 584; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 94 DCNKGSPPTKNSGATCQVNPDOCTPNCORRGTQACODLGMNFFCLCKAGWGRLC 153  
 DB 40 NCINKYSGPYTKNSGATCQVNPDOCTPNCORRGTQACODLGMNFFCLCKAGWGRLC 99  
 QY 154 DKDVNCSQENGGCLOICHNKPGSFHCSGSELSGRTCODIDECADSEAGERRC 213  
 DB 100 DKDVNCSQENGGCLOICHNKPGSFHCSGSELSGRTCODIDECADSEAGERRC 159  
 QY 214 NLEPGYSCLCDEGFAVSSQEKACRDVDECLQGRCEQCVNPSPSYTCDCGRGGLKLSQD 273  
 DB 160 NLEPGYSCLCDEGFAVSSQEKACRDVDECLQGRCEQCVNPSPSYTCDCGRGGLKLSQD 219  
 QY 274 MDTCEIILPCVPSVAKSVKSLYLGRMFSGTPVIRLRFKQLQPTRLVAEPDFPTPEGI 333  
 DB 220 MDTCEIILPCVPSVAKSVKSLYLGRMFSGTPVIRLRFKQLQPTRLVAEPDFPTPEGI 279  
 QY 334 LLEFAGGHODSTWVLLRAGRLLOLRVNGVGRVTSGGPYNHGMOTTSVEELARLVY 393  
 DB 280 LLEFAGGHODSTWVLLRAGRLLOLRVNGVGRVTSGGPYNHGMOTTSVEELARLVY 339  
 QY 394 KVNRAVMKIAVAGDLFOBERGLYHNLTVGGIPFHEKDLVOPINRLDCMSNMWLG 453  
 DB 340 KVNRAVMKIAVAGDLFOBERGLYHNLTVGGIPFHEKDLVOPINRLDCMSNMWLG 399  
 QY 454 EDTTIOETVKVNTMOCFSYTERGSPYPSGFAFSLDYKRTPLDVGTSETEVEVAHI 513  
 DB 400 EDTTIOETVKVNTMOCFSYTERGSPYPSGFAFSLDYKRTPLDVGTSETEVEVAHI 459  
 QY 514 RPAADTGVLPALWAPDLRAVPLSVLVDSYHSTKLLKKOLVLAVENTALALMEIKYCDQ 573  
 DB 460 RPAADTGVLPALWAPDLRAVPLSVLVDSYHSTKLLKKOLVLAVENTALALMEIKYCDQ 519  
 QY 574 EHVVTVSLRDEATLEVDGTGSGSEVSAQLOERLAVLERHLSPVLTFAAGLPDVPVTS 633  
 DB 520 EHVVTVSLRDEATLEVDGTGSGSEVSAQLOERLAVLERHLSPVLTFAAGLPDVPVTS 579  
 QY 634 APVTAFFRCMTLENNRRLDLDEAAVYKISDITFAHSCPPVEPAAA 678  
 DB 580 APVTAFFRCMTLENNRRLDLDEAAVYKISDITFAHSCPPVEPAAA 624

RESULT 14  
 AAM46462  
 ID AAM46462 standard; protein; 673 AA.  
 XX  
 AC AAM46462;  
 XX  
 DT 15-MAY-1998 (first entry)  
 XX  
 DE Murine growth arrest specific-gene 6 (gas6) protein.  
 XX  
 KM Growth arrest specific-gene 6; gas6; Raa; Axl; receptor; mitogenic agent;  
 KM receptor tyrosine kinase; regulation; protease cascade; insulin;  
 KM growth regulation; serum-free culture medium; human; Schwann cell;  
 KM receptor activator; erbB receptor; heregulin; cAMP level; proliferation;  
 KM treatment; nervous system injury.  
 XX  
 OS Mus sp.  
 XX  
 PN US5714385-A.  
 XX  
 PD 03-FEB-1998.  
 XX  
 PF 10-MAY-1995; 95US-00435434.  
 XX  
 PR 10-MAY-1995; 95US-00435434.  
 XX  
 PA (GENTH ) GENENTECH INC.  
 XX  
 PI Chen J, Mather JP, Li R;  
 XX  
 DR WPI; 1998-129864/12.  
 XX  
 PT Medium for culturing human Schwann cells - is serum-free and contains Rse  
 PT receptor activator and other mitogens.  
 XX  
 PS Disclosure; Fig 2; 51pp; English.  
 XX  
 CC The present sequence represents a murine growth arrest specific-gene 6  
 CC (gas6) protein which is able to activate the Rsa and Axl receptor. Rse is  
 CC a receptor tyrosine kinase that is preferentially expressed in the adult  
 CC brain. Gas6 is a vitamin K dependent protein which may play a role in the  
 CC regulation of a protease cascade relevant in growth regulation. The  
 CC protein is used in a serum-free culture medium for culturing human  
 CC Schwann cells, which does not support fibroblast growth. Gas6 functions  
 CC as a mitogenic agent which is a Rse/Axl receptor activator. A second  
 CC mitogenic agent e.g. insulin or an erbB receptor activator such as  
 CC heregulin, is also required to raise cAMP levels and enhance survival or  
 CC proliferation of human Schwann cells. The culture medium additionally  
 CC comprises a molecule or composition that provides Fe ions to the Schwann  
 CC cells, vitamin E, a protease inhibitor, and progesterone. The Schwann  
 CC cells can be used to treat patients with nervous system injuries  
 XX  
 SQ Sequence 673 AA;  
 Query Match 80.4%; Score 2955.5; DB 2; Length 673;  
 Best Local Similarity 81.6%; Pred. No. 1.2e-197;  
 Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;  
 QY 7 PCPAARARAPOLLILLIAECALALLPAREATQFLRPPORARFOVEEAKOHLRECV 66  
 DB 5 PCPAA-ALGTALLILLIAESSITVLLRREAQFLRPPORARFOVEEAKOHLRECV 63  
 QY 67 EELCSREAREVENDPEFDYPPRYLDCINKYSGPYTKNSGATCQVNPDOCTBNPCD 126  
 DB 64 EELCSREAREVENDPEFDYPPRYLDCINKYSGPYTKNSGATCQVNPDOCTBNPCD 123  
 QY 127 RKGTOACODLGMNFFCLCKAGWGRLCDKDVNCSQENGGCLOICHNKPGSFHCSGSHSP 186  
 DB 124 RKGTHICODLGMNFFCLCKAGWGRLCDKDVNCSQENGGCLOICHNKPGSFHCSGSHSP 183  
 QY 187 ELSDGRTCODIDECADSEAGERRCNPJSGYSCLCDEGFAVSSQEKACRDVDECLQGR 246

Db	184	SLASDGGCTCQDIDETSDTDCDARNCKDIPGSSYCLCBEGYIYSSEKTKCQVDEDCQDR	243
Qy	247	CEQCVANSFGSYTCHCDRGGIKLSQMDMDCEDILPCVPFSAKSVKSLYLGRMFSGTPEV	306
Db	244	CEQTCVANSFGSYTCHCDRGGIKLSRMDMTCEDILPCVPFSAKSVKSLYLGRMFSGTPEV	303
Qy	307	IRLRPKRIQPIRLVAEFDPFRTPDEPGILLFAGGHQDSTWIVLALRAGRLEQLRYNGVR	366
Db	304	IRLRFKRIQPIRLVAEPFRTPDEPGVLLFAGGRSDSTWIVGLRAGRLEQLRYNGVR	363
Qy	367	VTSSGPIVNHGMWQITISVEBELARNIVIKVNRDAWKKIAVAGDLFOBERGLYHNLTVGSI	426
Db	364	ITSSGPIVNHGMWQITISVEBELARNIVIKVNDVAWKKIAVAGELFQLEKGLYHNLTVGSI	423
Qy	427	PFEHKDVLQPIINPRIDGCMRSWNMLNGEDTTIOETVKVNTRMQCFSTVERGSPFYPSGPA	486
Db	424	PFKEBELVQPIINPRIDGCMRSWNMLNGEDSALQETVKATKMQCFSTVERGSPFPNGFA	483
Qy	487	FYSLDYMRTPLDVGESTWEVEVAHIRPADTGVLFALMAPDLRAVPLSVALVDYHSTK	546
Db	484	TYRLNLYRTSLDVGEGTETWEVKVARIIRPATDGVLLALVGDD--DVTISVALVDYHSTK	541
Qy	547	KLKQQLVVLAVENTLALMEIKVCPGQEHVNVVSLRDGEATLLEVDTGRGQSEVSAQLOE	606
Db	542	KLKQQLVVLAVEDVALALMEIKVCSQEHVTVVSLRGEATLLEVDTKGQSEVSTQLOE	601
Qy	607	RLAVERHLRSPVLTFPAGGLPDVPVTSAPVTAFTFYRCMTLEVNRRLLDDEAAVKHSDIT	666
Db	602	RLDTLKTHLQGSVHHYVGGLPPEVSIVASVTAFTFYRCMTLEVNKKLDDTASVKHSDIT	661
Qy	667	AHSCPPVEPA 676	
Db	662	SHSCPPVEHA 671	
RESULT 15			
ID	AAV29793	standard; protein; 673 AA.	
XX	AAV29793;		
AC	AAV29793;		
DT	15-NOV-1999	(first entry)	
XX			
DE		Murine growth arrest-specific gene 6 protein.	
XX			
OS		Rse receptor protein tyrosine kinase; Rse ligand; Rse-L; Gas6;	
XX		growth arrest-specific gene 6; proliferation; differentiation;	
KM		glial cell; Schwann cell; fusion protein.	
XX			
OS		Mus sp.	
XX			
PN		US5955420-A.	
XX			
PD		21-SEP-1999.	
XX			
PF		10-MAY-1995; 95US-00438864.	
XX			
PR		10-MAR-1995; 95US-00402253.	
XX			
PA		(GETH ) GENENTECH INC.	
PI		Mark MR, Mather JP, Li R, Chen J, Hammonds RG, Godowski PJ;	
XX		WPI; 1999-539585/45.	
DR			
XX			
PT		Activation of the Rse receptor on a cell, useful for promoting cell	
XX		proliferation and differentiation.	
PS		Disclosure; Fig 2; 48pp; English.	
CC		A method has been developed for activating the Rse receptor on a cell.	
CC		The method comprises exposing the receptor to the exogenous growth arrest	

CC -specific gene 6 (gas6) polypeptide. The method is useful for enhancing  
CC cell proliferation and cell differentiation. The present sequence  
CC represents murine gas6 given in the present invention  
XX  
SQ Sequence 673 AA;

SQ Sequence 673 AA;

Query Match	80.4%	Score 2955.5	DB 2	Length 673
-------------	-------	--------------	------	------------

Best Local Similarity 81.6%; Pred. No. 1.2e-197;  
Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2

7 PGPAALRRAPQLLLLLLAECALLALLPAREAIQFLRPRKRAQVEEBAQGHLEKCV 88

5 PGPAA-ALGTALLLLASSSHIVLLRAREAQVLRPRQRKAYQVFEANQGNENECV 65

6/ EELCSREAREVFENDPEIDHPRILDCINKIGSPIINNSGFAICVQNDPDCIFNECD 12

DB 64 EEVCSNEAREVFENDPEIEIFIKIUECMANIGFBEENFDTMUCVQNEIQQ.....

09  
12' KNOI QACQBEIN I CECIOFOMOCUCBIC VNECQZLHOCBIF :  
:  
:

**H** **N** **C** **O** **T** **E** **R** **S** **A** **D** **I** **C** **A** **T** **I** **O** **N**

[illegible]

100

Итого: 30

[illegible][illegible]

0. 367 1TMOCCBUTN1CMOCTI SVEFI ABNU VIKMIDPAVKTA VAGDI.FODERGI.YHI.NI.TVGGI 42

364 TTSCTPTNHGMWOTI SVEEI .ERNI.VI KYNKDAVMKI AVAGEL FOL ERGLYHNLTVGGI 42

427 PFHEKDI.VOPTNPRI.DGCMBSWNWLNGETTIOETVKVNTRMOCFSVTERGSFYPSGFA 48

424 PEKESL YOPINPR L D G C M R S W N W L N G E D S A I O E T V K A N T K M O C F S V T E R G S F F P G N G F A 48

OV 487 FYSLDYMRTPLDVGTESTWEVEVAHIRPADTGVLFALWAPDLRAVPLSVALVDYHSTK 54

Db 484 TYRLNYTRTSLDVGTETTWKVKVARIRPATDTGVLALLVGDD--DVVISVALVDYHSTK 54

547 KLKKQLVLAVENTALMEIKVCDGQEHVTVSLRDGEATLEVDGTRGQSEVSAQLOE 60

Db 542 KLKKQLVLAVEDVALALMEIKVCDSQEHVTVSLREGAATLEVDGKQOSEVSTAQLQE 60

607 RLAVLERHLSPLTFAGGLPDVPTSA PVTAFYRGCMILEVNRRLDLDDEAYKHSDI 608

Db 602 RLDLTKTHLQGSVHTYVGGLEPESVISAPVIAFYRGCMLLEVNGKLDDDIASINHSDI 60

667 AHSCPEPA 6/16 QY

Db 662 SHSCPEVEHA 6/1

Search completed: June 29, 2006, 11:10:39

JOB LINE : 0000000000

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OM protein - protein search, using sw model

Run on: June 29, 2006, 11:28:06 ; Search time 188 Seconds  
(without alignments)  
1690.241 Million cell updates/sec

Title: US-10-671-054-1

Perfect score: 3675  
Sequence: 1 MAPSLSPGPAALRRAPQLL.....AHSCPVEPAADYKDDDK 686

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_Main:  
1: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US07\_PUBCOMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US08\_PUBCOMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US09\_PUBCOMB.pep:\*  
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6: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3675	100.0	686	US-10-671-054-1	Sequence 1, Appl1
2	3628	98.7	678	US-10-671-054-3	Sequence 3, Appl1
3	3628	98.7	678	US-10-696-909A-41	Sequence 41, Appl1
4	3628	98.7	678	US-10-756-149-4949	Sequence 4949, Ap
5	2955.5	80.4	673	US-10-223-085-48	Sequence 48, Appl
6	2955.5	80.4	673	US-10-223-084-48	Sequence 48, Appl
7	2955.5	80.4	673	US-10-223-088-48	Sequence 48, Appl
8	2955.5	80.4	673	US-10-223-088-48	Sequence 48, Appl
9	2955.5	80.4	673	US-10-223-087-48	Sequence 48, Appl
10	2955.5	80.4	673	US-10-223-083-48	Sequence 48, Appl
11	2955.5	80.4	673	US-10-223-089-48	Sequence 48, Appl
12	2955.5	80.4	673	US-10-223-081-48	Sequence 48, Appl
13	2955.5	80.4	673	US-10-223-082-48	Sequence 48, Appl
14	2955.5	80.4	673	US-10-305-654-48	Sequence 48, Appl
15	2955.5	80.4	673	US-10-081-056-48	Sequence 48, Appl
16	2879	78.3	697	US-10-367-094-31	Sequence 31, Appl
17	2543	69.2	510	US-10-367-094-34	Sequence 34, Appl
18	1547.5	42.1	676	US-10-952-459-30	Sequence 30, Appl
19	1532	41.7	650	US-10-723-860-467	Sequence 467, App
20	359	9.8	1394	US-11-097-143-10302	Sequence 10302, A
21	358.5	9.8	957	US-09-855-824-6	Sequence 6, Appl1
22	358.5	9.8	957	US-10-476-542-6	Sequence 6, Appl1
23	358.5	9.8	997	US-09-747-371-3	Sequence 3, Appl1
24	358.5	9.8	997	US-09-930-512-66	Sequence 66, Appl
25	358.5	9.8	997	US-10-231-813-90	Sequence 90, Appl
26	358.5	9.8	997	US-10-029-020-37	Sequence 37, Appl
27	358.5	9.8	997	US-11-113-424-37	Sequence 37, Appl

28	357.5	9.7	911	3	US-09-855-824-4	Sequence 4, Appl1
29	357.5	9.7	911	5	US-10-476-542-4	Sequence 4, Appl1
30	357.5	9.7	961	3	US-09-930-512-67	Sequence 67, Appl
31	357.5	9.7	961	4	US-10-406-073-13	Sequence 13, Appl
32	357.5	9.7	961	4	US-10-231-913-88	Sequence 88, Appl
33	357.5	9.7	961	4	US-10-029-020-35	Sequence 35, Appl
34	357.5	9.7	961	6	US-11-113-424-35	Sequence 35, Appl
35	354.5	9.6	1587	4	US-10-016-248-77	Sequence 77, Appl
36	354.5	9.6	1587	5	US-10-287-436A-565	Sequence 565, App
37	353.5	9.6	775	4	US-10-016-248-78	Sequence 78, Appl
38	353.5	9.6	888	4	US-10-016-248-75	Sequence 75, Appl
39	353.5	9.6	1354	4	US-10-016-248-32	Sequence 32, Appl
40	353.5	9.6	1356	4	US-10-016-248-30	Sequence 30, Appl
41	353.5	9.6	1425	4	US-10-112-944-315	Sequence 315, App
42	353.5	9.6	1467	4	US-10-016-248-28	Sequence 28, Appl
43	353.5	9.6	1469	4	US-10-016-248-26	Sequence 26, Appl
44	353.5	9.6	1511	4	US-10-016-248-76	Sequence 76, Appl
45	352	9.6	2871	4	US-10-015-115-57	Sequence 57, Appl

## ALIGNMENTS

RESULT 1									
US-10-671-054-1									
; Sequence 1, Application US/10671054									
; Publication No. US20040157774A1									
; GENERAL INFORMATION:									
; APPLICANT: Johnson & Johnson									
; TITLE OF INVENTION: EPITOPE TAGGED RECOMBINANT GROWTH ARREST SPECIFIC GENE 6									
; FILE REFERENCE: GEN-5015USNP									
; CURRENT APPLICATION NUMBER: US/10/671,054									
; PRIOR FILING DATE: 2003-09-24									
; PRIOR APPLICATION NUMBER: 60/413157									
; NUMBER OF SEQ ID NOS: 3									
; SOFTWARE: Patentin version 3.2									
; SEQ ID NO 1									
; LENGTH: 686									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
US-10-671-054-1									
Query Match									
Best Local Similarity 100.0%; Score 3675; DB 4; Length 686;									
Matches 686; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MAPSLSPGPAALRRAPQLLLLLAECALAAALPAREATOTFLRPRORARQVFEBAKQGH	60						
DB	1	MAPSLSPGPAALRRAPQLLLLLAECALAAALPAREATOTFLRPRORARQVFEBAKQGH	60						
QY	61	LEEEVEELCSREAREVEFENDEBTDFYPRYLDCINKYGSPTKNSGFATCVQNLPDQC	120						
DB	61	LEEEVEELCSREAREVEFENDEBTDFYPRYLDCINKYGSPTKNSGFATCVQNLPDQC	120						
QY	121	TPMPCCRKGTQACODIMGNFCLCKAGWGRLLCDKXVNBESQNGCGLQICNKKPSFHC	180						
DB	121	TPMPCCRKGTQACODIMGNFCLCKAGWGRLLCDKXVNBESQNGCGLQICNKKPSFHC	180						
QY	181	SCISGFEISDGTCDIDECADSEAGKRCNKLPGSYCLDEGFAYSSQKACRDVD	240						
DB	181	SCISGFEISDGTCDIDECADSEAGKRCNKLPGSYCLDEGFAYSSQKACRDVD	240						
QY	241	ECLQGRCEOVCVNPSGYSYCHCDRGGLKLSQDMTCEDLPCVPSPVAKSVKSLYLGRM	300						
DB	241	ECLQGRCEOVCVNPSGYSYCHCDRGGLKLSQDMTCEDLPCVPSPVAKSVKSLYLGRM	300						
QY	301	FSGTPVIRLRPRKLOTRLVAEFDFPTDPEGILLFAGGHOSHTWTVALRAGRLQLR	360						
DB	301	FSGTPVIRLRPRKLOTRLVAEFDFPTDPEGILLFAGGHOSHTWTVALRAGRLQLR	360						
QY	361	YNGVGRVTSAGPVINHGMMQTTISVEELARNLVIKVNRDAVMKIAVAGDLFQPERGLYHIN	420						

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Db 361 YNGGVRVSSGPGVINHGMMQTISVEELARNLVIKNRDAVMKIAVAGDLFQGERGLYHLN 420
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Db 421 LTVGGIPFHEKDLVOPINRDLDCNRSNWMNGEDTTIOETVKVNTRMCCFSYTERGSFY 480
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Db 481 PGSGFAFYSLDYMRPLDVGTSTWEEVVAHIRPAADTGVLPALMAPLRAVPISVALY 540
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Qy 601 AAQOERLAVLERHRLRSPVLTFRAGGLPDVPTVSAPVTAFTYRCGNTLEVNRLDLDEAY 660
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## RESULT 2

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US-10-671-054-3
; Sequence 3, Application US/10671054
; Publication No. US20040157744A1
; GENERAL INFORMATION:
; APPLICANT: Johnson & Johnson
; TITLE OF INVENTION: EPITOPE TAGGED RECOMBINANT GROWTH ARREST SPECIFIC GENE 6
; FILE REFERENCE: CEN-5015USNP
; CURRENT APPLICATION NUMBER: US/10/671,054
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: 60/413157
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 678
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-671-054-3
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Query Match 98.7%; Score 3628; DB 4; Length 678;  
Best Local Similarity 100.0%; Pred. No. 7.9e-289;  
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 LRECEVEELCSRBEAREVEFENDEPETYFYPRIYDCINKTGSPTTKNSGFATCVQNLDDC 120
Qy 121 TNPDCDRKGTQACODLMGNFCLCKRAGWGRLCDKDVNCSQENGGCLQICHKPKGSFHC 180
Db 121 TNPDCDRKGTQACODLMGNFCLCKRAGWGRLCDKDVNCSQENGGCLQICHKPKGSFHC 180
Qy 181 SCHSGFELSSDGRTCODIDECADSEACGEARCKNLPGSYSCLCDEGFAYSSOEKACRDV 240
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Db 241 ECLQGRCEQVCVNSPGSYTCHCDGRGGLKLSQDMTCEDLLPCVPPSVAKSVKSLYIGNM 300
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Db 361 YNGGVRVSSGPGVINHGMMQTISVEELARNLVIKNRDAVMKIAVAGDLFQGERGLYHLN 420
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Db 421 LTVGGIPFHEKDLVOPINRDLDCNRSNWMNGEDTTIOETVKVNTRMCCFSYTERGSFY 480
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Db 661 KHSDDITAHSCPVEPAA 678
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## RESULT 3

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US-10-696-909A-41
; Sequence 41, Application US/10696909A
; Publication No. US20050118604A1
; GENERAL INFORMATION:
; APPLICANT: Lorens, James B.
; APPLICANT: Atchison, Robert E.
; APPLICANT: Frieria, Anabella
; APPLICANT: Holland, Sacha
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: Modulators of Angiogenesis and Tumorigenesis
; FILE REFERENCE: 021044-005820US
; CURRENT APPLICATION NUMBER: US/10/696,909A
; CURRENT FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: US 60/512,251
; PRIOR FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US 60/421,989
; PRIOR FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 678
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: growth arrest-specific 6 (GAS6), AXL stimulatory
US-10-696-909A-41
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Query Match 98.7%; Score 3628; DB 5; Length 678;  
Best Local Similarity 100.0%; Pred. No. 7.9e-289;  
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAPSLSPGPAALRRAPQULLLLLAECALALLPAEATQFLRPRORAFVVEEAKQGH 60
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QY 301 FSGTPIVRLRFKRLQPTRLVAEPDFTFDEGILLFAGHQDSTWIVLALRAGRLLEQLR 360  
DB 301 FSGTPIVRLRFKRLQPTRLVAEPDFTFDEGILLFAGHQDSTWIVLALRAGRLLEQLR 360  
QY 361 YNGVGRVTSGGPVINHGMQOTISVEELARNLVIVKNDVAWKIAVADLFQPERGLYHLN 420  
DB 361 YNGVGRVTSGGPVINHGMQOTISVEELARNLVIVKNDVAWKIAVADLFQPERGLYHLN 420  
QY 421 LTVGGIFPHEKDLVQPINPRLDGCMSNMNLNGEDTTIOETVKVNTMQCSYTERGSFY 480  
DB 421 LTVGGIFPHEKDLVQPINPRLDGCMSNMNLNGEDTTIOETVKVNTMQCSYTERGSFY 480  
QY 481 PGSGFAFYSLDYMRTPLDVGTSTWEVEVAHIRPADTGVLFALMAPDLRAVPLSVALV 540  
DB 481 PGSGFAFYSLDYMRTPLDVGTSTWEVEVAHIRPADTGVLFALMAPDLRAVPLSVALV 540  
QY 541 DYHSTKLLKKQVLAVEHTALALMEIKVCDGQEHVTVSLRDGEATLEVDGTRGQSEVS 600  
DB 541 DYHSTKLLKKQVLAVEHTALALMEIKVCDGQEHVTVSLRDGEATLEVDGTRGQSEVS 600  
QY 601 AAQLOERLAVLEHRLSPVLTFAAGLPDVPTSAPTYAFYRGCTMLEVNRRLDLDBAAY 660  
DB 601 AAQLOERLAVLEHRLSPVLTFAAGLPDVPTSAPTYAFYRGCTMLEVNRRLDLDBAAY 660  
QY 661 KHSIDITAHSCPVEPAAA 678  
DB 661 KHSIDITAHSCPVEPAAA 678

## RESULT 4

US-10-756-149-4949  
Sequence 4949, Application US/10756149  
Publication No. US20050181375A1  
GENERAL INFORMATION:  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND  
FILE REFERENCE: file  
CURRENT APPLICATION NUMBER: US/10/756,149  
NUMBER OF SEQ ID NOS: 5818  
SOFTWARE: Patentin version 3.2  
SEQ ID NO 4949  
LENGTH: 678  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-10-756-149-4949

Query Match 98.7%; Score 3628; DB 5; Length 678;  
Best Local Similarity 100.0%; Pred. No. 7, 9e-289;  
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPSISPGPALRRAPQILLILIAECALALIPAREATQFLRPRORAFVFEBAKQGH 60  
DB 1 MAPSISPGPALRRAPQILLILIAECALALIPAREATQFLRPRORAFVFEBAKQGH 60  
QY 61 LERECVEELCSREAREVEENDEPETYFYPRYUDCTNKXGSPYTKSGPATCVQNLDDC 120  
DB 61 LERECVEELCSREAREVEENDEPETYFYPRYUDCTNKXGSPYTKSGPATCVQNLDDC 120  
QY 121 TNPDCRKTQACQDLMGNFPCICRAGWGGRLCDKDVNECSQENGGCLOICHNKPSGPHC 180  
DB 121 TNPDCRKTQACQDLMGNFPCICRAGWGGRLCDKDVNECSQENGGCLOICHNKPSGPHC 180  
QY 181 SCHSGFELSSDGTCTODIDECADSEACGEARCNLPGSYSCLCDEGFAVSSQEKACRDVD 240  
DB 181 SCHSGFELSSDGTCTODIDECADSEACGEARCNLPGSYSCLCDEGFAVSSQEKACRDVD 240

QY 241 ECLQRCBOYCVNSPGSYTCHCDGRGGI.KLSQDMDCEDILPCVPFSVAKSVKSL.YLGRM 300  
DB 241 ECLQRCBOYCVNSPGSYTCHCDGRGGI.KLSQDMDCEDILPCVPFSVAKSVKSL.YLGRM 300  
QY 301 FSGTPIVRLRFKRLQPTRLVAEPDFTFDEGILLFAGHQDSTWIVLALRAGRLLEQLR 360  
DB 301 FSGTPIVRLRFKRLQPTRLVAEPDFTFDEGILLFAGHQDSTWIVLALRAGRLLEQLR 360  
QY 361 YNGVGRVTSGGPVINHGMQOTISVEELARNLVIVKNDVAWKIAVADLFQPERGLYHLN 420  
DB 361 YNGVGRVTSGGPVINHGMQOTISVEELARNLVIVKNDVAWKIAVADLFQPERGLYHLN 420  
QY 421 LTVGGIFPHEKDLVQPINPRLDGCMSNMNLNGEDTTIOETVKVNTMQCSYTERGSFY 480  
DB 421 LTVGGIFPHEKDLVQPINPRLDGCMSNMNLNGEDTTIOETVKVNTMQCSYTERGSFY 480  
QY 481 PGSGFAFYSLDYMRTPLDVGTSTWEVEVAHIRPADTGVLFALMAPDLRAVPLSVALV 540  
DB 481 PGSGFAFYSLDYMRTPLDVGTSTWEVEVAHIRPADTGVLFALMAPDLRAVPLSVALV 540  
QY 541 DYHSTKLLKKQVLAVEHTALALMEIKVCDGQEHVTVSLRDGEATLEVDGTRGQSEVS 600  
DB 541 DYHSTKLLKKQVLAVEHTALALMEIKVCDGQEHVTVSLRDGEATLEVDGTRGQSEVS 600  
QY 601 AAQLOERLAVLEHRLSPVLTFAAGLPDVPTSAPTYAFYRGCTMLEVNRRLDLDBAAY 660  
DB 601 AAQLOERLAVLEHRLSPVLTFAAGLPDVPTSAPTYAFYRGCTMLEVNRRLDLDBAAY 660  
QY 661 KHSIDITAHSCPVEPAAA 678  
DB 661 KHSIDITAHSCPVEPAAA 678

## RESULT 5

US-10-223-085-48  
Sequence 48, Application US/10223085  
Publication No. US20030100497A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austen L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Marsters, Scot A.  
APPLICANT: Pan, James  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Ye, Weilian  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
FILE REFERENCE: P3235P1C10  
CURRENT APPLICATION NUMBER: US/10/223,085  
PRIOR FILING DATE: 2002-08-16  
PRIOR APPLICATION NUMBER: US 10/081,056  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: US 60/213,637  
PRIOR FILING DATE: 2000-06-23  
PRIOR APPLICATION NUMBER: US 60/219,556  
PRIOR FILING DATE: 2000-07-20  
PRIOR APPLICATION NUMBER: US 60/220,624  
PRIOR FILING DATE: 2000-07-25  
PRIOR APPLICATION NUMBER: US 60/220,664  
PRIOR FILING DATE: 2000-07-25  
PRIOR APPLICATION NUMBER: PCT/US00/20710  
PRIOR FILING DATE: 2000-07-28  
PRIOR APPLICATION NUMBER: US 60/222,695  
PRIOR FILING DATE: 2000-08-02

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; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
; US-10-223-085-48

```

```

Query Match      80.4%; Score 2955.5; DB 4; Length 673;
Best Local Similarity 81.6%; Pred. No. 1.4e-233;
Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;

```

```

QY 7 PGPALRRAPOLLILLIAECALALLPAREATOPFRPQRAFOVEEAKOGLHERECV 66
DB 5 PGPAA-ALGTALLILLASSESHYVLRAREAAQFRPQRAFOVEEAKOGLHERECV 63
QY 67 BELCSREAREVENDPETDYFYPRLDCKINXGSPYTKNSGFATCVQNLPOQCTPNPCD 126
DB 64 BEVCSKEAREVENDPETEYFYPRIQECMRKXGRPEEKNDPAKCVQNLPOQCTPNPCD 123
QY 127 RKGTOACODLMGNFPCLCAGWGGRCLCDVNECQENGGCQICHNKRGSPHSCSHGF 186
DB 124 KKGTHICODLMGNFPCVCTDGNWGRCLCDVNECQENGGCQICHNKRGSPHSCSHGF 183
QY 187 ELSDGRTQODIDECADSEACGEARCKNPGSYSCLCDEGFAVSSOEKACRDVDECLQGR 246
DB 184 SLASDQGTQODIDECADSDTCGDARCKNPGSYSCLCDEGTYSSSEKTCQDVDEQOQR 243
QY 247 CEQVCNPSGSYTCHCDGRGGLKLSQDMOTCEDILPCVFPVSAKYSKSLYLGSMFSGTPV 306
DB 244 CEQVCNPSGSYTCHCDGRGGLKLSQDMOTCEDILPCVFPVSAKYSKSLYLGSMFSGTPV 303
QY 307 IRLRFRLOPTRLVAEFDRTDPBGILLFAGGHODSTWIVALARGRLEQLRYNGVR 366
DB 304 IRLRFRLOPTRLVAEFDRTDPBGILLFAGGRSDSTWIVALARGRLEQLRYNGVR 363
QY 367 VTSGSPVINGMWTISVEELARNLYIKNRDAVMKIAVAGDLFQPERGLYHLNLTVGSI 426
DB 364 ITSSGPTINGMWTISVEELARNLYIKNRDAVMKIAVAGDLFQPERGLYHLNLTVGSI 423
QY 427 PHEKDLVOPINPRLDGCMRSNMWLNGBDTTIOETVYKVTNQCFSVTERGSPYSGSPA 486
DB 424 PKESEELVOPINPRLDGCMRSNMWLNGBDSALQETVKANTKQCFSVTERGSPYSGSPA 483
QY 487 FVSLDYMRTPLVGESTVEVEVAHIRPAADTGVLFALMAPDLRAVPLSVALLVDYHSTK 546
DB 484 TRLNTRKSLDVGELTWEVKVARIRPAIDTGVLLAVGDD--DVIVSVALVDYHSTK 541
QY 547 KLLKQDLVLAVENTALALMEIKVCGQEHVVTVSLRDEGATLEVDGTRQSEVSAQLOE 606
DB 542 KLLKQDLVLAVENTALALMEIKVCGQEHVVTVSLRDEGATLEVDGTRQSEVSAQLOE 601
QY 607 RLAVLERHLSRYLTPFAGGLPDVPUTSAVTAFTYRCQMTLEVNRLDIDEAAYKASDIT 666
DB 602 RLDTLTKTHLQSGVHTVGGIPEVSVISABVTAFTYRCQMTLEVNKILIDDTASYSKSDIT 661
QY 667 AHSCEPVEPA 676
DB 662 SHSCEPVEPA 671

```

```

RESULT 6
US-10-223-084-48
; Sequence 48, Application US/10223084
; Publication No. US20030105011A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.

```

```

; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilian
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235P1C5
; CURRENT APPLICATION NUMBER: US/10/223,084
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
; US-10-223-084-48

```

```

Query Match      80.4%; Score 2955.5; DB 4; Length 673;
Best Local Similarity 81.6%; Pred. No. 1.4e-233;
Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;

```

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QY 7 PGPALRRAPOLLILLIAECALALLPAREATOPFRPQRAFOVEEAKOGLHERECV 66
DB 5 PGPAA-ALGTALLILLASSESHYVLRAREAAQFRPQRAFOVEEAKOGLHERECV 63
QY 67 BELCSREAREVENDPETDYFYPRLDCKINXGSPYTKNSGFATCVQNLPOQCTPNPCD 126
DB 64 BEVCSKEAREVENDPETEYFYPRIQECMRKXGRPEEKNDPAKCVQNLPOQCTPNPCD 123
QY 127 RKGTOACODLMGNFPCLCAGWGGRCLCDVNECQENGGCQICHNKRGSPHSCSHGF 186
DB 124 KKGTHICODLMGNFPCVCTDGNWGRCLCDVNECQENGGCQICHNKRGSPHSCSHGF 183
QY 187 ELSDGRTQODIDECADSEACGEARCKNPGSYSCLCDEGFAVSSOEKACRDVDECLQGR 246
DB 184 SLASDQGTQODIDECADSDTCGDARCKNPGSYSCLCDEGTYSSSEKTCQDVDEQOQR 243
QY 247 CEQVCNPSGSYTCHCDGRGGLKLSQDMOTCEDILPCVFPVSAKYSKSLYLGSMFSGTPV 306
DB 244 CEQVCNPSGSYTCHCDGRGGLKLSQDMOTCEDILPCVFPVSAKYSKSLYLGSMFSGTPV 303
QY 307 IRLRFRLOPTRLVAEFDRTDPBGILLFAGGHODSTWIVALARGRLEQLRYNGVR 366

```

```

Db      304 IRLRFKRLQPTRLLAEPDFRTPDEBGLFFPAGGRSDSTWIVLGLRAGRLLEQLRYNGVR 363
Qy      367 VTSSGPVNHGMQOTISVEELARNLVKVRDAVMKIAVAGDLFQPERGLVHMLTYVGI 426
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      364 ITSSGPTINHGMQOTISVEELARNLVKVRDAVMKIAVAGDLFQPERGLVHMLTYVGI 423
Qy      427 PFHEKDLVQPINRPLDGCMSMWLNAGEDTTIOETVKVNTMOCFSYTERGSPYPSGFA 486
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      424 PFKESELVQPINRPLDGCMSMWLNAGEDSAIOETVKANTMOCFSYTERGSPFGNGFA 483
Qy      487 FYSLDVNRTPLDVGTSTWTEVEVVAHTRPADTGVLFALMAPDLRAVPLSALVDYHSTK 546
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      484 TYRLNTRYTSLDVGTSTWTEVEVVAHTRPADTGVLFALVGD--DVVISVALVDYHSTK 541
Qy      547 KLKQQLVLAVEHTALAMEIKVCDGQEHVTVSLRDEATLEVDGTRGQSEVSAOLOE 606
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      542 KLKQQLVLAVEHTALAMEIKVCDGQEHVTVSLRDEATLEVDGTRGQSEVSAOLOE 601
Qy      607 RLAVLEHRLSPVLTFAGGLPDVPTSAVTAFAFYRGCMTELVNRRLDLDEAAVXSHDIT 666
        :|||||:|||||:|||||:|||||:|||||:|||||:
Db      602 RLDTLTKHLQGSVHTVYGGLEPEVSISAPVTAFAFYRGCMTELVNRRLDLDTASYKHSDIT 661
Qy      667 AHSCPVEPA 676
        :|||||:
Db      662 SHSCPVEHA 671

```

## RESULT 7

```

US-10-223-088-48
; Sequence 48, Application US/10223088
; Publication No. US20030105012A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrari, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltzen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scott A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P3235PIC6
; CURRENT APPLICATION NUMBER: US/10/223.088
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See file wrapper or PALM.

```

```

; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
; US-10-223-088-48

```

```

Query Match      80.4%; Score 2955.5; DB 4; Length 673;
Best Local Similarity 81.6%; Pred. No. 1.4e-233;
Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;

```

```

Qy      7  PGPAAARRAPDLLLLLLAEECALAALLPAREATQFLRPRQRAFOVEEAKQHLERECV 66
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      5  PGPAA-ALGTAALLLLASSSHVLLRARAAPFLRPRQRAFOVEEAKQHLERECV 63
Qy      67  BELCSREAAEVEFNDDETDYFFRYRLDCINKYGSPTYKSGFATCYQNLPDQCTPNPCD 126
        :|||||:|||||:|||||:|||||:|||||:|||||:
Db      64  EEWCSKEAREVEFNDDETDYFFRYRYOECMRKGRPEEKNPDPFAKCVQNLPDQCTPNPCD 123
Qy      127  RKGTQACODLMGNFECCKAGWGGRLCDKQVNECSQNGGCTQI CHNKPQS FHCCHSGF 186
        :|||||:|||||:|||||:|||||:|||||:|||||:
Db      124  KKGTHICQDLMGNFECCTDGMGGRLCDKQVNECSQNGGCTQI CHNKPQS FHCCHSGF 183
Qy      187  ELSSDGRTCODIDECADSEACGEARCKNLPGYSCLDEGFAYSSQEKACRDVDECTQGR 246
        :|||||:|||||:|||||:|||||:|||||:|||||:
Db      184  SLASDQGTQDIDECTSDTCGDARCKNLPGYSCLDEGTAYSSKKECTQDVEDCQDR 243
Qy      247  CEQVCVNSPGSYTCHCDGRGGLKLSQDMTCEDTLPVCPSPVAKSVKSLYGRMFGSTPV 306
        :|||||:|||||:|||||:|||||:|||||:|||||:
Db      244  CEQVCVNSPGSYTCHCDGRGGLKLSQDMTCEDTLPVCPSPMAKSVKSLYGRMFGSTPV 303
Qy      307  IRLRFKRLQPTRLLAEPDFRTPDEBGLFFPAGGHQSDTWIVLGLRAGRLLEQLRYNGVR 366
        :|||||:|||||:|||||:|||||:|||||:|||||:
Db      304  IRLRFKRLQPTRLLAEPDFRTPDEBGLFFPAGGRSDSTWIVLGLRAGRLLEQLRYNGVR 363
Qy      367  VTSSGPVNHGMQOTISVEELARNLVKVRDAVMKIAVAGDLFQPERGLVHMLTYVGI 426
        :|||||:|||||:|||||:|||||:|||||:|||||:
Db      364  ITSSGPTINHGMQOTISVEELARNLVKVRDAVMKIAVAGDLFQPERGLVHMLTYVGI 423
Qy      427  PFHEKDLVQPINRPLDGCMSMWLNAGEDTTIOETVKVNTMOCFSYTERGSPYPSGFA 486
        :|||||:|||||:|||||:|||||:|||||:|||||:
Db      424  PFKESELVQPINRPLDGCMSMWLNAGEDSAIOETVKANTMOCFSYTERGSPFGNGFA 483
Qy      487  FYSLDVNRTPLDVGTSTWTEVEVVAHTRPADTGVLFALMAPDLRAVPLSALVDYHSTK 546
        :|||||:|||||:|||||:|||||:|||||:|||||:
Db      484  TYRLNTRYTSLDVGTSTWTEVEVVAHTRPADTGVLFALVGD--DVVISVALVDYHSTK 541
Qy      547  KLKQQLVLAVEHTALAMEIKVCDGQEHVTVSLRDEATLEVDGTRGQSEVSAOLOE 606
        :|||||:|||||:|||||:|||||:|||||:|||||:
Db      542  KLKQQLVLAVEHTALAMEIKVCDGQEHVTVSLRDEATLEVDGTRGQSEVSAOLOE 601
Qy      607  RLAVLEHRLSPVLTFAGGLPDVPTSAVTAFAFYRGCMTELVNRRLDLDEAAVXSHDIT 666
        :|||||:|||||:|||||:|||||:|||||:|||||:
Db      602  RLDTLTKHLQGSVHTVYGGLEPEVSISAPVTAFAFYRGCMTELVNRRLDLDTASYKHSDIT 661
Qy      667  AHSCPVEPA 676
        :|||||:
Db      662  SHSCPVEHA 671

```

## RESULT 8

```

US-10-223-090-48
; Sequence 48, Application US/10223090
; Publication No. US20030105013A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrari, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltzen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.

```

```

/ APPLICANT: Marsters, Scot A.
/ APPLICANT: Pan, James
/ APPLICANT: Stephan, Jean-Philippe F.
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Ye, Weilan
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
/ TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
/ FILE REFERENCE: P3235P1C2
/ CURRENT APPLICATION NUMBER: US/10/223,090
/ CURRENT FILING DATE: 2002-08-16
/ PRIOR APPLICATION NUMBER: US 10/081,056
/ PRIOR FILING DATE: 2002-02-20
/ PRIOR APPLICATION NUMBER: US 60/213,637
/ PRIOR FILING DATE: 2000-06-23
/ PRIOR APPLICATION NUMBER: US 60/219,556
/ PRIOR FILING DATE: 2000-07-20
/ PRIOR APPLICATION NUMBER: US 60/220,624
/ PRIOR FILING DATE: 2000-07-25
/ PRIOR APPLICATION NUMBER: US 60/220,664
/ PRIOR FILING DATE: 2000-07-25
/ PRIOR APPLICATION NUMBER: PCT/US00/20710
/ PRIOR FILING DATE: 2000-07-28
/ PRIOR APPLICATION NUMBER: US 60/222,695
/ PRIOR FILING DATE: 2000-08-02
/ PRIOR APPLICATION NUMBER: US 09/643,657
/ PRIOR FILING DATE: 2000-08-17
/ PRIOR APPLICATION NUMBER: PCT/US00/23522
/ PRIOR FILING DATE: 2000-08-23
/ PRIOR APPLICATION NUMBER: PCT/US00/23328
/ PRIOR FILING DATE: 2000-08-24
/ Remaining Prior Application data removed - See file wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 383
/ SEQ ID NO 48
/ LENGTH: 673
/ TYPE: PRT
/ ORGANISM: Murine
US-10-223-090-48

Query Match      80.4%; Score 2955.5; DB 4; Length 673;
Best Local Similarity 81.6%; Pred. No. 1.4e-233;
Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;

QY 7 PGPAAARRAPOLLILLALABCAALALPBEATOFIPRRORRAFOVFEAKOGHLRECV 66
DB 5 PGPAA-ALGTALLLLASSSHHTVILRREAQPLRPRORRAVOVFEAKOGHLRECV 63
QY 67 BEICSRREAREVENDPETDYFYPRYLDCINKYGSPTKNSGFATCVONLPDOCTPNPCD 126
DB 64 BEVCSREAREVENDPETDYFYPRYQJECMRKXGRBEKNPDPRAKCVONLPDOCTPNPCD 123
QY 127 RKGTQACQDLMGNFCLCAAGWCGRLCDKDVNCSQENGGCLQICHNKPGSFHSCGSGF 186
DB 124 KKGTHICQDLMGNFCLCAAGWCGRLCDKDVNCSQENGGCLQICHNKPGSFHSCGSGF 183
QY 187 ELSSDRTQDIDECADSEACGARKCNLPGSYSCLCDEGFAVSSEKARQDVECLQGR 246
DB 184 SLASDQOTQDIDECADSEACGARKCNLPGSYSCLCDBSGYTSSEKRTQDVECLQGR 243
QY 247 CEQVCNVSPEGSYCHCDGRGGLKLSQDMDCEDILPCVPSFVAKSVKSLYLGMFSGSTPV 306
DB 244 CBQTCNVSPEGSYCHCDGRGGLKLSQDMDCEDILPCVPSFVAKSVKSLYLGMFSGSTPV 303
QY 307 IRLRFRLOFTRLVAEFDFPTPEBEGILLFAGGHQDSTWIVLALRAGRLQLRYNGVGR 366
DB 304 IRLRFRLOFTRLVAEFDFPTPEBEGVLFAGGRSSTWIVLGLRAGRLQLRYNGVGR 363
QY 367 VUSGGVINHGMOQTSVEELARNIVKXNDAMKIAVAGDLFOPERGGLYHNLATVGGI 426
DB 364 ITSSGPTINNGMOQTSVEELERNIVKXNDAMKIAVAGELFQLRGGLYHNLATVGGI 423
QY 427 PFHEKDLVQPINRLDGCMSNMWLNEDTTIOETVKNVTRMOCFSVTERGSEFPYPSGFA 486
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DB 424 PFKESELVQPINRLDGCMSNMWLNEDSAIQETVKANTKQCFSVTERGSEFPFNGPFA 483
QY 487 FVSLDYMRPLPDVGNESHTWEVVAHIRPAADTVLFLMAPDLAVPLSVLVDYHSRK 546
DB 484 TYRLNVTFTSLDVGHTTEVVAHIRPAADTVLFLMAPDLAVPLSVLVDYHSRK 541
QY 547 KKKQVLVAVENTLALMEIKVCDGQEHVTVSLRDEGATLEVDGTRGQSEVSAQLOE 606
DB 542 KKKQVLVAVENTLALMEIKVCDGQEHVTVSLRDEGATLEVDGTRGQSEVSAQLOE 601
QY 607 RLAVERRHRSPLTPAGGLPVYTSAPVTAIFYGCMTELVNRRLLDEANVYKSDIT 666
DB 602 RLDTLKTHLQSGVHTYVGLPEVSVISAPVTAIFYGCMTELVNRRLLDEANVYKSDIT 661
QY 667 AHSCEPVEPA 676
DB 662 SHSCPEVEHA 671

RESULT 9
US-10-223-087-48
/ Sequence 48, Application US/10223087
/ Publication No. US20030109438A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerlitsen, Maty E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Marsters, Scot A.
/ APPLICANT: Pan, James
/ APPLICANT: Stephan, Jean-Philippe F.
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Ye, Weilan
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
/ TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
/ FILE REFERENCE: P3235P1C4
/ CURRENT APPLICATION NUMBER: US/10/223,087
/ CURRENT FILING DATE: 2002-08-16
/ PRIOR APPLICATION NUMBER: US 10/081,056
/ PRIOR FILING DATE: 2002-02-20
/ PRIOR APPLICATION NUMBER: US 60/213,637
/ PRIOR FILING DATE: 2000-06-23
/ PRIOR APPLICATION NUMBER: US 60/219,556
/ PRIOR FILING DATE: 2000-07-20
/ PRIOR APPLICATION NUMBER: US 60/220,624
/ PRIOR FILING DATE: 2000-07-25
/ PRIOR APPLICATION NUMBER: US 60/220,664
/ PRIOR FILING DATE: 2000-07-28
/ PRIOR APPLICATION NUMBER: PCT/US00/20710
/ PRIOR FILING DATE: 2000-08-02
/ PRIOR APPLICATION NUMBER: US 60/222,695
/ PRIOR FILING DATE: 2000-08-17
/ PRIOR APPLICATION NUMBER: US 09/643,657
/ PRIOR FILING DATE: 2000-08-23
/ PRIOR APPLICATION NUMBER: PCT/US00/23522
/ PRIOR FILING DATE: 2000-08-24
/ PRIOR APPLICATION NUMBER: PCT/US00/23328
/ PRIOR FILING DATE: 2000-09-07
/ PRIOR APPLICATION NUMBER: US 60/230,978
/ PRIOR FILING DATE: 2000-09-15
/ PRIOR APPLICATION NUMBER: US 60/232,887
/ PRIOR FILING DATE: 2000-09-18
/ PRIOR APPLICATION NUMBER: US 09/664,610
/ PRIOR FILING DATE: 2000-09-18
/ PRIOR APPLICATION NUMBER: US 09/665,350
/ PRIOR FILING DATE: 2000-09-18
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; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
; US-10-223-083-48

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Query Match      80.4%; Score 2955.5; DB 4; Length 673;
Best Local Similarity 81.6%; Pred. No. 1.4e-233;
Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;

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7  PGPALRRAPOLLLLLLLAECALALLPAREATOFLEPRORAFQVFEBAKQGHLERECV 66
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5  PGPAA-ALGTALLLLLLAESSHVTLLRAREAAQFLRPRQRRAYQVFEBAKQGHLERECV 63
67  BELCSREAREVENDPETDYFPRYLDCINKYGSBYTKNSGPATCVQNLPOQCTPNPCD 126
|||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
64  BEVCSKEAREVENDPETEYFPRYOECMRKYGRPEEKNDPFAKCVQNLPOQCTPNPCD 123
127  RKGTOACDLMGNFPCLCAGWGRLCDVNECSGSENGGCIQICHNKGSFHCCHSGF 186
|||||  |||||||  :  |||||||  :  |||||||  :  |||||||  :  |||||||  :
124  KKGTHICODLMGNFPCVCTDGMGRLCDVNECVQKNGGCSQVCHNKGSFQACACHSGF 183
187  ELSDGRTCODIDECADSEACGEARCKNLPGSYSCLCDEGFAYSSQEKACRDVDECTQGR 246
|||||  |||||||  :  |||||||  :  |||||||  :  |||||||  :  |||||||  :
184  SLASDQGTODIDECDDSDTCGDARCKNLPGSYSCLCDEGYTSSSEKTCQDVDECOQGR 243
247  CEQVCVNSPGSYTCHCDGRGGLKLSQMDTCEDIILFCVPSVAKSYKSLYLGRMFSGTIV 306
|||||  |||||||  :  |||||||  :  |||||||  :  |||||||  :  |||||||  :
244  CEQTCVNSPGSYTCHCDGRGGLKLSQMDTCEDIILFCVPSVAKSYKSLYLGRMFSGTIV 303
307  IRLRFRLOPRTLVAEFDRTPDPSGILLFAGSHODSTWIVLALRAGRLELOLRVYGV 366
|||||  |||||||  :  |||||||  :  |||||||  :  |||||||  :  |||||||  :
304  IRLRFRLOPRTLVAEFDRTPDPSGILLFAGSRSDSTWIVLALRAGRLELOLRVYGV 363
367  VTSQGFVINGMWQOTISVEELANLVIKVRDAVMKIAVAGDLFQDERGLYHLNLTVGGI 426
|||||  |||||||  :  |||||||  :  |||||||  :  |||||||  :  |||||||  :
364  ITSSGFTINGMWQOTISVEELANLVIKVRDAVMKIAVAGELFQDERGLYHLNLTVGGI 423
427  PHEKDLVOPINPRLDGCKRSWMLNGEOTTOETIYKVNTRQCFSEVTERGSGYPSGGA 486
|||||  |||||||  :  |||||||  :  |||||||  :  |||||||  :  |||||||  :
424  PKESSELVOPINPRLDGCKRSWMLNGEOTTOETIYKVNTRQCFSEVTERGSGYPSGGA 483
487  FVSLQVMTPLVYGESTVEVEVAHIRPAADTGVLFALMAPLRAVPISVALVDHSHK 546
|||||  |||||||  :  |||||||  :  |||||||  :  |||||||  :  |||||||  :
484  TYRLNTRTSLDVGITVEVKVARIIRAITDTGILLALVGD--DVIISVALVDHSHK 541
547  KLLKQDLVLAVEHTALALMEIKVCDQBEHVTVSLRDGEATLEVDTRQGEVSAALOQ 606
|||||  |||||||  :  |||||||  :  |||||||  :  |||||||  :  |||||||  :
542  KLLKQDLVLAVEHTALALMEIKVCDQBEHVTVSLRDGEATLEVDTRQGEVSAALOQ 601
607  RLAVLERHRLRSPVLTAGCLPDVPTVSAPVATYARCGMTLEVRRLDLDEAAKYKSDIT 666
|||||  |||||||  :  |||||||  :  |||||||  :  |||||||  :  |||||||  :
602  RLDTLFTLHLOGSVHTVYVGLPEVSVISAPVATYARCGMTLEVRRLDLDEAAKYKSDIT 661
667  AHSCEPVEBA 676
|||||  |||||||  :  |||||||  :  |||||||  :  |||||||  :  |||||||  :
662  SHSCPEVEBA 671

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RESULT 11

US-10-223-089-48

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; Sequence 48, Application US/10223089
; Publication No. US20030125521A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerriksen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gunney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Masters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilian
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235P1C9
; CURRENT APPLICATION NUMBER: US/10/223,089
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
; US-10-223-089-48

```

```

Query Match      80.4%; Score 2955.5; DB 4; Length 673;
Best Local Similarity 81.6%; Pred. No. 1.4e-233;
Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;

```

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7  PGPALRRAPOLLLLLLLAECALALLPAREATOFLEPRORAFQVFEBAKQGHLERECV 66
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5  PGPAA-ALGTALLLLLLAESSHVTLLRAREAAQFLRPRQRRAYQVFEBAKQGHLERECV 63
67  BELCSREAREVENDPETDYFPRYLDCINKYGSBYTKNSGPATCVQNLPOQCTPNPCD 126
|||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
64  BEVCSKEAREVENDPETEYFPRYOECMRKYGRPEEKNDPFAKCVQNLPOQCTPNPCD 123
127  RKGTOACDLMGNFPCLCAGWGRLCDVNECSGSENGGCIQICHNKGSFHCCHSGF 186
|||||  |||||||  :  |||||||  :  |||||||  :  |||||||  :  |||||||  :
124  KKGTHICODLMGNFPCVCTDGMGRLCDVNECVQKNGGCSQVCHNKGSFQACACHSGF 183
187  ELSDGRTCODIDECADSEACGEARCKNLPGSYSCLCDEGFAYSSQEKACRDVDECTQGR 246
|||||  |||||||  :  |||||||  :  |||||||  :  |||||||  :  |||||||  :
184  SLASDQGTODIDECDDSDTCGDARCKNLPGSYSCLCDEGYTSSSEKTCQDVDECOQGR 243
247  CEQVCVNSPGSYTCHCDGRGGLKLSQMDTCEDIILFCVPSVAKSYKSLYLGRMFSGTIV 306

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; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilian
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P3235P1C3
; CURRENT APPLICATION NUMBER: US/10/223,082
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
US-10-223-082-48

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```

Query Match      80.4%; Score 2955.5; DB 4; Length 673;
Best Local Similarity 81.6%; Pred. No. 1.4e-233;
Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;

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; 7 PGPALRRAPOLLILLILAAACALALPAREATQFRRPQRRAPQVFEBAKQGHLERECV 66
; 5 PGPAA-ALGTALLILLILASSSHITVLLRRRRAQFRRPQRRAPQVFEBAKQGHLERECV 63
; 67 EELCSREAREVEFENDPETDYFYPRYLDCINKYGSPTYNKSGFATCVQNLPDQCTNPDC 126
; 64 EEVCSKEAREVEFENDPETEYFYPRYOECMRKRGREKKNPDPKACVQNLPDQCTNPDC 123
; 127 RKGTQACCOLMGNFPLCLCAAGWGRCLCDVNECSENGGCLQICNNKGSFHCCHSGF 186
; 124 KKGTHICODLMGNFVCCTDGMWGRCLCDVNECVQNGKGSQVCHNKPSSFQACCHSGF 183
; 187 ELISDRTQODIDECADSEACGEARCKNPGSYSGCDEGFAVSSQEKACRDVDECLQGG 246
; 184 SLASDQOTQODIDECADSEACGEARCKNPGSYSGCDEGFAVSSQEKACRDVDECLQGG 243
; 247 CEQVSNVSPGSYTCCHCDGRGGLKLSQMDTCEBILPCVPEPSVAKSVKSLVIGMFGSTPV 306
; 244 CEGTCVNSPGSYTCCHCDGRGGLKLSQMDTCEBILPCVPEPSVAKSVKSLVIGMFGSTPV 303
; 307 IRLRFRLQPTRLVAPDRPTPEGLILPAGGHQSTWVLLARAGRLQLQRYNGVR 366
; 304 IRLRFRLQPTRLVAPDRPTPEGLILPAGGHQSTWVLLARAGRLQLQRYNGVR 363

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; 367 VTSSGPVINGMWTQISVEBELARNLVIKVRDPAVKIAVAGDLFQPERGLYHLNTLVGGI 426
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; 427 PFERKDLVQPINRDLDCGRSMWNLNGEDTTIQEYKXNTRQCSYTERGSFYGSGFA 486
; 424 PFERKDLVQPINRDLDCGRSMWNLNGEDTTIQEYKXNTRQCSYTERGSFYGSGFA 483
; 487 FVSLDYNRTPLDVGESTWVEVVAHIRPAADTVGLPALMAPDLRAVPLSLVLDYHSTR 546
; 484 TYRLNVTISLVDGELITWVEVVAHIRPAADTVGLPALMAPDLRAVPLSLVLDYHSTR 541
; 547 KKKQVLVAVENHTALAMEIKVCDQGEHVTVSLRDEATLEVDGTRQSEVSAQLOE 606
; 542 KKKQVLVAVENHTALAMEIKVCDQGEHVTVSLRDEATLEVDGTRQSEVSAQLOE 601
; 607 RLAVLERHRSVYLTFFAGLPVPTSAVTAFFYGCMTLENNRLLDLEAAYHSDIT 666
; 602 RLDTLKLHQSVMHYVGLPEVSVIASVTAFFYGCMTLENNRLLDLEAAYHSDIT 661
; 667 AHSCPEVEPA 676
; 662 SHSCPEVEHA 671

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# RESULT 14

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; US-10-305-654-48
; Sequence 48, Application US/10305654
; Publication No. US20030224984A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hans-Peter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, J.
; APPLICANT: Paoni, N. F.
; APPLICANT: Stephan, J-P. F.
; APPLICANT: Matanabe, C.K.
; APPLICANT: Wood, W.I.
; APPLICANT: Williams, P.M.
; APPLICANT: Ye, Weilian
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P3235R1C1
; CURRENT APPLICATION NUMBER: US/10/305,654
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
US-10-305-654-48

```

```

Query Match      80.4%; Score 2955.5; DB 4; Length 673;
Best Local Similarity 81.6%; Pred. No. 1.4e-233;
Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;

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; 7 PGPALRRAPOLLILLILAAACALALPAREATQFRRPQRRAPQVFEBAKQGHLERECV 66
; 5 PGPAA-ALGTALLILLILASSSHITVLLRRRRAQFRRPQRRAPQVFEBAKQGHLERECV 63
; 67 EELCSREAREVEFENDPETDYFYPRYLDCINKYGSPTYNKSGFATCVQNLPDQCTNPDC 126
; 64 EEVCSKEAREVEFENDPETEYFYPRYOECMRKRGREKKNPDPKACVQNLPDQCTNPDC 123
; 127 RKGTQACCOLMGNFPLCLCAAGWGRCLCDVNECSENGGCLQICNNKGSFHCCHSGF 186
; 124 KKGTHICODLMGNFVCCTDGMWGRCLCDVNECVQNGKGSQVCHNKPSSFQACCHSGF 183

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QY 187 ELSSDGRTCODIDECADSEACGEARCKNLPSSYCLCEGFAVSSOEKACRDVDECQGR 246  
DB 184 SLASDGTCCODIDECTSDTCTGDARCKNLPSSYCLCEGTYSSKETTCODVDECQDR 243  
QY 247 CEQCVNPSPGSYTCHCGRGGLKLSQDMTCEDILLPCVPFSAKSVKSLVYGRMFSGTPV 306  
DB 244 CEQCVNPSPGSYTCHCGRGGLKLSQDMTCEDILLPCVPFSAKSVKSLVYGRMFSGTPV 303  
QY 307 IRLRFKLOPRLVAEPDPRTEDEGILLFAGCHODSTWYALRAGRLLEQLRYNGVR 366  
DB 304 IRLRFKLOPRLVAEPDPRTEDEGILLFAGCHODSTWYALRAGRLLEQLRYNGVR 363  
QY 367 VTSSGPVNHGMQOTISVEBELARNLVKVRNDAMKIAVAGDLFQPERGLYHNLTVGGI 426  
DB 364 ITSSGPTNHGMQOTISVEBELARNLVKVRNDAMKIAVAGDLFQPERGLYHNLTVGGI 423  
QY 427 PFHEKDLVOPINPRLDCMRSMNMLNGEDTTIOETVKNVTRMOCFSYTERGSPYSGGFA 486  
DB 424 PFHEKDLVOPINPRLDCMRSMNMLNGEDTTIOETVKNVTRMOCFSYTERGSPYSGGFA 483  
QY 487 FYSLDVNRTPLDJGTESTWEVAVAHIRPADTGVFLAAMPDLRAVPLSVALVDYHSTK 546  
DB 484 TYRLNTRISLDJGTESTWEVAVAHIRPADTGVFLAAMPDLRAVPLSVALVDYHSTK 541  
QY 547 KLKKOLVLAVENTALAMEIKVCDQEHVTVSLRDEGATLEVDGTRGQSEVSAQLOE 606  
DB 542 KLKKOLVLAVENTALAMEIKVCDQSEHVTYSLRGEATLEVDGTRGQSEVSAQLOE 601  
QY 607 RLAVLEHRLSPVLTFAGSLPDVPTVSAPYAFYRGCMTELVNRLLDLDEAAKHSIDT 666  
DB 602 RLUTLXTHLQGSVHTYVGGLEPVSISAPYAFYRGCMTELVNGKILDLDTASKHSIDT 661  
QY 667 AHSCPEPEPA 676  
DB 662 SHSCPEPEHA 671

RESULT 15  
US-10-081-056-48  
Sequence 48, Application US/10081056  
Publication No. US2004043927A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Gerber, Hanpetere  
APPLICANT: Geritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Marsters, Scot A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Ye, Weilan  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
FILE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS  
FILE REFERENCE: P3235P1C1  
CURRENT APPLICATION NUMBER: US/10/081,056  
CURRENT FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: PCT/US01/21735  
PRIOR FILING DATE: 2001-07-09  
PRIOR APPLICATION NUMBER: US 60/219,556  
PRIOR FILING DATE: 2000-07-20  
PRIOR APPLICATION NUMBER: US 60/220,624  
PRIOR FILING DATE: 2000-07-25  
PRIOR APPLICATION NUMBER: US 60/220,664  
PRIOR FILING DATE: 2000-07-25  
PRIOR APPLICATION NUMBER: PCT/US00/20710

PRIOR FILING DATE: 2000-07-28  
PRIOR APPLICATION NUMBER: US 60/222,695  
PRIOR FILING DATE: 2000-08-02  
PRIOR APPLICATION NUMBER: US 09/643,657  
PRIOR FILING DATE: 2000-08-17  
PRIOR APPLICATION NUMBER: PCT/US00/23522  
PRIOR FILING DATE: 2000-08-23  
PRIOR APPLICATION NUMBER: PCT/US00/23328  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US 60/230,978  
PRIOR FILING DATE: 2000-09-07  
PRIOR APPLICATION NUMBER: US 60/000,000  
PRIOR FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: US 09/664,610  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: US 09/665,350  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: US 60/242,922  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 09/709,238  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: PCT/US00/30952  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: PCT/US00/30873  
PRIOR FILING DATE: 2000-11-10  
PRIOR APPLICATION NUMBER: PCT/US00/32678  
PRIOR FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: US 09/747,259  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/34956  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: US 09/767,609  
PRIOR FILING DATE: 2001-01-22  
PRIOR APPLICATION NUMBER: US 09/796,498  
PRIOR FILING DATE: 2001-02-28  
PRIOR APPLICATION NUMBER: PCT/US01/06520  
PRIOR FILING DATE: 2001-02-28  
PRIOR APPLICATION NUMBER: PCT/US01/06666  
PRIOR FILING DATE: 2001-03-01  
PRIOR APPLICATION NUMBER: US 09/802,706  
PRIOR FILING DATE: 2001-03-09  
PRIOR APPLICATION NUMBER: US 09/808,689  
PRIOR FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: US 09/816,744  
PRIOR FILING DATE: 2001-03-22  
PRIOR APPLICATION NUMBER: US 09/828,366  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: US 09/854,208  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: US 09/854,280  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: US 09/866,028  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: US 09/866,034  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: PCT/US01/17092  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: US 09/870,574  
PRIOR FILING DATE: 2001-05-30  
PRIOR APPLICATION NUMBER: PCT/US01/17443  
PRIOR FILING DATE: 2001-05-30  
PRIOR APPLICATION NUMBER: PCT/US01/17800  
PRIOR FILING DATE: 2001-06-01  
PRIOR APPLICATION NUMBER: PCT/US01/19692  
PRIOR FILING DATE: 2001-06-20  
PRIOR APPLICATION NUMBER: PCT/US01/00000  
PRIOR FILING DATE: 2001-06-28  
NUMBER OF SEQ ID NOS: 383  
SEQ ID NO 48  
LENGTH: 673  
TYPE: PRT  
ORGANISM: Murine  
US-10-081-056-48

Query Match 80.4%; Score 2955.5; DB 4; Length 673;  
 Best Local Similarity 81.6%; Pred. No. 1.4e-233;  
 Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;

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Db 5 PGPAA-ALGTALLLLILASSSHVTLRRAREAAQFLRPRORARAYQVEEAKQGHLERECV 63
   ||||| ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 67 BELCSREAREVEFENDPETDYFPRYLDCINKYGSPTYKNSGFATCVQNLPDQCTPNPCD 126
   ||||| ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
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   ||||| ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 127 RKGTCACODLMGNFCLCKAGWGRLCDKDVNCSQENGSCLOICHNKPSFHGCSHGF 186
   ||||| ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 124 KKGTHI CODLMGNFPCVCTDGMWGRLCDKDVNCSQENGSCLOICHNKPSFHGCSHGF 183
   ||||| ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 187 ELSDGRTCODIDECADEACGEARCKNLPGSYSCLDEGFAYSSQEKACRDVDECTQGR 246
   ||||| ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 184 SLASDGQTCODIDECTDSPTCCDARCKNLPGSYSCLDEGYTSSKEKTCQDVDECOQDR 243
   ||||| ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 247 CEQVCVNSPGSYTCHCDGRGGLKLSQDMTCEBILFCVPPSVAKSVKSLYLGRMFSGTPV 306
   ||||| ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 244 CEQTCVNSPGSYTCHCDGRGGLKLSQDMTCEBILFCVPPSVAKSVKSLYLGRMFSGTPV 303
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QY 307 IRLRFRLQPTRLVAEPDFTFDPBEGILLFAGGHODSTWIVLALRAGRLELOLRVNGVR 366
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QY 367 VTSSEGVINHGMMQITISVEELARNLVIKVNRDAVMKIAVAGDLFQPERGLYHLNLTVGSI 426
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QY 487 FYSLDYMTPLDVGTSTWEVEVVAHIRPADTGVLFALMAPDLRAVPLSVVALVDYHSTK 546
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   ||||| ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 547 KLKKQDLVLAVENTALALMEIKVCQGEHVTVSLRDGEATLEVDGTRGQSEVSAALQGE 606
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Db 542 KLKKQDLVLAVENTALALMEIKVCDSQEHVTVSLRDGEATLEVDGTRGQSEVSTALQGE 601
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QY 607 RLAVLERHURSPVLTFAAGLPDVPTSAVPTAFYRCMTLEVNRLLDDEAAYKHSDDT 666
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Db 662 SHSCPVEHA 671
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Search completed: June 29, 2006, 11:31:30  
 Job time : 190 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 29, 2006, 11:16:01 ; Search time 51 Seconds  
(without alignments)  
1177.373 Million cell updates/sec

Title: US-10-671-054-1

Perfect score: 3675  
Sequence: 1 MAPSLSPGPAALRRAPQLLL.....AHSCPVEPAADYKDDDK 686

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued Patents\_AA:\*  
2: /EMC\_Celerra\_SIDS3/prodata/2/1aa/5\_COMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/prodata/2/1aa/6\_COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/prodata/2/1aa/7\_COMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/prodata/2/1aa/H\_COMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/prodata/2/1aa/RE\_COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/prodata/2/1aa/Backfill1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3628	98.7	678	1	US-08-282-141-2 Sequence 2, Appl1
2	3628	98.7	678	1	US-08-435-434-2 Sequence 2, Appl1
3	3628	98.7	678	1	US-08-435-436-2 Sequence 2, Appl1
4	3628	98.7	678	1	US-08-438-863-2 Sequence 2, Appl1
5	3628	98.7	678	1	US-08-438-864-2 Sequence 2, Appl1
6	3628	98.7	678	2	US-08-438-862-2 Sequence 2, Appl1
7	3628	98.7	678	2	US-08-402-253-2 Sequence 2, Appl1
8	3628	98.7	678	2	US-08-443-868-2 Sequence 2, Appl1
9	3620	98.5	678	2	US-08-628-747-2 Sequence 2, Appl1
10	2955.5	80.4	673	1	US-08-282-141-3 Sequence 3, Appl1
11	2955.5	80.4	673	1	US-08-435-434-1 Sequence 1, Appl1
12	2955.5	80.4	673	1	US-08-435-436-1 Sequence 1, Appl1
13	2955.5	80.4	673	1	US-08-438-863-1 Sequence 1, Appl1
14	2955.5	80.4	673	1	US-08-438-864-1 Sequence 1, Appl1
15	2955.5	80.4	673	2	US-08-438-862-1 Sequence 1, Appl1
16	2955.5	80.4	673	2	US-08-402-253-1 Sequence 1, Appl1
17	2955.5	80.4	673	2	US-08-443-868-1 Sequence 1, Appl1
18	2945.5	80.1	673	2	US-08-628-747-1 Sequence 1, Appl1
19	1547.5	42.1	676	1	US-08-282-141-4 Sequence 4, Appl1
20	1543	42.0	676	1	US-08-435-434-3 Sequence 3, Appl1
21	1543	42.0	676	1	US-08-435-436-3 Sequence 3, Appl1
22	1543	42.0	676	1	US-08-438-863-3 Sequence 3, Appl1
23	1543	42.0	676	1	US-08-438-864-3 Sequence 3, Appl1
24	1543	42.0	676	2	US-08-438-862-3 Sequence 3, Appl1
25	1543	42.0	676	2	US-08-402-253-3 Sequence 3, Appl1
26	1543	42.0	676	2	US-08-443-868-3 Sequence 3, Appl1

#### ALIGNMENTS

27	1543	42.0	676	2	US-08-443-868-3	Sequence 3, Appl1
28	1510.5	41.1	635	1	US-07-907-190-1	Sequence 1, Appl1
29	1510.5	41.1	635	1	US-07-985-691-2	Sequence 2, Appl1
30	1510.5	41.1	635	1	US-08-436-804-2	Sequence 2, Appl1
31	1510.5	41.1	635	1	US-08-267-387-2	Sequence 2, Appl1
32	1505	41.0	652	2	5258288-4	Patent No. 5258288
33	1413	38.4	675	7	5258288-1	Patent No. 5258288
34	358.5	9.8	997	2	US-09-747-371-3	Sequence 3, Appl1
35	354.5	9.6	1587	2	US-09-949-002-354	Sequence 354, App
36	353.5	9.6	1581	2	US-09-949-002-414	Sequence 414, App
37	352	9.6	1935	2	US-09-949-016-10403	Sequence 10403, A
38	352	9.6	2871	2	US-09-538-092-1076	Sequence 1076, Appl1
39	345.5	9.4	999	2	US-09-747-371-2	Sequence 2, Appl1
40	344.5	9.4	677	2	US-09-949-016-11369	Sequence 11369, A
41	344.5	9.4	677	2	US-09-949-016-11370	Sequence 11370, A
42	344.5	9.4	677	2	US-09-949-016-11371	Sequence 11371, A
43	344.5	9.4	677	2	US-09-949-016-11372	Sequence 11372, A
44	339.5	9.2	1394	2	US-09-949-016-5971	Sequence 5971, Ap
45	339.5	9.2	1394	7	5177197-30	Patent No. 5177197

#### RESULT 1

US-08-282-141-2  
Sequence 2, Application US/08282141  
Patent No. 5538861  
GENERAL INFORMATION:  
APPLICANT: Schneider, Claudio  
APPLICANT: Varnum, Brian  
APPLICANT: Avanzzi, Giancarlo  
APPLICANT: Biancolini, Claudio  
APPLICANT: Manfioletti, Guidalberto  
TITLE OF INVENTION: Stimulating factor for the AXL Receptor  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Amgen Inc.  
STREET: 1840 Dehavenland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: United States  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/282,141  
FILING DATE:  
CLASSIFICATION: 435  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 678 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-282-141-2

Query Match 98.7%; Score 3628; DB 1; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.5e-309; Indels 0; Gaps 0;

Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPSLSPGPAALRRAPQLLLLAECALALPAREATQFLPRORAFVFEAKQGH 60  
DB 1 MAPSLSPGPAALRRAPQLLLLAECALALPAREATQFLPRORAFVFEAKQGH 60  
QY 61 LRECEVEELCSREAREVEFENDPETYPRYLDCINKYSGPYTKNSGATCVQNLDDC 120  
DB 61 LRECEVEELCSREAREVEFENDPETYPRYLDCINKYSGPYTKNSGATCVQNLDDC 120

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QY 121 TPNPCDRKCTQACODLMGNFCLCRAGWGRLCDKDVNCSQENGGCLQICHNKPGSFHC 180
DB 121 TPNPCDRKCTQACODLMGNFCLCRAGWGRLCDKDVNCSQENGGCLQICHNKPGSFHC 180
QY 181 SCHSGFELSSDRTCODIDECADSEACGACRKNLPGSYSCLCDEGFAVSQEKACRDVD 240
DB 181 SCHSGFELSSDRTCODIDECADSEACGACRKNLPGSYSCLCDEGFAVSQEKACRDVD 240
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DB 241 ECLQRCBCEVCVNSPGSYTCHDGRGGLKLSQDMOTCEDILPCVPFSVAKSVKSLYLGM 300
QY 301 FSGTPVIRLRFKRLQPTRLVAEFDFRTFDPBEGILLFAGGHODSTWIVLALRAGRLELQJR 360
DB 301 FSGTPVIRLRFKRLQPTRLVAEFDFRTFDPBEGILLFAGGHODSTWIVLALRAGRLELQJR 360
QY 361 YNGVGRVTSSGPIVNHGMQTTISVEELARNLVIKVRDAVMKIAVAGDLFQPERGLYHNL 420
DB 361 YNGVGRVTSSGPIVNHGMQTTISVEELARNLVIKVRDAVMKIAVAGDLFQPERGLYHNL 420
QY 421 LTVGGIPFHEKDLVQPINRDLGCMRSNMWLNGETTTIETVKNTRMOCFSVTERGSPY 480
DB 421 LTVGGIPFHEKDLVQPINRDLGCMRSNMWLNGETTTIETVKNTRMOCFSVTERGSPY 480
QY 481 PGSGFAFYSLDYMRTPLDVGTESTWEVEVAHIRPADTGVLFALMAPDLRAVPLSVALY 540
DB 481 PGSGFAFYSLDYMRTPLDVGTESTWEVEVAHIRPADTGVLFALMAPDLRAVPLSVALY 540
QY 541 DYHSTYKLLKKQVLVAVEHTALAMEIKVCDGGEHVTVSLRDEATLEVDGTRGSEVS 600
DB 541 DYHSTYKLLKKQVLVAVEHTALAMEIKVCDGGEHVTVSLRDEATLEVDGTRGSEVS 600
QY 601 AAQLOERLAVLEBHLSPVLTFAGGLPDVPTVSAPYTAFFRGCMTELVNRRLLDLEAAY 660
DB 601 AAQLOERLAVLEBHLSPVLTFAGGLPDVPTVSAPYTAFFRGCMTELVNRRLLDLEAAY 660
QY 661 KHSIDITAHSCPVEPAAA 678
DB 661 KHSIDITAHSCPVEPAAA 678

RESULT 2
US-08-435-434-2
; Sequence 2, Application US/08435434
; Patent No. 5714385
; GENERAL INFORMATION:
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,434
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000

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; REFERENCE/DOCKET NUMBER: 946-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 678 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-435-434-2

Query Match      98.7%; Score 3628; DB 1; Length 678;
Best Local Similarity 100.0%; Pred.No. 1.5e-309;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPSLSPGPAALRRAPQLLLLLLAAECALALLPAREAQFLRPPORAFQVPEEAKQGH 60
DB 1 MAPSLSPGPAALRRAPQLLLLLLAAECALALLPAREAQFLRPPORAFQVPEEAKQGH 60
QY 61 LRECEVEELCSREAREVEFENDPETDYFYPRYLDCINKYGSPTYKNSGFATCVQNLPDQC 120
DB 61 LRECEVEELCSREAREVEFENDPETDYFYPRYLDCINKYGSPTYKNSGFATCVQNLPDQC 120
QY 121 TPNPCDRKCTQACODLMGNFCLCRAGWGRLCDKDVNCSQENGGCLQICHNKPGSFHC 180
DB 121 TPNPCDRKCTQACODLMGNFCLCRAGWGRLCDKDVNCSQENGGCLQICHNKPGSFHC 180
QY 181 SCHSGFELSSDRTCODIDECADSEACGACRKNLPGSYSCLCDEGFAVSQEKACRDVD 240
DB 181 SCHSGFELSSDRTCODIDECADSEACGACRKNLPGSYSCLCDEGFAVSQEKACRDVD 240
QY 241 ECLQRCBCEVCVNSPGSYTCHDGRGGLKLSQDMOTCEDILPCVPFSVAKSVKSLYLGM 300
DB 241 ECLQRCBCEVCVNSPGSYTCHDGRGGLKLSQDMOTCEDILPCVPFSVAKSVKSLYLGM 300
QY 301 FSGTPVIRLRFKRLQPTRLVAEFDFRTFDPBEGILLFAGGHODSTWIVLALRAGRLELQJR 360
DB 301 FSGTPVIRLRFKRLQPTRLVAEFDFRTFDPBEGILLFAGGHODSTWIVLALRAGRLELQJR 360
QY 361 YNGVGRVTSSGPIVNHGMQTTISVEELARNLVIKVRDAVMKIAVAGDLFQPERGLYHNL 420
DB 361 YNGVGRVTSSGPIVNHGMQTTISVEELARNLVIKVRDAVMKIAVAGDLFQPERGLYHNL 420
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DB 421 LTVGGIPFHEKDLVQPINRDLGCMRSNMWLNGETTTIETVKNTRMOCFSVTERGSPY 480
QY 481 PGSGFAFYSLDYMRTPLDVGTESTWEVEVAHIRPADTGVLFALMAPDLRAVPLSVALY 540
DB 481 PGSGFAFYSLDYMRTPLDVGTESTWEVEVAHIRPADTGVLFALMAPDLRAVPLSVALY 540
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DB 541 DYHSTYKLLKKQVLVAVEHTALAMEIKVCDGGEHVTVSLRDEATLEVDGTRGSEVS 600
QY 601 AAQLOERLAVLEBHLSPVLTFAGGLPDVPTVSAPYTAFFRGCMTELVNRRLLDLEAAY 660
DB 601 AAQLOERLAVLEBHLSPVLTFAGGLPDVPTVSAPYTAFFRGCMTELVNRRLLDLEAAY 660
QY 661 KHSIDITAHSCPVEPAAA 678
DB 661 KHSIDITAHSCPVEPAAA 678

RESULT 3
US-08-435-436-2
; Sequence 2, Application US/08435436
; Patent No. 5721139
; GENERAL INFORMATION:
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; APPLICANT: Chen, Jjian

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: TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: patin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/435,436
: FILING DATE: 10-MAY-1995
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Lee, Wendy M.
: REGISTRATION NUMBER: 00,000
: REFERENCE/DOCKET NUMBER: 946-3
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-1994
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 678 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
US-08-435-436-2

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Query Match      98.7%; Score 3628; DB 1; Length 678;
Best local Similarity 100.0%; Pred. No. 1.5e-309;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 LERECEVEELCSREAREVEENDEPETYFPRYLDCINKGSPYTKSGFATCVQNLPDQC 120
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DB 121 TNPICDRKGTQACQDLMGNFCLCKAGWGRLCDKDVNECSQENGGCLQICHNKPQSFHC 180
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DB 181 SCHSGFELSSDGTTCODIDECADSEACGEARCNLPQSYSCLCDEGFAYSSQEKACRDVD 240
QY 181 SCHSGFELSSDGTTCODIDECADSEACGEARCNLPQSYSCLCDEGFAYSSQEKACRDVD 240
DB 181 SCHSGFELSSDGTTCODIDECADSEACGEARCNLPQSYSCLCDEGFAYSSQEKACRDVD 240
QY 241 ECLQGRCEQVCVNSPGSYTCHCDGRGGLKLSQDMDCEDLLPCVPFSAVSXSLYIGRM 300
DB 241 ECLQGRCEQVCVNSPGSYTCHCDGRGGLKLSQDMDCEDLLPCVPFSAVSXSLYIGRM 300
QY 301 FSGTPVIRLRFKRLQPTRLVAEFDFRTPDEGILLFAGGHQSDTWLVALLRAGRLQLQR 360
DB 301 FSGTPVIRLRFKRLQPTRLVAEFDFRTPDEGILLFAGGHQSDTWLVALLRAGRLQLQR 360
QY 361 YNGVGVTVSSGPIYINQMOTISVEBELARLVKVRDAVMKIAVAGDLFQPERGLYHLN 420
DB 361 YNGVGVTVSSGPIYINQMOTISVEBELARLVKVRDAVMKIAVAGDLFQPERGLYHLN 420
QY 421 LTVGGPFPFEKDLVQINPRLDGCMRSMMNLNGEDTTIOETVAVNTRMOCFSYTERGSEF 480
DB 421 LTVGGPFPFEKDLVQINPRLDGCMRSMMNLNGEDTTIOETVAVNTRMOCFSYTERGSEF 480
QY 481 PSSGFAFYSLDYWRTEPLDVGTSEWEVEVAHIRPADTQGLPALWAPDLRAVPLSVALY 540

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DB 481 PSSGFAFYSLDYWRTEPLDVGTSEWEVEVAHIRPADTQGLPALWAPDLRAVPLSVALY 540
QY 541 DYHSTKLLKQQLVVLVAEHTALALMEIKVCDGQEHVTVTSIRDEBATLEVDGTGQSEVS 600
DB 541 DYHSTKLLKQQLVVLVAEHTALALMEIKVCDGQEHVTVTSIRDEBATLEVDGTGQSEVS 600
QY 601 AAOLQERLAVLERHRSPLVTFPAGGLPDVPTSAFPTAFYRGCMTELVNRRLLDDEAY 660
DB 601 AAOLQERLAVLERHRSPLVTFPAGGLPDVPTSAFPTAFYRGCMTELVNRRLLDDEAY 660
QY 661 KHSIDTAHSCPPVEPAAA 678
DB 661 KHSIDTAHSCPPVEPAAA 678

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# RESULT 4 US-08-438-863-2

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: Sequence 2, Application US/0843863
: Patent No. 5849585
: GENERAL INFORMATION:
: APPLICANT: Mather, Jennie P.
: APPLICANT: Ronghao Li
: APPLICANT: Chen, Jian
: TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080

```

```

: COMPUTER READABLE FORM:
: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: patin (Genentech)

```

```

: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/438,863
: FILING DATE: 10-MAY-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:

```

```

: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Lee, Wendy M.
: REGISTRATION NUMBER: 00,000
: REFERENCE/DOCKET NUMBER: 946
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-1994
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168

```

```

: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 678 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
US-08-438-863-2

```

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Query Match      98.7%; Score 3628; DB 1; Length 678;
Best local Similarity 100.0%; Pred. No. 1.5e-309;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY 1 MAPSLSPGPAALRRAPQQLLLLLAECALALLPAREATQFLRPRORAFQVFEAKQGH 60
DB 1 MAPSLSPGPAALRRAPQQLLLLLAECALALLPAREATQFLRPRORAFQVFEAKQGH 60
QY 61 LERECEVEELCSREAREVEENDEPETYFPRYLDCINKGSPYTKSGFATCVQNLPDQC 120
DB 61 LERECEVEELCSREAREVEENDEPETYFPRYLDCINKGSPYTKSGFATCVQNLPDQC 120
QY 121 TNPICDRKGTQACQDLMGNFCLCKAGWGRLCDKDVNECSQENGGCLQICHNKPQSFHC 180

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Db      121  |TNPDCRKTQACODLMGNFCLCKAGWGRLCDXDVNCSQENGGCLOICHNKGSFHC|180
Qy      181  |SCHSGFELSSDGRTCODIDECADSEACGEARCKNLPGSYSCLDCBGFAYSQEKACRDVD|240
Db      181  |SCHSGFELSSDGRTCODIDECADSEACGEARCKNLPGSYSCLDCBGFAYSQEKACRDVD|240
Qy      241  |ECLQRCCEQVCVNSPGSYTCHCDGRGGLKLSQDMTCEDILPCVPSVAKSVKSLYLGM|300
Db      241  |ECLQRCCEQVCVNSPGSYTCHCDGRGGLKLSQDMTCEDILPCVPSVAKSVKSLYLGM|300
Qy      301  |FSGTFVIRLRFKRLQPTRLVAEFDFRTDPBEGILLFAGGHQDSTWIVLALRAGRLELQJR|360
Db      301  |FSGTFVIRLRFKRLQPTRLVAEFDFRTDPBEGILLFAGGHQDSTWIVLALRAGRLELQJR|360
Qy      361  |YNGVGRVITSSGPIVNHGMQTTISVEELANLVIKVRDAVMKIAVAGDLFOBERGLYHIN|420
Db      361  |YNGVGRVITSSGPIVNHGMQTTISVEELANLVIKVRDAVMKIAVAGDLFOBERGLYHIN|420
Qy      421  |LTVGGIPFHEKLVOPINRLDGCMSNMWNLNGEDTTIOETVKVNTRMOCFSVTERGSPY|480
Db      421  |LTVGGIPFHEKLVOPINRLDGCMSNMWNLNGEDTTIOETVKVNTRMOCFSVTERGSPY|480
Qy      481  |PSSGFAFYSLDYMRTPLDVGTSTWEVEVAHIRPAADTGVLFALMAPDLRAVPLSVALY|540
Db      481  |PSSGFAFYSLDYMRTPLDVGTSTWEVEVAHIRPAADTGVLFALMAPDLRAVPLSVALY|540
Qy      541  |DYHSTKCLKKQVLVAVEHTALALMEIKVCDQGEHVTVSLRDEGATLEVDGTRGSEVS|600
Db      541  |DYHSTKCLKKQVLVAVEHTALALMEIKVCDQGEHVTVSLRDEGATLEVDGTRGSEVS|600
Qy      601  |AAOLOERLAVLERHLSPLVTFAGGLPDVPTVSAPVTAIFYRCGCMTEVNRRLLDDEAY|660
Db      601  |AAOLOERLAVLERHLSPLVTFAGGLPDVPTVSAPVTAIFYRCGCMTEVNRRLLDDEAY|660
Qy      661  |KXSDITAHSCPVEPAAA 678
Db      661  |KXSDITAHSCPVEPAAA 678

RESULT 5
US-08-438-864-2
; Sequence 2, Application US/08438864
; Patent No. 5955420
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Hammonds, R. Glenn
; APPLICANT: Godowski, Paul J.
; APPLICANT: Mark, Melanie R.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; TITLE OF INVENTION: RSE RECEPTOR ACTIVATION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,864
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/402253
; FILING DATE: 10-MAR-1995
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Wendy M. Lee
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 929P1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/225-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 678 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-438-864-2

Query Match      98.7%; Score 3628; DB 1; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.5e-309;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  |MAPSLSPGPAALRRAPQULILLALAEALALLPAREATQFLRPRQRAFOVFEAKQGH|60
Db      1  |MAPSLSPGPAALRRAPQULILLALAEALALLPAREATQFLRPRQRAFOVFEAKQGH|60
Qy      61  |LERECVEBELCSREARBEVFENDPETDYFPRYLDICINKKGSFYTKNSGFATCVQNLPDQC|120
Db      61  |LERECVEBELCSREARBEVFENDPETDYFPRYLDICINKKGSFYTKNSGFATCVQNLPDQC|120
Qy      121  |TNPDCRKTQACODLMGNFCLCKAGWGRLCDXDVNCSQENGGCLOICHNKGSFHC|180
Db      121  |TNPDCRKTQACODLMGNFCLCKAGWGRLCDXDVNCSQENGGCLOICHNKGSFHC|180
Qy      181  |SCHSGFELSSDGRTCODIDECADSEACGEARCKNLPGSYSCLDCBGFAYSQEKACRDVD|240
Db      181  |SCHSGFELSSDGRTCODIDECADSEACGEARCKNLPGSYSCLDCBGFAYSQEKACRDVD|240
Qy      241  |ECLQRCCEQVCVNSPGSYTCHCDGRGGLKLSQDMTCEDILPCVPSVAKSVKSLYLGM|300
Db      241  |ECLQRCCEQVCVNSPGSYTCHCDGRGGLKLSQDMTCEDILPCVPSVAKSVKSLYLGM|300
Qy      241  |ECLQRCCEQVCVNSPGSYTCHCDGRGGLKLSQDMTCEDILPCVPSVAKSVKSLYLGM|300
Db      241  |ECLQRCCEQVCVNSPGSYTCHCDGRGGLKLSQDMTCEDILPCVPSVAKSVKSLYLGM|300
Qy      301  |FSGTFVIRLRFKRLQPTRLVAEFDFRTDPBEGILLFAGGHQDSTWIVLALRAGRLELQJR|360
Db      301  |FSGTFVIRLRFKRLQPTRLVAEFDFRTDPBEGILLFAGGHQDSTWIVLALRAGRLELQJR|360
Qy      361  |YNGVGRVITSSGPIVNHGMQTTISVEELANLVIKVRDAVMKIAVAGDLFOBERGLYHIN|420
Db      361  |YNGVGRVITSSGPIVNHGMQTTISVEELANLVIKVRDAVMKIAVAGDLFOBERGLYHIN|420
Qy      421  |LTVGGIPFHEKLVOPINRLDGCMSNMWNLNGEDTTIOETVKVNTRMOCFSVTERGSPY|480
Db      421  |LTVGGIPFHEKLVOPINRLDGCMSNMWNLNGEDTTIOETVKVNTRMOCFSVTERGSPY|480
Qy      481  |PSSGFAFYSLDYMRTPLDVGTSTWEVEVAHIRPAADTGVLFALMAPDLRAVPLSVALY|540
Db      481  |PSSGFAFYSLDYMRTPLDVGTSTWEVEVAHIRPAADTGVLFALMAPDLRAVPLSVALY|540
Qy      541  |DYHSTKCLKKQVLVAVEHTALALMEIKVCDQGEHVTVSLRDEGATLEVDGTRGSEVS|600
Db      541  |DYHSTKCLKKQVLVAVEHTALALMEIKVCDQGEHVTVSLRDEGATLEVDGTRGSEVS|600
Qy      601  |AAOLOERLAVLERHLSPLVTFAGGLPDVPTVSAPVTAIFYRCGCMTEVNRRLLDDEAY|660
Db      601  |AAOLOERLAVLERHLSPLVTFAGGLPDVPTVSAPVTAIFYRCGCMTEVNRRLLDDEAY|660
Qy      661  |KXSDITAHSCPVEPAAA 678
Db      661  |KXSDITAHSCPVEPAAA 678

RESULT 6
US-08-438-862-2
; Sequence 2, Application US/08438862
; Patent No. 6033660
; GENERAL INFORMATION:
; APPLICANT: Mather, Jennie P.

```

APPLICANT: Li, Ronghao  
APPLICANT: Chen, Jian  
TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/438,862  
FILING DATE: 10-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 00,000  
REFERENCE/DOCKET NUMBER: 946-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 678 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-438-862-2

Query Match 98.7%; Score 3628; DB 2; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.5e-309;

Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPSLSPGPAALRRAPQQLLLLLAABCALAALLPAREATQFLRPRORAFQVEEAKQGH 60  
DB 1 MAPSLSPGPAALRRAPQQLLLLLAABCALAALLPAREATQFLRPRORAFQVEEAKQGH 60  
QY 61 LERECVEELCSREAREVEFENDEPDTDFYPRYLDCKINKYGSPTKNSGFATCVQNLPDQC 120  
DB 61 LERECVEELCSREAREVEFENDEPDTDFYPRYLDCKINKYGSPTKNSGFATCVQNLPDQC 120  
QY 121 TPNPCDRKGTQACODLMGNFECCKAGWGRLCDKVNNECSQENGCLOICHNKPSFHC 180  
DB 121 TPNPCDRKGTQACODLMGNFECCKAGWGRLCDKVNNECSQENGCLOICHNKPSFHC 180  
QY 181 SCHSGFELSSDGTTCODIDECADSEAGSEARCKNLPGSYCLCDEGFASSQKACRDV 240  
DB 181 SCHSGFELSSDGTTCODIDECADSEAGSEARCKNLPGSYCLCDEGFASSQKACRDV 240  
QY 241 ECLQGRCEQVCNPSSTYCHCDGRGGLKLSQDMTCEDTLPCVPSVAKSVKSLYLGM 300  
DB 241 ECLQGRCEQVCNPSSTYCHCDGRGGLKLSQDMTCEDTLPCVPSVAKSVKSLYLGM 300  
QY 301 FSGTPYIRLRFKRLQPTRLVAEPDFTFPPEGILLFAGGHODSTWLVLLRAGRLQLR 360  
DB 301 FSGTPYIRLRFKRLQPTRLVAEPDFTFPPEGILLFAGGHODSTWLVLLRAGRLQLR 360  
QY 361 YNGVGVTSSGPIVNHGMQTSIVBELANLVKVRDAMVKIAVAGDLFQPERGLYHLN 420  
DB 361 YNGVGVTSSGPIVNHGMQTSIVBELANLVKVRDAMVKIAVAGDLFQPERGLYHLN 420  
QY 421 LTVGGIPFHEKDLVQINRLDGCMSNMWLNAGEPTTIOETVKNTRMOCFSVTERGSFY 480  
DB 421 LTVGGIPFHEKDLVQINRLDGCMSNMWLNAGEPTTIOETVKNTRMOCFSVTERGSFY 480

QY 481 PGSGFAFYSIDYMRTPLDVGSTWEVEVVAHTRPADTGVLFALMA PDLRAYPLSVLV 540  
DB 481 PGSGFAFYSIDYMRTPLDVGSTWEVEVVAHTRPADTGVLFALMA PDLRAYPLSVLV 540  
QY 541 DYHSTKKLKKQVLVAEHTALAMEIKVCDGSHVTVTSIRDEATLEVDGTGQSEVS 600  
DB 541 DYHSTKKLKKQVLVAEHTALAMEIKVCDGSHVTVTSIRDEATLEVDGTGQSEVS 600  
QY 601 AAQLOERLAVLERHLSRSPVLTFAAGLPDVPVTSAPVTAFFRGCTLEVNRLDLDEAY 660  
DB 601 AAQLOERLAVLERHLSRSPVLTFAAGLPDVPVTSAPVTAFFRGCTLEVNRLDLDEAY 660  
QY 661 KHSIDTAHSCPPVEPAAA 678  
DB 661 KHSIDTAHSCPPVEPAAA 678

RESULT 7

US-08-402-253-2  
Sequence 2, Application US/08402253

Patent No. 6211142

GENERAL INFORMATION:

APPLICANT: Chen, Jian

APPLICANT: Hammonds, R. Glenn

APPLICANT: Godowski, Paul J.

APPLICANT: Mark, Melanie R.

TITLE OF INVENTION: RSE RECEPTOR ACTIVATION

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/402,253

FILING DATE: 10-MAR-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Wendy M. Lee

REGISTRATION NUMBER: 00,000

REFERENCE/DOCKET NUMBER: 929

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-1994

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 678 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-402-253-2

Query Match 98.7%; Score 3628; DB 2; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.5e-309;

Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPSLSPGPAALRRAPQQLLLLLAABCALAALLPAREATQFLRPRORAFQVEEAKQGH 60  
DB 1 MAPSLSPGPAALRRAPQQLLLLLAABCALAALLPAREATQFLRPRORAFQVEEAKQGH 60  
QY 61 LERECVEELCSREAREVEFENDEPDTDFYPRYLDCKINKYGSPTKNSGFATCVQNLPDQC 120  
DB 61 LERECVEELCSREAREVEFENDEPDTDFYPRYLDCKINKYGSPTKNSGFATCVQNLPDQC 120

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Db      61 LERECVEBLCSEBEAREVFEENDPETDYFPRYLDCINKGSPYTKNSGFATCVQNLDPQC 120
Qy      121 TPNPCDRKGTQACODLMGNFCLCAAGWGRLCDXDVNCSQENGGCLOICHNKGSFHC 180
Db      121 TPNPCDRKGTQACODLMGNFCLCAAGWGRLCDXDVNCSQENGGCLOICHNKGSFHC 180
Qy      181 SCHSGFELSSDRTQODIDECADSEACGEARCKNLPGSYSCLCDEGFAYSQEKACRDVD 240
Db      181 SCHSGFELSSDRTQODIDECADSEACGEARCKNLPGSYSCLCDEGFAYSQEKACRDVD 240
Qy      241 ECLQRCRCBOVCVNSPGSYTCHCDGRGGLKLSQDMOTCEDILPCVPSVAKSVKSYLYLGM 300
Db      241 ECLQRCRCBOVCVNSPGSYTCHCDGRGGLKLSQDMOTCEDILPCVPSVAKSVKSYLYLGM 300
Qy      301 FSGTPIRLRFKRLQPTRLVAEFDRTPPEGILLFAGGHQDSTWVIALRAGRLEQLR 360
Db      301 FSGTPIRLRFKRLQPTRLVAEFDRTPPEGILLFAGGHQDSTWVIALRAGRLEQLR 360
Qy      361 YNGVRVTVSSGPIVNHGMQTTISVEELARNLVIKVRDAVMKIAVAGDLFOBERGLYHLN 420
Db      361 YNGVRVTVSSGPIVNHGMQTTISVEELARNLVIKVRDAVMKIAVAGDLFOBERGLYHLN 420
Qy      421 LTVGGIPFHEKDLVQPINRDLGCMKSNMNLNGEDTTIOETVKVNTRMOCFSVTERGSFY 480
Db      421 LTVGGIPFHEKDLVQPINRDLGCMKSNMNLNGEDTTIOETVKVNTRMOCFSVTERGSFY 480
Qy      481 PGSGFAFYSLDYMRTPLDVGSTEWEEVVAHIRPADTGVLFALMAPDLRAVPLSVALLY 540
Db      481 PGSGFAFYSLDYMRTPLDVGSTEWEEVVAHIRPADTGVLFALMAPDLRAVPLSVALLY 540
Qy      541 DYHSTKCLKKQOLVLAVENTALALMEIKVCDGQEHVTVSLRDGEATLEVDGTGSGSEVS 600
Db      541 DYHSTKCLKKQOLVLAVENTALALMEIKVCDGQEHVTVSLRDGEATLEVDGTGSGSEVS 600
Qy      601 AAQOLERLAVLBERHLSPVLTTFAGGLPDVPTSAPTYAFRGCMTELVNRRLLDLDEAAY 660
Db      601 AAQOLERLAVLBERHLSPVLTTFAGGLPDVPTSAPTYAFRGCMTELVNRRLLDLDEAAY 660
Qy      661 KHSIDITAHSCPVEPAAA 678
Db      661 KHSIDITAHSCPVEPAAA 678

RESULT 8
US-08-443-866B-2
; Sequence 2, Application US/08443866B
; Patent No. 6255068
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Hammonds, R. Glenn
; TITLE OF INVENTION: RSE RECEPTOR ACTIVATION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,866B
; FILING DATE: 31-May-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/402253
; FILING DATE: 10-MAR-1995
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: P0929D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 678 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-443-866B-2

Query Match      98.7%; Score 3628; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.5e-309;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MAPSLSPGPAALRRAPOLLILLILAAECALALPARAATQFLRPRORAFQVFEAKQGH 60
Db      1 MAPSLSPGPAALRRAPOLLILLILAAECALALPARAATQFLRPRORAFQVFEAKQGH 60
Qy      61 LERECVEBLCSEBEAREVFEENDPETDYFPRYLDCINKGSPYTKNSGFATCVQNLDPQC 120
Db      61 LERECVEBLCSEBEAREVFEENDPETDYFPRYLDCINKGSPYTKNSGFATCVQNLDPQC 120
Qy      121 TPNPCDRKGTQACODLMGNFCLCAAGWGRLCDXDVNCSQENGGCLOICHNKGSFHC 180
Db      121 TPNPCDRKGTQACODLMGNFCLCAAGWGRLCDXDVNCSQENGGCLOICHNKGSFHC 180
Qy      181 SCHSGFELSSDRTQODIDECADSEACGEARCKNLPGSYSCLCDEGFAYSQEKACRDVD 240
Db      181 SCHSGFELSSDRTQODIDECADSEACGEARCKNLPGSYSCLCDEGFAYSQEKACRDVD 240
Qy      241 ECLQRCRCBOVCVNSPGSYTCHCDGRGGLKLSQDMOTCEDILPCVPSVAKSVKSYLYLGM 300
Db      241 ECLQRCRCBOVCVNSPGSYTCHCDGRGGLKLSQDMOTCEDILPCVPSVAKSVKSYLYLGM 300
Qy      241 ECLQRCRCBOVCVNSPGSYTCHCDGRGGLKLSQDMOTCEDILPCVPSVAKSVKSYLYLGM 300
Db      241 ECLQRCRCBOVCVNSPGSYTCHCDGRGGLKLSQDMOTCEDILPCVPSVAKSVKSYLYLGM 300
Qy      301 FSGTPIRLRFKRLQPTRLVAEFDRTPPEGILLFAGGHQDSTWVIALRAGRLEQLR 360
Db      301 FSGTPIRLRFKRLQPTRLVAEFDRTPPEGILLFAGGHQDSTWVIALRAGRLEQLR 360
Qy      361 YNGVRVTVSSGPIVNHGMQTTISVEELARNLVIKVRDAVMKIAVAGDLFOBERGLYHLN 420
Db      361 YNGVRVTVSSGPIVNHGMQTTISVEELARNLVIKVRDAVMKIAVAGDLFOBERGLYHLN 420
Qy      421 LTVGGIPFHEKDLVQPINRDLGCMKSNMNLNGEDTTIOETVKVNTRMOCFSVTERGSFY 480
Db      421 LTVGGIPFHEKDLVQPINRDLGCMKSNMNLNGEDTTIOETVKVNTRMOCFSVTERGSFY 480
Qy      481 PGSGFAFYSLDYMRTPLDVGSTEWEEVVAHIRPADTGVLFALMAPDLRAVPLSVALLY 540
Db      481 PGSGFAFYSLDYMRTPLDVGSTEWEEVVAHIRPADTGVLFALMAPDLRAVPLSVALLY 540
Qy      541 DYHSTKCLKKQOLVLAVENTALALMEIKVCDGQEHVTVSLRDGEATLEVDGTGSGSEVS 600
Db      541 DYHSTKCLKKQOLVLAVENTALALMEIKVCDGQEHVTVSLRDGEATLEVDGTGSGSEVS 600
Qy      601 AAQOLERLAVLBERHLSPVLTTFAGGLPDVPTSAPTYAFRGCMTELVNRRLLDLDEAAY 660
Db      601 AAQOLERLAVLBERHLSPVLTTFAGGLPDVPTSAPTYAFRGCMTELVNRRLLDLDEAAY 660
Qy      661 KHSIDITAHSCPVEPAAA 678
Db      661 KHSIDITAHSCPVEPAAA 678

RESULT 9
US-08-628-747-2
; Sequence 2, Application US/08628747
; Patent No. 6169070
; GENERAL INFORMATION:
; APPLICANT: Chen, Jjian

```

APPLICANT: Godowski, Paul J.  
APPLICANT: Hammond, R. Glenn  
APPLICANT: Mark, Melanie  
APPLICANT: Mather, Jennie P.  
APPLICANT: Li, Ronghao  
TITLE OF INVENTION: RECEPTOR ACTIVATION BY GAS6  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: One DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/628,747  
FILING DATE: 17-APR-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/402,253  
FILING DATE: 10-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/438,861  
FILING DATE: 10-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 00,000  
REFERENCE/DOCKET NUMBER: P929P2PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-225-1994  
TELEFAX: 650-952-9881  
TELEX: 910-371-7168  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 678 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-628-747-2

Query Match 98.5%; Score 3620; DB 2; Length 678;  
Best Local Similarity 99.9%; Pred. No. 7.8e-309;  
Matches 677; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPSLSPGPAALRRAPOLLILLAAECALAAALPAREATQFLPRORAROVEEAAQGH 60  
DB 1 MAPSLSPGPAALRRAPOLLILLAAECALAAALPAREATQFLPRORAROVEEAAQGH 60

QY 61 LERECEVEELCSREAREVEFENDEPDTDFYPRYLDCINKYSPYTKNSGFATCVQNLPPDQC 120  
DB 61 LERECEVEELCSREAREVEFENDEPDTDFYPRYLDCINKYSPYTKNSGFATCVQNLPPDQC 120

QY 121 TTPPCDCKRGTQAQODLMGNFCLCKAGWGRLCDKDVNCSQENGGLQI CHNKPSSFHC 180  
DB 121 TTPPCDCKRGTQAQODLMGNFCLCKAGWGRLCDKDVNCSQENGGLQI CHNKPSSFHC 180

QY 181 SCHSGFELSDGRTCODIDECADSEAGSEARCKNLGSGVSCLCDEGFAVSSQKACARDVD 240  
DB 181 SCHSGFELSDGRTCODIDECADSEAGSEARCKNLGSGVSCLCDEGFAVSSQKACARDVD 240

QY 241 ECLQSGCEQYCVNPSPSYTCDCGRGGLKLSQMDTCEBILPCVPSPVAKSIVSLYGRM 300  
DB 241 ECLQSGCEQYCVNPSPSYTCDCGRGGLKLSQMDTCEBILPCVPSPVAKSIVSLYGRM 300

QY 301 FSGTPIVIRLRFKRLQPTRLVAEPDFRDEGILLPAGGHQDSTWIVLAIARGLQLR 360  
DB 301 FSGTPIVIRLRFKRLQPTRLVAEPDFRDEGILLPAGGHQDSTWIVLAIARGLQLR 360

QY 361 YNGVGRVTSQGPVINHGMWOTISVEBLARNLVIKVNDPAVKIYVAGDLFQPERGLYHLN 420  
DB 361 YNGVGRVTSQGPVINHGMWOTISVEBLARNLVIKVNDPAVKIYVAGDLFQPERGLYHLN 420

QY 421 LTVGIPFHEKDLVQINPRLDGCRSMNMLNGEDTTIQTETVKVTRMQCSYTERGSFY 480  
DB 421 LTVGIPFHEKDLVQINPRLDGCRSMNMLNGEDTTIQTETVKVTRMQCSYTERGSFY 480

QY 481 PGSGFARYSLDYMTPLDVGRTSWVEVVAHHPADTGVLPALMAPDLRAVPLSVLV 540  
DB 481 PGSGFARYSLDYMTPLDVGRTSWVEVVAHHPADTGVLPALMAPDLRAVPLSVLV 540

QY 541 DYHSTKLLKQVLVAVENTALAMEIKVCGQEHVTVLSRDEGATLEVGTRGSGSFS 600  
DB 541 DYHSTKLLKQVLVAVENTALAMEIKVCGQEHVTVLSRDEGATLEVGTRGSGSFS 600

QY 601 AAQLQERLAVLERHLSRSPVLTFAAGLPDVPTSAFVTAFRGCMTELVNRRLDLDEAY 660  
DB 601 AAQLQERLAVLERHLSRSPVLTFAAGLPDVPTSAFVTAFRGCMTELVNRRLDLDEAY 660

QY 661 KHSDTIHSCPPVEPAAA 678  
DB 661 KHSDTIHSCPPVEPAAA 678

RESULT 10  
US-08-282-141-3  
Sequence 3, Application US/08282141  
Patent No. 5538861  
GENERAL INFORMATION:  
APPLICANT: Schneider, Claudio  
APPLICANT: Varnum, Brian  
APPLICANT: Avanzi, Giancarlo  
APPLICANT: Mancioletti, Guido  
TITLE OF INVENTION: Stimulating Factor for the AXL Receptor  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Dehavenland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: United States  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/282,141  
FILING DATE:  
CLASSIFICATION: 435  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 673 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-282-141-3

Query Match 80.4%; Score 2955.5; DB 1; Length 673;  
Best Local Similarity 81.6%; Pred. No. 1.7e-250;  
Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;

QY 7 PGPAALRRAPOLLILLAAECALAAALPAREATQFLPRORAROVEEAAQGHLEBEV 66  
DB 5 PGPAALRRAPOLLILLAAECALAAALPAREATQFLPRORAROVEEAAQGHLEBEV 63

QY 67 EBLCSREAREVEFENDEPDTDFYPRYLDCINKYSPYTKNSGFATCVQNLPPDQTPNPD 126  
DB 67 EBLCSREAREVEFENDEPDTDFYPRYLDCINKYSPYTKNSGFATCVQNLPPDQTPNPD 126

```

Db      64  EVCSKEARAEVENDPETEYFPRYOBCMRKYGRPEEKNDPFAKCVQNLDPQCTPNPCD 123
Qy      127 RKGTOACODLMGNFCLCKAGNGRLCDKDVNECSQENGGCLQICHNKGSHGCHSGF 186
Db      124 KKGTHICODLMGNFCLCKAGNGRLCDKDVNECSQENGGCLQICHNKGSHGCHSGF 183
Qy      187 ELSDGRTCODIDECADSEACGEARCKNLPGSYSLCDEGFAYSSQEKACRVDDECLQR 246
Db      184 SLASDGTQCODIDECADSEACGEARCKNLPGSYSLCDEGFAYSSQEKACRVDDECLQR 243
Qy      247 CEQVCNPSGTYTCHCDGGRGKLKLSQDMPTCEDILPCVPFSAKSVKSLYLGRMFSGTPV 306
Db      244 CEQVCNPSGTYTCHCDGGRGKLKLSQDMPTCEDILPCVPFSAKSVKSLYLGRMFSGTPV 303
Qy      307 IRLRFRLOPTRLVAEPDRTFDPREGILLFAGGHODSTWIVLALPAGRLLEQLRNGVGR 366
Db      304 IRLRFRLOPTRLVAEPDRTFDPREGILLFAGGHODSTWIVLALPAGRLLEQLRNGVGR 363
Qy      367 VTSAGPVINHGMWQITISVELEARNLVIKVRDAVNMKIAVAGDLFQPERGLYHLNLTVGSI 426
Db      364 ITSSGPTINHGMWQITISVELEARNLVIKVRDAVNMKIAVAGDLFQPERGLYHLNLTVGSI 423
Qy      427 PFHEKDLVOPINPRLDGCKRSNMWNLNGEDTTIOETVKVNTRMQCFSVTERGSPFGSGFA 486
Db      424 PFHEKDLVOPINPRLDGCKRSNMWNLNGEDTTIOETVKVNTRMQCFSVTERGSPFGSGFA 483
Qy      487 FYSLDYMRTPLDVGESTWEVVAHIRPAADTGVLFALMADPLRAVPLVALVDYHSTRK 546
Db      484 TYRLNVTYRTSLDVGESTWEVVAHIRPAADTGVLFALMADPLRAVPLVALVDYHSTRK 541
Qy      547 KKKKQVLVAVENTALALMEIKVCDQGEHVTVSLRDGEATLEVDGTQSGSEVSAALOGE 606
Db      542 KKKKQVLVAVENTALALMEIKVCDQGEHVTVSLRDGEATLEVDGTQSGSEVSAALOGE 601
Qy      607 RLAVLERHLRSPVLPFAGGLPDVPTSAVTAFFYRCMTLEVNRLLDDEAYKXSDIT 666
Db      602 RLAVLERHLRSPVLPFAGGLPDVPTSAVTAFFYRCMTLEVNRLLDDEAYKXSDIT 661
Qy      667 AHSCPEVEPA 676
Db      662 SHSCPEVEPA 671

RESULT 11
US-08-435-434-1
; Sequence 1, Application US/08435434
; Patent No. 5714385
; GENERAL INFORMATION:
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; APPLICANT: Chen, Jian
; TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,434
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 946-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-435-434-1

Query Match      80.4%; Score 2955.5; DB 1; Length 673;
Best Local Similarity 81.6%; Pred. No. 1.7e-250;
Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;

Qy      7  PGPALRRAPOLLILLLLAECALALPAREATOPLRPRORARFQVFEAKQGLERECV 66
Db      5  PGPAL-ALGTALLILLLLASBSHTVLLRAREAQFLRPRORARVQVFEAKQGLERECV 63
Qy      67  BELCSKEARAEVENDPETDYFPRYLDICINKYSPYTKNSGFATCVQNLDPQCTPNPCD 126
Db      64  EVCSKEARAEVENDPETEYFPRYOBCMRKYGRPEEKNDPFAKCVQNLDPQCTPNPCD 123
Qy      127 RKGTOACODLMGNFCLCKAGNGRLCDKDVNECSQENGGCLQICHNKGSHGCHSGF 186
Db      124 KKGTHICODLMGNFCLCKAGNGRLCDKDVNECSQENGGCLQICHNKGSHGCHSGF 183
Qy      187 ELSDGRTCODIDECADSEACGEARCKNLPGSYSLCDEGFAYSSQEKACRVDDECLQR 246
Db      184 SLASDGTQCODIDECADSEACGEARCKNLPGSYSLCDEGFAYSSQEKACRVDDECLQR 243
Qy      247 CEQVCNPSGTYTCHCDGGRGKLKLSQDMPTCEDILPCVPFSAKSVKSLYLGRMFSGTPV 306
Db      244 CEQVCNPSGTYTCHCDGGRGKLKLSQDMPTCEDILPCVPFSAKSVKSLYLGRMFSGTPV 303
Qy      307 IRLRFRLOPTRLVAEPDRTFDPREGILLFAGGHODSTWIVLALPAGRLLEQLRNGVGR 366
Db      304 IRLRFRLOPTRLVAEPDRTFDPREGILLFAGGHODSTWIVLALPAGRLLEQLRNGVGR 363
Qy      367 VTSAGPVINHGMWQITISVELEARNLVIKVRDAVNMKIAVAGDLFQPERGLYHLNLTVGSI 426
Db      364 ITSSGPTINHGMWQITISVELEARNLVIKVRDAVNMKIAVAGDLFQPERGLYHLNLTVGSI 423
Qy      427 PFHEKDLVOPINPRLDGCKRSNMWNLNGEDTTIOETVKVNTRMQCFSVTERGSPFGSGFA 486
Db      424 PFHEKDLVOPINPRLDGCKRSNMWNLNGEDTTIOETVKVNTRMQCFSVTERGSPFGSGFA 483
Qy      487 FYSLDYMRTPLDVGESTWEVVAHIRPAADTGVLFALMADPLRAVPLVALVDYHSTRK 546
Db      484 TYRLNVTYRTSLDVGESTWEVVAHIRPAADTGVLFALMADPLRAVPLVALVDYHSTRK 541
Qy      547 KKKKQVLVAVENTALALMEIKVCDQGEHVTVSLRDGEATLEVDGTQSGSEVSAALOGE 606
Db      542 KKKKQVLVAVENTALALMEIKVCDQGEHVTVSLRDGEATLEVDGTQSGSEVSAALOGE 601
Qy      607 RLAVLERHLRSPVLPFAGGLPDVPTSAVTAFFYRCMTLEVNRLLDDEAYKXSDIT 666
Db      602 RLAVLERHLRSPVLPFAGGLPDVPTSAVTAFFYRCMTLEVNRLLDDEAYKXSDIT 661
Qy      667 AHSCPEVEPA 676
Db      662 SHSCPEVEPA 671

RESULT 12
US-08-435-436-1
; Sequence 1, Application US/08435436
; Patent No. 5721139
; GENERAL INFORMATION:
; APPLICANT: Mather, Jennie P.

```

```

APPLICANT: Li, Ronghao
APPLICANT: Chen, Jian
TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,436
FILING DATE: 10-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 946-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-435-436-1

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```

Query Match      80.4%; Score 2955.5; DB 1; Length 673;
Best Local Similarity 81.6%; Pred. No. 1.7e-250;
Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;

```

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QY 7 PGPALRRAPOLLILLIAECALALLLPAREATQFLRPRORAFQVFEAKQGHLERECV 66
DB 5 PGPAA-ALGTALLILLSSSHITVLLRREAQFLRPRORAYQVFEAKQGHLERECV 63
QY 67 BELCSREAREVENDPETDYFYPRLDCINKYSGPYTKNSGFATCVQNLPDQCTPNPCD 126
DB 64 BEVCSKEAREVENDPETEYFYPRYOECMRKRYGRPEEKNPDPFAKCVQNLPDQCTPNPCD 123
QY 127 RKGTAQCOLMGNFCLCKAGNGRLCDVDVNECSQENGCLQICNNKSGSPFCCHSGP 186
DB 124 KKGTHICQDMGNFVCTDVGWGRLLCDVNECVKNGSCSVCNNKSGSPFCACHSGP 183
QY 187 ELSDGRTQODIDECADSEACGEARCKNPGSYSCLCDEGFAYSQEKACRPVDECLQGR 246
DB 184 SLASDQGTQODIDECDSPTCCDARCKNPGSYSCLCDEGYTSSSEKTCQDVDEQQR 243
QY 247 CEQVCNVSFGSYTCHCDGGRGLKLSQMDTCEDILPCVPFSAKYSKSLYLGMFSGTPV 306
DB 244 CEQTCNVSFGSYTCHCDGGRGLKLSQMDTCEDILPCVPFSAKYSKSLYLGMFSGTPV 303
QY 307 ILRLPRLQPTLVAEFDRTPDREGILLFAGHDSSTIVLALRAGRLQLQRYNGVR 366
DB 304 ILRLPRLQPTLVAEFDRTPDREGILLFAGHDSSTIVLALRAGRLQLQRYNGVR 363
QY 367 VTSAGPVINHGMMQOTISVEELANLVIKYNRDAVMKIAVAGDLFQPERGLYHLNLTVGSI 426
DB 364 ITSSGPTINHGMMQOTISVEELANLVIKYNRDAVMKIAVAGDLFQPERGLYHLNLTVGSI 423
QY 427 PHEKDLVQPINRDLGCKRSMWMLNGEDTTTIOETVKVTRMOCPSVTERGSPYGGSGFA 486
DB 424 PKESELVQPINRDLGCKRSMWMLNGEDSAIOETVKANTKMQCFSEVTERGSPFPNGPA 483

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QY 487 FYSLDWMTPLDVGSTSEWEVVAHTRPADGVLFALNAPDLRAVPLSVALVDYHSTK 546
DB 484 TYRLNRYTRISLDGTEETWEKVVARRIPATDGVLLALVGD--DVVISVALVDYHSTK 541
QY 547 KKKQVLLVAVENTALAMEIKVCDQGEHVVTSLRDEGATLEVDGTRGQSEVSAQLOE 606
DB 542 KKKQVLLVAVEDVALAMEIKVCDQGEHVVTSLRDEGATLEVDGTRGQSEVSTAQLOE 601
QY 607 RLAVLERHLSPVLTFAGLPDVPTVSAPYTAFFRGMTLEVNRLDLDEAAVKHSIDT 666
DB 602 RLDTLKTHTLOGSVHTVYVGLPEVSVISAPYTAFFRGMTLEVNKILDLDTASKHSIDT 661
QY 667 AHSCPYEPA 676
DB 662 SHSCPYEHA 671

```

## RESULT 13

US-08-438-863-1

```

Sequence 1, Application US/08438863
Patent No. 5849585
GENERAL INFORMATION:
APPLICANT: Mather, Jennie P.
APPLICANT: Ronghao Li
APPLICANT: Chen, Jian
TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,863
FILING DATE: 10-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 946
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-438-863-1

```

```

Query Match      80.4%; Score 2955.5; DB 1; Length 673;
Best Local Similarity 81.6%; Pred. No. 1.7e-250;
Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;

```

```

QY 7 PGPALRRAPOLLILLIAECALALLLPAREATQFLRPRORAFQVFEAKQGHLERECV 66
DB 5 PGPAA-ALGTALLILLSSSHITVLLRREAQFLRPRORAYQVFEAKQGHLERECV 63
QY 67 BELCSREAREVENDPETDYFYPRLDCINKYSGPYTKNSGFATCVQNLPDQCTPNPCD 126
DB 64 BEVCSKEAREVENDPETEYFYPRYOECMRKRYGRPEEKNPDPFAKCVQNLPDQCTPNPCD 123

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127 RKGTQACDLMGNFCLCKAGGRLCDKDVNECSQENGGCLQICHNKGSTHSCCHSGF 186
124 KKGTTHICDMLGNFPCVCTDGGGRLCDKDVNECVQKNGGCSQVCHNKGSTHSCCHSGF 183
187 ELSSDGTCCODIDECADSEAGCEARCKNLPGSYSLCDEGFAYSSQEKACRVDDECLQGR 246
184 SLASDGTCCODIDECADSEAGCEARCKNLPGSYSLCDEGFAYSSQEKACRVDDECLQGR 243
247 CEQVCVNSPGSYTCHCDGRGGLKLSQMDTCEDILPCVPFSVAKSVKSLYLGRMFSGTPV 306
244 CEQVCVNSPGSYTCHCDGRGGLKLSQMDTCEDILPCVPFSVAKSVKSLYLGRMFSGTPV 303
307 IRLRFRKRLQPTRLAEFDFRTDPPEGVLFFAGGRSDSTWIVGLRAGRLLEQLRYNGVR 366
304 IRLRFRKRLQPTRLAEFDFRTDPPEGVLFFAGGRSDSTWIVGLRAGRLLEQLRYNGVR 363
367 VTSSEPVINHGMMQITISVEELARNLVYKVRDAVMKIAVAGDLFQPERGLYHNLTVGCI 426
364 ITSSGPTINHGMMQITISVEELARNLVYKVRDAVMKIAVAGDLFQPERGLYHNLTVGCI 423
427 PFHEKDLVOPINPRLDGCMRSNMWLNGBEDTTIOETVKVNTMOCFSVTERGSPYSGGFA 486
424 PFKESELVOPINPRLDGCMRSNMWLNGBEDSALIOETVKANTKMOCFSVTERGSPFGNGFA 483
487 FYSLDYMRTPLDVGTSTVEVEVAHIRPAADTVGLFALMAADLRAVPLSVALLVDYHSRK 546
484 TYRLNTRYTRSLDVGETTWEVKVVARIRPATDTGVLLALVGD--DVIVSVALVDYHSRK 541
547 KKKKQVLVAVEHTALALMEIKVCDGQBEHVVTYSLRDEGATLEVDSTRQSEVSAQLOE 606
542 KKKKQVLVAVEHTALALMEIKVCDGQBEHVVTYSLRDEGATLEVDSTRQSEVSAQLOE 601
607 RLAVLERHLRSPVLTFFAGGLPDVPTVSAPVTAFFRCGMLTEVNRLLIDEAAYKXSDT 666
602 RLDTLKLTHLQGSVHTVVGGLPEVSIVASPVTAFFRCGMLTEVNGKILDDTASYKXSDT 661
667 AHSCEPVEPA 676
662 SHSCPEVEHA 671

```

RESULT 14  
 US-08-438-864-1  
 ; Sequence 1, Application US/08438864  
 ; Patent No. 5955420  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Hammonds, R. Glenn  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Mark, Melanie R.  
 ; APPLICANT: Mather, Jennie P.  
 ; APPLICANT: Li, Ronghao  
 ; TITLE OF INVENTION: RSE RECEPTOR ACTIVATION  
 ; NUMBER OF SEQUENCES: 22  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: patin (Genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/438,864  
 ; FILING DATE: 10-MAY-1995  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/402253

```

; FILING DATE: 10-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wendy M. Lee
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 929P1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO. 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-438-864-1

Query Match
Best Local Similarity 80.4%; Score 2955.5; DB 1; Length 673;
Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;

7 PGPALRRAPQULLLLLAECALALPAREATOPIRPROBRAFQVFEAKQHLERECV 66
5 PGPAA-ALGTALLLLASSESHVLLRAREAPQFLRORARAYVFEAKQHLERECV 63
67 EELCSREAREVEFENDPEPTYFPRYLDCINKYGSPTYKNSGFATCVONLPDQCTPNPCD 126
64 BEVCSKEAREVEFENDPEPTYFPRYQCMRYGRPEEKNPDFACVONLPDQCTPNPCD 123
127 RKGTQACDLMGNFCLCKAGGRLCDKDVNECSQENGGCLQICHNKGSTHSCCHSGF 186
124 KKGTTHICDMLGNFPCVCTDGGGRLCDKDVNECVQKNGGCSQVCHNKGSTHSCCHSGF 183
187 ELSSDGTCCODIDECADSEAGCEARCKNLPGSYSLCDEGFAYSSQEKACRVDDECLQGR 246
184 SLASDGTCCODIDECADSEAGCEARCKNLPGSYSLCDEGFAYSSQEKACRVDDECLQGR 243
247 CEQVCVNSPGSYTCHCDGRGGLKLSQMDTCEDILPCVPFSVAKSVKSLYLGRMFSGTPV 306
244 CEQVCVNSPGSYTCHCDGRGGLKLSQMDTCEDILPCVPFSVAKSVKSLYLGRMFSGTPV 303
307 IRLRFRKRLQPTRLAEFDFRTDPPEGVLFFAGGRSDSTWIVGLRAGRLLEQLRYNGVR 366
304 IRLRFRKRLQPTRLAEFDFRTDPPEGVLFFAGGRSDSTWIVGLRAGRLLEQLRYNGVR 363
367 VTSSEPVINHGMMQITISVEELARNLVYKVRDAVMKIAVAGDLFQPERGLYHNLTVGCI 426
364 ITSSGPTINHGMMQITISVEELARNLVYKVRDAVMKIAVAGDLFQPERGLYHNLTVGCI 423
427 PFHEKDLVOPINPRLDGCMRSNMWLNGBEDTTIOETVKVNTMOCFSVTERGSPYSGGFA 486
424 PFKESELVOPINPRLDGCMRSNMWLNGBEDSALIOETVKANTKMOCFSVTERGSPFGNGFA 483
487 FYSLDYMRTPLDVGTSTVEVEVAHIRPAADTVGLFALMAADLRAVPLSVALLVDYHSRK 546
484 TYRLNTRYTRSLDVGETTWEVKVVARIRPATDTGVLLALVGD--DVIVSVALVDYHSRK 541
547 KKKKQVLVAVEHTALALMEIKVCDGQBEHVVTYSLRDEGATLEVDSTRQSEVSAQLOE 606
542 KKKKQVLVAVEHTALALMEIKVCDGQBEHVVTYSLRDEGATLEVDSTRQSEVSAQLOE 601
607 RLAVLERHLRSPVLTFFAGGLPDVPTVSAPVTAFFRCGMLTEVNRLLIDEAAYKXSDT 666
602 RLDTLKLTHLQGSVHTVVGGLPEVSIVASPVTAFFRCGMLTEVNGKILDDTASYKXSDT 661
667 AHSCEPVEPA 676
662 SHSCPEVEHA 671

```

RESULT 15  
 US-08-438-862-1  
 ; Sequence 1, Application US/08438862  
 ; Patent No. 6033660



GENERAL INFORMATION:  
APPLICANT: Mather, Jennie P.  
APPLICANT: Li, Ronghao  
APPLICANT: Chen, Jian  
TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: pacin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/438,862  
FILING DATE: 10-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 00,000  
REFERENCE/DOCKET NUMBER: 946-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEO ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 673 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-438-862-1

Query Match 80.4%; Score 2955.5; DB 2; Length 673;  
Best Local Similarity 81.6%; Pred. No. 1.7e-250;  
Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;  
Qy 7 PGPALRRAPQULLLLAECALALLPAREATQPLRPORARRAFOVEEAKOGHLEBECV 66  
Db 5 PGPAA-ALGTALLLLASSSHTVLLRAREAAQFLPRORRAYOVFEAKOGHLEBECV 63  
Qy 67 BELCSREAREVENDEPETDYFYPRYLDCKINKYSPYTKNSGFATCVQNLPDCTPNPCD 126  
Db 64 EEVCSKEAREVENDEPETDYFYPRYQECMRKYGREBEKNPDPKACVQNLPDCTPNPCD 123  
Qy 127 RKGTQACQDLMGNFCLCAWGGRLCDKDVNCSQENGGCLQICHNKPGSPHCSCHSGF 186  
Db 124 KKGTHICQDLMGNFCLCAWGGRLCDKDVNCSQENGGCLQICHNKPGSPHCSCHSGF 183  
Qy 187 BLSSDRTQDIDECADSEACGEARCKNPGSYSCIDBGFAYSSOEKACRDVDECLQGR 246  
Db 184 SLASDQTCQDIDECADSEACGEARCKNPGSYSCIDBGFAYSSOEKACRDVDECLQGR 243  
Qy 247 CEQVCNAPSGSYTCHCDGRGGLKLSQDMTCEDILPCVPPSVAKSVKSLYLGRMFGSTPY 306  
Db 244 CEQVCNAPSGSYTCHCDGRGGLKLSQDMTCEDILPCVPPSVAKSVKSLYLGRMFGSTPY 303  
Qy 307 IRLRFRLQPTRLVAFDRTFDPBEGILLPAGGHQDSTWIVLALRAGRLLEQLRYNGVGR 366  
Db 304 IRLRFRLQPTRLVAFDRTFDPBEGILLPAGGHQDSTWIVLALRAGRLLEQLRYNGVGR 363  
Qy 367 VTSSEGVINHGMMQTSVEBELARNLYIKNRDAVMKIAVAGDLFOBERGILYHNLTVGGI 426  
Db 364 ITSSGPTINHGMQTSVEBELARNLYIKNRDAVMKIAVAGDLFOBERGILYHNLTVGGI 423  
Qy 427 PFEKDLVQPINRLDGMRSNMWLNGBDPTTIOETVKVNTRMQCFSTERGSPYPSGFA 486

Db 424 PFEKSELVQPINRLDGMRSNMWLNGBDPTTIOETVKVNTRMQCFSTERGSPYPSGFA 483  
Qy 487 FYSLDYMRTPLDVGTSTESTWEYEVVAHIRPAADTGVLPALNAPDIRAIVPLSYALVDYHSTK 546  
Db 484 TYRLNTRYTSIDVGTETTWEEKVVARIRPATDGVLLALVGD--DVIVSVALVDYHSTK 541  
Qy 547 KLKKQVLVLAVERHALAMEIKVCDGQEHVTVSLRGEATLEVDGTRGQSEVSAQLOE 606  
Db 542 KLKKQVLVLAVERHALAMEIKVCDGQEHVTVSLRGEATLEVDGTRGQSEVSAQLOE 601  
Qy 607 RLAVLERHLRSPVLTFFAGGLPDVPTSAPTYAFYRGCMTELVNRRLLDLDEAAVYKHSIDT 666  
Db 602 RLDTLKTHLGGSVHTYVGLPEVSVISAPVTAFYRGCMTELVNRRLLDLDEAAVYKHSIDT 661  
Qy 667 AHSCEPVEPA 676  
Db 662 SHSCPPVEHA 671

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Job time : 53 secs

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OM protein - protein search, using sw model

Run on: June 29, 2006, 11:28:31 ; Search time 20 Seconds  
(without alignments)  
810.155 Million cell updates/sec

Title: US-10-671-054-1  
Perfect score: 3675  
Sequence: 1 MAPSLSPGPAALRRAPQLL.....AHSCPYEPAADYKDDDK 686

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 103426 seqs, 23619683 residues

Total number of hits satisfying chosen parameters: 103426

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: Published Applications AA New:  
2: /EMC\_Celerra\_SIDS3/prodata/1/pubppaa/US09\_NEW\_PUB pep.\*  
3: /EMC\_Celerra\_SIDS3/prodata/1/pubppaa/US06\_NEW\_PUB pep.\*  
4: /EMC\_Celerra\_SIDS3/prodata/1/pubppaa/US07\_NEW\_PUB pep.\*  
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8: /EMC\_Celerra\_SIDS3/prodata/1/pubppaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	325.5	8.9	1821	US-10-505-928-451	Sequence 451, App
2	323.5	8.8	448	US-11-267-942-5	Sequence 5, Appli
3	321	8.7	493	US-10-505-928-676	Sequence 676, App
4	320	8.7	493	US-11-267-942-2	Sequence 2, Appli
5	319	8.7	448	US-11-267-942-3	Sequence 3, Appli
6	319	8.7	493	US-10-196-749-408	Sequence 408, App
7	319	8.7	493	US-11-267-942-4	Sequence 4, Appli
8	316	8.6	1418	US-11-217-997-38	Sequence 38, Appli
9	300	8.2	5635	US-10-766-760-2	Sequence 2, Appli
10	296	8.1	444	US-10-511-937-2962	Sequence 2962, Ap
11	296	8.1	444	US-10-511-937-3014	Sequence 3014, Ap
12	296	8.1	444	US-11-183-218-8	Sequence 8, Appli
13	277.5	7.6	462	US-11-183-218-10	Sequence 10, Appli
14	275.5	7.5	1594	US-11-217-997-18	Sequence 18, Appli
15	275.5	7.5	2003	US-11-217-997-8	Sequence 8, Appli
16	272.5	7.4	289	US-11-264-243-8	Sequence 28, Appli
17	272.5	7.4	472	US-11-217-997-28	Sequence 28, Appli
18	272.5	7.4	1198	US-11-217-997-26	Sequence 26, Appli
19	272.5	7.4	1398	US-11-217-997-4	Sequence 4, Appli
20	272.5	7.4	1403	US-11-217-997-12	Sequence 12, Appli
21	272.5	7.4	1404	US-11-217-997-2	Sequence 2, Appli
22	272.5	7.4	1450	US-11-217-997-6	Sequence 6, Appli
23	272.5	7.4	1547	US-11-217-997-22	Sequence 22, Appli
24	272.5	7.4	1577	US-11-217-997-16	Sequence 16, Appli
25	272.5	7.4	1577	US-11-217-997-20	Sequence 20, Appli

26	272.5	7.4	1620	US-11-217-997-42	Sequence 42, Appli
27	272.5	7.4	1653	US-11-217-997-40	Sequence 40, Appli
28	267	7.3	1218	US-11-178-724-21	Sequence 21, Appli
29	263.5	7.2	2556	US-11-264-243-6	Sequence 6, Appli
30	263	7.2	1247	US-10-505-928-371	Sequence 371, App
31	262.5	7.1	439	US-11-293-697-2765	Sequence 2765, Ap
32	261.5	7.1	1953	US-11-264-243-16	Sequence 16, Appli
33	255	6.9	509	US-10-196-749-52	Sequence 52, Appli
34	251	6.8	406	US-10-512-754-2	Sequence 2, Appli
35	249	6.8	575	US-10-511-937-2625	Sequence 2625, Ap
36	247	6.7	1238	US-11-178-724-22	Sequence 22, Appli
37	246.5	6.7	713	US-11-175-714-5	Sequence 5, Appli
38	246.5	6.7	720	US-11-175-714-4	Sequence 4, Appli
39	246.5	6.7	786	US-10-504-973-31	Sequence 31, Appli
40	238.5	6.5	801	US-10-504-973-38	Sequence 38, Appli
41	234.5	6.4	1523	US-10-196-749-290	Sequence 290, App
42	233	6.3	729	US-11-175-714-8	Sequence 8, Appli
43	231.5	6.3	229	US-11-293-697-4810	Sequence 4810, Ap
44	231.5	6.3	724	US-11-293-697-3263	Sequence 3263, Ap
45	231	6.3	723	US-11-178-724-18	Sequence 18, Appli

## ALIGNMENTS

RESULT 1  
US-10-505-928-451  
; Sequence 451, Application US/10505928  
; Publication No. US20060088532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ludwig Institute for Cancer Research et al.  
; TITLE OR INVENTION: LYMPHATIC ENDOTHELIAL GENES  
; FILE REFERENCE: 28967/39178  
; CURRENT APPLICATION NUMBER: US/10/505,928  
; PRIOR FILING DATE: 2004-08-27  
; PRIOR APPLICATION NUMBER: US 60/363,019  
; NUMBER OF SEQ ID NOS: 866  
; SOFTWARE: PatentIn 3.2  
; SEQ ID NO 451  
; LENGTH: 1821  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-505-928-451

Query Match 8.9%; Score 325.5; DB 6; Length 1821;  
Best Local Similarity 26.8%; Pred. No. 7.3e-18;  
Matches 84; Conservative 35; Mismatches 77; Indels 117; Gaps 13;

83 PENTDFPRRLDCLINKGSPYTKNSGPAATCVOLPD-----Q 119  
832 PSTDVLTSTPGIDRCAGATVNCGPGTCV-NLPDGYRCVSPGYQLHPSQAYCTDNE 890  
120 CTNPCCDRKGTQACODIMGNFCLCKRAG-----GGRL--- 152  
891 CLADPC--KKKGCINRVGSYSCFCYPTGYLTATSGATQECODINECRQPVCSGGQCTNT 948  
153 -----CD-----KDVNECSQ-----ENGCC 167  
949 EGSYHCECDGQYIMVRKGHQODINECRHPGTCPDGRCVNSPGSYTCLACEGVRGGGSC 1008  
168 LQI-----CHKPGSFHSGHGFSLSSGRICODIDEADSEACGEARCN 214  
1009 VDVNECTPGVCAHGKCTINSGSFRCSCEGQYVTSDEKCCQVDECAASASCPYTGCLN 1068  
215 LPSYSYC-LDDEGFAVSSQKACRDVDEC-LQGRCEQ-VCVNSPGSYTC-HCDGRGGLKL 270  
1069 TEGSFACACENGYWNEDEGTACEDJDECAFPVCPISGVCTNAGSFSCDCD--GGYRP 1126  
271 SQDMTCEDILPC 283  
Db 1127 SPUGDSCEVDDEC 1139

RESULT 2  
 US-11-267-942-5  
 ; Sequence 5, Application US/11267942  
 ; Publication No. US20060094054A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schiemann, William P.  
 ; APPLICANT: Albis, Allan R.  
 ; TITLE OF INVENTION: Fibulin-3 and Uses Thereof  
 ; FILE REFERENCE: 2879-109  
 ; CURRENT APPLICATION NUMBER: US/11/267,942  
 ; CURRENT FILING DATE: 2005-11-04  
 ; PRIOR APPLICATION NUMBER: 60/625,598  
 ; PRIOR FILING DATE: 2004-11-04  
 ; PRIOR APPLICATION NUMBER: 60/687,129  
 ; PRIOR FILING DATE: 2005-06-03  
 ; NUMBER OF SEQ ID NOS: 19  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 5  
 ; LENGTH: 448  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-11-267-942-5

Query Match 8.8%; Score 323.5; DB 7; Length 448;  
 Best Local Similarity 33.6%; Pred. No. 1.6e-18;  
 Matches 87; Conservative 31; Mismatches 94; Indels 47; Gaps 15;

QY 55 EAKQHLRECYBE---LC---SREARBEFBNDEPTDYF-----YP--- 90  
 DB 51 EACRG--DMYCVNQNGYLCIPRTNPVYKGPYSNPSTSGPYAAPVPASNPPTS 108  
 QY 91 RYLDICNKXGSPYTKNSGFATCYQNLPDCTPNCORRKQAOQODMGNPFCLCKXGW-- 148  
 DB 109 RPLVC--RFG--YQDEG--NQVD--VDECATDSHCNPTQICINIEGGTSCCTDGYML 161  
 QY 149 --GGRLCDKDVNECSQENGGLQICHNKSGFHCSCSGFELSDDRTCODIDECADSEA 206  
 DB 162 LRGQCL---DIEBC--RYGVCQQLCANVPGSYSCCTGNPTLDDRSQODVNECETEMP 216  
 QY 207 CGBARCKNLPGSYSLCDEBFAVSSEKACRDVDEC--LOGRGEQVCVNSPGSYTHCHG 264  
 DB 217 CVQY--CVNYGSGTICRCDPGELEEDGHCSDMDECSFSEFLCQHCVCVNPQSGYFSCP- 274  
 QY 265 RGGLKLSQDMDTCEIDLPC 283  
 DB 275 -PGYVLLDNRSCQDINEC 292

RESULT 3  
 US-10-505-928-676  
 ; Sequence 676, Application US/10505928  
 ; Publication No. US20060088532A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ludwig Institute for Cancer Research et al.  
 ; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
 ; FILE REFERENCE: 28967/39178  
 ; CURRENT APPLICATION NUMBER: US/10/505,928  
 ; CURRENT FILING DATE: 2004-08-27  
 ; PRIOR APPLICATION NUMBER: US 60/363,019  
 ; PRIOR FILING DATE: 2002-03-07  
 ; NUMBER OF SEQ ID NOS: 866  
 ; SOFTWARE: PatentIn 3.2  
 ; SEQ ID NO 676  
 ; LENGTH: 493  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-505-928-676

Query Match 8.7%; Score 321; DB 6; Length 493;  
 Best Local Similarity 38.2%; Pred. No. 3e-18;  
 Matches 65; Conservative 30; Mismatches 65; Indels 10; Gaps 7;

QY 118 DOCTPNCBRKGTQACODMGNPFCLCKXGW--GGRLCDKDVNECSQENGGLQICHNKP 175  
 DB 175 DECTAGTHNCRADQVCINIRGSPACQCPGYQKRGQC--VDIDECTIP--PYCHQRCVNTP 232  
 QY 176 GSFHCSCSGFELSDDRTCODIDECADSEACGEARCKNLPSSYSLCDEBFAVSSEKXA 235  
 DB 233 GSFYCCGSPGFQLAANNYTCVDINECDASNQCAQ--QCVNIILSFLCQCNQGYELSSDRLN 291  
 QY 236 CRDVECLQGR--CEQVCVNSPGSYTHCHDGRGGLKLSQDMDTCEIDLPC 283  
 DB 292 CEDIDECRTSSYLQYQVCVNEBPKFSQCP--QGYQVRSR--TCQDINEC 338

RESULT 4  
 US-11-267-942-2  
 ; Sequence 2, Application US/11267942  
 ; Publication No. US20060094054A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schiemann, William P.  
 ; APPLICANT: Albis, Allan R.  
 ; TITLE OF INVENTION: Fibulin-3 and Uses Thereof  
 ; FILE REFERENCE: 2879-109  
 ; CURRENT APPLICATION NUMBER: US/11/267,942  
 ; CURRENT FILING DATE: 2005-11-04  
 ; PRIOR APPLICATION NUMBER: 60/625,598  
 ; PRIOR FILING DATE: 2004-11-04  
 ; PRIOR APPLICATION NUMBER: 60/687,129  
 ; PRIOR FILING DATE: 2005-06-03  
 ; NUMBER OF SEQ ID NOS: 19  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 2  
 ; LENGTH: 493  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-11-267-942-2

Query Match 8.7%; Score 321; DB 7; Length 493;  
 Best Local Similarity 38.2%; Pred. No. 3e-18;  
 Matches 65; Conservative 30; Mismatches 65; Indels 10; Gaps 7;

QY 118 DOCTPNCBRKGTQACODMGNPFCLCKXGW--GGRLCDKDVNECSQENGGLQICHNKP 175  
 DB 175 DECTAGTHNCRADQVCINIRGSPACQCPGYQKRGQC--VDIDECTIP--PYCHQRCVNTP 232  
 QY 176 GSFHCSCSGFELSDDRTCODIDECADSEACGEARCKNLPSSYSLCDEBFAVSSEKXA 235  
 DB 233 GSFYCCGSPGFQLAANNYTCVDINECDASNQCAQ--QCVNIILSFLCQCNQGYELSSDRLN 291  
 QY 236 CRDVECLQGR--CEQVCVNSPGSYTHCHDGRGGLKLSQDMDTCEIDLPC 283  
 DB 292 CEDIDECRTSSYLQYQVCVNEBPKFSQCP--QGYQVRSR--TCQDINEC 338

RESULT 5  
 US-11-267-942-3  
 ; Sequence 3, Application US/11267942  
 ; Publication No. US20060094054A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schiemann, William P.  
 ; APPLICANT: Albis, Allan R.  
 ; TITLE OF INVENTION: Fibulin-3 and Uses Thereof  
 ; FILE REFERENCE: 2879-109  
 ; CURRENT APPLICATION NUMBER: US/11/267,942  
 ; CURRENT FILING DATE: 2005-11-04  
 ; PRIOR APPLICATION NUMBER: 60/625,598  
 ; PRIOR FILING DATE: 2004-11-04  
 ; PRIOR APPLICATION NUMBER: 60/687,129  
 ; PRIOR FILING DATE: 2005-06-03  
 ; NUMBER OF SEQ ID NOS: 19  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 3  
 ; LENGTH: 493  
 ; TYPE: PRT





QY 134 QDLMGNFFCLCKAGWGRLCDKDVNE---CSOENGGCLQICHNKPFSFH-CSCHSGFELS 189  
 Db 100 KDQLQSYICFCFLPAFEGRNCEHTKDDQLICVNENGGCEQYCSHTGTGRSCRCHEGYSLL 159  
 QY 190 SDGRTC 195  
 Db 160 ADGVSC 165

## RESULT 11

US-10-511-937-3014  
 ; Sequence 3014, Application US/10511937  
 ; Publication No. US2006008836A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: EXPRESSION DIAGNOSTICS, INC.  
 ; APPLICANT: Mohlgemuth, Jay  
 ; APPLICANT: Fry, Kirk  
 ; APPLICANT: Woodward, Robert  
 ; APPLICANT: Ly, Ngoc  
 ; APPLICANT: Prentice, James  
 ; APPLICANT: Morris, Macdonald  
 ; APPLICANT: Rosenberg, Steven  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
 ; FILE OF INVENTION: AND MONITORING TRANSPLANT REJECTION  
 ; FILE REFERENCE: 506612000104  
 ; CURRENT FILING DATE: 2004-10-19  
 ; PRIOR APPLICATION NUMBER: PCT/US2003/012946  
 ; PRIOR FILING DATE: 2003-04-24  
 ; PRIOR APPLICATION NUMBER: US 10/131,831  
 ; PRIOR FILING DATE: 2002-04-24  
 ; PRIOR APPLICATION NUMBER: US 10/325,899  
 ; PRIOR FILING DATE: 2002-12-20  
 ; NUMBER OF SEQ ID NOS: 3117  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 3014  
 ; LENGTH: 444  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-511-937-3014

Query Match 8.1%; Score 296; DB 6; Length 444;  
 Best Local Similarity 35.5%; Pred. No. 2,7e-16;  
 Matches 66; Conservative 27; Mismatches 65; Indels 28; Gaps 4;

QY 14 RAPQLLLLLAALCALAALLPAREATQFLRPRQRAQVFEBAKQGHLEBCEVHELCSRE 73  
 Db 4 QALRLCLLGLGQCLAAVFTQBEAHGVLHRRRRANAFLBELRPGSLEREBCEQCSFE 63  
 QY 74 EAREVEFENDEPDTYFPRYVDCJNKYGSPTTKNSGFATCVQNLPDQCTPMPCDRKGTOAC 133  
 Db 64 EAREIFKDAERTKLFMTSYSD-----GDCASSPCQNG--SC 99  
 QY 134 QDLMGNFFCLCKAGWGRLCDKDVNE---CSOENGGCLQICHNKPFSFH-CSCHSGFELS 189  
 Db 100 KDQLQSYICFCFLPAFEGRNCEHTKDDQLICVNENGGCEQYCSHTGTGRSCRCHEGYSLL 159  
 QY 190 SDGRTC 195  
 Db 160 ADGVSC 165

## RESULT 12

US-11-183-218-8  
 ; Sequence 8, Application US/11183218  
 ; Publication No. US20060088906A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Neose Technologies, Inc.  
 ; APPLICANT: Defrees, Shawn  
 ; APPLICANT: Zopf, David  
 ; APPLICANT: Bayer, Robert  
 ; APPLICANT: Hakes, David  
 ; APPLICANT: Chen, Xi

APPLICANT: Bove, Caryne  
 ; TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND  
 ; FILE OF INVENTION: GLYCOCONJUGATION OF ERYTHROPOIETIN  
 ; FILE REFERENCE: 040853-01-5083-US02  
 ; CURRENT FILING DATE: 2005-07-15  
 ; PRIOR APPLICATION NUMBER: US/11/183,218  
 ; PRIOR FILING DATE: 2005-07-15  
 ; PRIOR APPLICATION NUMBER: US 10/410,945  
 ; PRIOR FILING DATE: 2003-04-09  
 ; PRIOR APPLICATION NUMBER: PCT/US02/32263  
 ; PRIOR FILING DATE: 2002-10-09  
 ; PRIOR APPLICATION NUMBER: US 60/407,527  
 ; PRIOR FILING DATE: 2002-08-28  
 ; PRIOR APPLICATION NUMBER: US 60/404,249  
 ; PRIOR FILING DATE: 2002-08-16  
 ; PRIOR APPLICATION NUMBER: US 60/396,594  
 ; PRIOR FILING DATE: 2002-07-17  
 ; PRIOR APPLICATION NUMBER: US 60/391,777  
 ; PRIOR FILING DATE: 2002-06-25  
 ; PRIOR APPLICATION NUMBER: US 60/387,292  
 ; PRIOR FILING DATE: 2002-06-07  
 ; PRIOR APPLICATION NUMBER: US 60/344,692  
 ; PRIOR FILING DATE: 2001-11-19  
 ; PRIOR APPLICATION NUMBER: US 60/334,301  
 ; PRIOR FILING DATE: 2001-11-28  
 ; PRIOR APPLICATION NUMBER: US 60/334,233  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 75  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 8  
 ; LENGTH: 444  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-11-183-218-8

Query Match 8.1%; Score 296; DB 7; Length 444;  
 Best Local Similarity 35.5%; Pred. No. 2,7e-16;  
 Matches 66; Conservative 27; Mismatches 65; Indels 28; Gaps 4;

QY 14 RAPQLLLLLAALCALAALLPAREATQFLRPRQRAQVFEBAKQGHLEBCEVHELCSRE 73  
 Db 4 QALRLCLLGLGQCLAAVFTQBEAHGVLHRRRRANAFLBELRPGSLEREBCEQCSFE 63  
 QY 74 EAREVEFENDEPDTYFPRYVDCJNKYGSPTTKNSGFATCVQNLPDQCTPMPCDRKGTOAC 133  
 Db 64 EAREIFKDAERTKLFMTSYSD-----GDCASSPCQNG--SC 99  
 QY 134 QDLMGNFFCLCKAGWGRLCDKDVNE---CSOENGGCLQICHNKPFSFH-CSCHSGFELS 189  
 Db 100 KDQLQSYICFCFLPAFEGRNCEHTKDDQLICVNENGGCEQYCSHTGTGRSCRCHEGYSLL 159  
 QY 190 SDGRTC 195  
 Db 160 ADGVSC 165

## RESULT 13

US-11-183-218-10  
 ; Sequence 10, Application US/11183218  
 ; Publication No. US20060088906A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Neose Technologies, Inc.  
 ; APPLICANT: Defrees, Shawn  
 ; APPLICANT: Zopf, David  
 ; APPLICANT: Bayer, Robert  
 ; APPLICANT: Hakes, David  
 ; APPLICANT: Chen, Xi  
 ; APPLICANT: Bove, Caryne  
 ; TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND  
 ; FILE OF INVENTION: GLYCOCONJUGATION OF ERYTHROPOIETIN  
 ; FILE REFERENCE: 040853-01-5083-US02  
 ; CURRENT FILING DATE: US/11/183,218  
 ; CURRENT FILING DATE: 2005-07-15

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; PRIOR APPLICATION NUMBER: US 10/410,945
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: PCT/US02/32263
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/334,301
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/334,233
; PRIOR FILING DATE: 2001-11-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 10
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-183-218-10
```

```

Query Match      7.6%; Score 277.5; DB 7; Length 462;
Best Local Similarity 34.0%; Pred. No. 8,7e-15;
Matches 65; Conservative 30; Mismatches 63; Indels 33; Gaps 6;

QY      12 LRAAPOLLL-----LAAECALALLPAREATQFLRPRORAFQVFEAKQGHLEECY 66
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      8 MAESPILITCLGYLSAATV--FLDHNANKILNRPKRYNSGLBEFVQGNLERECM 65
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      67 BELCSEERREVPENDPETYPRYLDCINKGSPYTKNSGFATCVQNLPDQCTNPDC 126
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      66 BEKCSSEERREVPENETKTERFKQYD-----GDQCESNPCL 103
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      127 RKGTOACODLMGNFCLCKAGWGRLCDKDVNCSOENGCLQICHNK-PGSFHCSCHG 185
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      104 NGG--SCRDINSYECMCFEGFEGKNCELDVT-CNKNKGCEQFCGNSADNKKVVCSTG 160
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      186 FELSSDGRTCQ 196
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      161 YRLAENQKSC 171
```

```

RESULT 14
US-11-217-997-18
; Sequence 18, Application US/11217997
; Publication No. US20060111561A1
; GENERAL INFORMATION:
; APPLICANT: Valerie L. Gerlach
; APPLICANT: Elma R. Fernandes
; APPLICANT: Richard A. Shinkels
; APPLICANT: Weera Patlurajan
; APPLICANT: Vladimir Y. Gusev
; APPLICANT: Stacie (Caeman) Navara
; APPLICANT: Velizar T. Tchernov
; APPLICANT: David W. Anderson
; APPLICANT: Xiaojia (Sasha) Guo
; APPLICANT: Luca Raetelli
; APPLICANT: Mei Zhong
; APPLICANT: Murallidhara Padigaru
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODED THEREBY
; FILE REFERENCE: Cura 551 CIP
; CURRENT FILING DATE: US/11/217,997
; PRIOR APPLICATION NUMBER: 2005-08-31
; PRIOR FILING DATE: 2003-06-03
```

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; PRIOR APPLICATION NUMBER: 10/055,877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: Curesqlst version 0.1
; SEQ ID NO 18
; LENGTH: 1594
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-217-997-18
```

```

Query Match      7.5%; Score 275.5; DB 7; Length 1594;
Best Local Similarity 26.0%; Pred. No. 6,6e-14;
Matches 94; Conservative 33; Mismatches 118; Indels 117; Gaps 15;

QY      5 LSPGPAALRRAPOLLLLLAAECALALLPAREATQFLRPRORAFQVFEAKQGHLEEC 64
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      4 LBEARAGAAVVALVALLLPVPVGSVPRP---LPLDQGMVHCABQGLTLVGR 59
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      65 --CVELL-----CSREERREVPENDPETYPRYLDCINKGSPYTKN 106
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      60 QPCVQALSHTVPMVRAGCGMAVCVGERRTVY-----YMG---YROYTTTE 103
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      107 S-GFATCVQN-----LPDQCTNPDCRKG-----TOACODLMGNFCLCKAGWG 149
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      104 ARTVLRCGCGWTOQPDSECLNBSASLCFHGRCVPSSAOPCH-----CFPGFQ 154
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      150 GRLCDVDNCSOENGCLQICHNKPFSFHCSCSGFELSDDRTCODIDECA----- 202
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      155 GPRCQYDVDECRTHNGCCQHRCVNTPGSYLCECKPFRLLHTDSRTCLAINSCALGNGCC 214
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      203 -----DSEAC-----GEA--RCKNLPGSYSLCDEGF 227
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      215 HHCVQLTTRHRCQCRPGFQLOEDGRHCVRRSPCANRNGSCMRCCVVRGLARCECHVG 274
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      228 AVSSQEKACRDVDECLQG--RCQVCVNSPGSYTCH-----DGRGGLKLSOD-MDT 276
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      275 QLAADGKACEDVDECAAGLAQCAHGLNTQGSFKVCVCHAGYELGADGRCYRIEMELVNS 334
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      277 CE 278
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      335 CE 336
```

```

RESULT 15
US-11-264-243-8
; Sequence 8, Application US/11264243
; Publication No. US20060134121A1
; GENERAL INFORMATION:
; APPLICANT: Thurston, Gavin
; APPLICANT: Gale, Nicholas
; APPLICANT: Noguera, Irene
; TITLE OF INVENTION: D1d4 Antagonists, Assays and Therapeutic
; FILE REFERENCE: 2070A
; CURRENT APPLICATION NUMBER: US/11/264,243
; PRIOR FILING DATE: 2005-10-31
```





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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: June 29, 2006, 11:31:46 ; Search time 195 Seconds  
(without alignments)  
18.758 Million cell updates/sec

Title: US-10-671-054-2  
Perfect score: 47  
Sequence: 1 DYKDDDK 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues  
Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database : A\_Geneseq\_8:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*
- 9: geneseqp2005s:\*
- 10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	8	1	AB999240
2	47	100.0	8	1	AA700024
3	47	100.0	8	2	AA809327
4	47	100.0	8	2	AA844496
5	47	100.0	8	2	AA877283
6	47	100.0	8	2	AA887022
7	47	100.0	8	2	AA876469
8	47	100.0	8	2	AA803656
9	47	100.0	8	2	AA831066
10	47	100.0	8	2	AA891045
11	47	100.0	8	2	AA889288
12	47	100.0	8	2	AA894931
13	47	100.0	8	2	AA818236
14	47	100.0	8	2	AA832484
15	47	100.0	8	2	AA800971
16	47	100.0	8	2	AA809824
17	47	100.0	8	2	AA846330
18	47	100.0	8	2	AA80476
19	47	100.0	8	2	AA854166
20	47	100.0	8	2	AA854166
21	47	100.0	8	2	AA856763
22	47	100.0	8	2	AA82555
23	47	100.0	8	2	AA875874

24	47	100.0	8	2	AA899286	AA899286 FLAG pep
25	47	100.0	8	2	AA854280	AA854280 Peptide s
26	47	100.0	8	2	AA844300	AA844300 Human ser
27	47	100.0	8	2	AA859269	AA859269 Type II I
28	47	100.0	8	2	AA854434	AA854434 Human PSI
29	47	100.0	8	2	AA858571	AA858571 FLAG pep
30	47	100.0	8	2	AA876424	AA876424 FLAG affi
31	47	100.0	8	2	AA817552	AA817552 Synthetic
32	47	100.0	8	2	AA879682	AA879682 Human CSI
33	47	100.0	8	2	AA879770	AA879770 FLAG pep
34	47	100.0	8	2	AA856033	AA856033 Chimeric
35	47	100.0	8	2	AA830566	AA830566 FLAG tag
36	47	100.0	8	2	AA875806	AA875806 FLAG pep
37	47	100.0	8	2	AA854266	AA854266 FLAG pep
38	47	100.0	8	2	AA829748	AA829748 Synthetic
39	47	100.0	8	2	AA879562	AA879562 FLAG pep
40	47	100.0	8	2	AA869953	AA869953 FLAG pep
41	47	100.0	8	2	AA847353	AA847353 Chimeric
42	47	100.0	8	2	AA876407	AA876407 Human PAR
43	47	100.0	8	2	AA856251	AA856251 FLAG pep
44	47	100.0	8	2	AA846969	AA846969 Peptide s
45	47	100.0	8	2	AA868289	AA868289 FLAG pep
46	47	100.0	8	2	AA844008	AA844008 FLAG pep
47	47	100.0	8	2	AA880478	AA880478 Peptide s
48	47	100.0	8	2	AA870592	AA870592 FLAG sequ
49	47	100.0	8	2	AA808734	AA808734 FLAG tag
50	47	100.0	8	2	AA896772	AA896772 Human TRA
51	47	100.0	8	2	AA806471	AA806471 Epitope t
52	47	100.0	8	2	AA899020	AA899020 FLAG pep
53	47	100.0	8	2	AA888371	AA888371 FLAG pep
54	47	100.0	8	2	AA897660	AA897660 FLAG pep
55	47	100.0	8	2	AA808479	AA808479 Human BS2
56	47	100.0	8	2	AA81534	AA81534 FLAG pep
57	47	100.0	8	2	AA806792	AA806792 FLAG pep
58	47	100.0	8	2	AA895670	AA895670 FLAG tag
59	47	100.0	8	2	AA895645	AA895645 Human BS1
60	47	100.0	8	2	AA811721	AA811721 FLAG pep
61	47	100.0	8	2	AA811944	AA811944 FLAG pep
62	47	100.0	8	2	AA82256	AA82256 FLAG pep
63	47	100.0	8	2	AA807740	AA807740 Human bre
64	47	100.0	8	2	AA894250	AA894250 FLAG pep
65	47	100.0	8	2	AA882735	AA882735 Adenoviru
66	47	100.0	8	2	AA842254	AA842254 Synthetic
67	47	100.0	8	2	AA849544	AA849544 FLAG pep
68	47	100.0	8	2	AA806609	AA806609 Human IL-
69	47	100.0	8	2	AA892410	AA892410 Human IL-
70	47	100.0	8	2	AA806911	AA806911 FLAG pep
71	47	100.0	8	2	AA823636	AA823636 Octapepti
72	47	100.0	8	2	AA868029	AA868029 FLAG pep
73	47	100.0	8	2	AA872153	AA872153 Peptide e
74	47	100.0	8	2	AA897648	AA897648 FLAG pep
75	47	100.0	8	2	AA896302	AA896302 C-termina
76	47	100.0	8	2	AA895562	AA895562 FLAG pep
77	47	100.0	8	2	AA809543	AA809543 Human TAB
78	47	100.0	8	2	AA882718	AA882718 Human ZCH
79	47	100.0	8	2	AA806900	AA806900 FLAG affi
80	47	100.0	8	2	AA815328	AA815328 Human pan
81	47	100.0	8	2	AA813471	AA813471 FLAG pep
82	47	100.0	8	2	AA804141	AA804141 Human sli
83	47	100.0	8	2	AA849750	AA849750 Compact s
84	47	100.0	8	2	AA816563	AA816563 Epitope t
85	47	100.0	8	2	AA877538	AA877538 FLAG pep
86	47	100.0	8	2	AA803362	AA803362 N-termina
87	47	100.0	8	2	AA899877	AA899877 FLAG pep
88	47	100.0	8	2	AA810961	AA810961 FLAG pep
89	47	100.0	8	2	AA87937	AA87937 Intracell
90	47	100.0	8	2	AA810094	AA810094 Combinato
91	47	100.0	8	2	AA81938	AA81938 FLAG pep
92	47	100.0	8	2	AA822877	AA822877 FLAG pep
93	47	100.0	8	2	AA86126	AA86126 Human TGF
94	47	100.0	8	2	AA828432	AA828432 FLAG pep
95	47	100.0	8	3		
96	47	100.0	8	3		

97	47	100.0	8	3	AAV95914	AAV95914 FLAG pept	170	47	100.0	8	4	AA849284	AA849284 FLAG tag
98	47	100.0	8	3	AAV53260	AAV53260 Mouse neu	171	47	100.0	8	4	AAE00931	AAE00931 FLAG octa
99	47	100.0	8	3	AAV97366	AAV97366 FLAG pept	172	47	100.0	8	4	AA873625	AA873625 FLAG pept
100	47	100.0	8	3	AAV83142	AAV83142 FLAG pept	173	47	100.0	8	4	AA851513	AA851513 FLAG pept
101	47	100.0	8	3	AAV67423	AAV67423 FLAG pept	174	47	100.0	8	4	AAE11989	AAE11989 Tag #6, t
102	47	100.0	8	3	AA813358	AA813358 FLAG pept	175	47	100.0	8	4	ABR00925	ABr00925 FLAG pept
103	47	100.0	8	3	AAV97132	AAV97132 FLAG pept	176	47	100.0	8	4	AA874300	AA874300 FLAG pept
104	47	100.0	8	3	AAV97183	AAV97183 FLAG pept	177	47	100.0	8	4	AAE08007	AAE08007 FLAG pept
105	47	100.0	8	3	AA808424	AA808424 Peptide d	178	47	100.0	8	4	AA851726	AA851726 FSH alpha
106	47	100.0	8	3	AA803808	AA803808 FLAG pept	179	47	100.0	8	4	AA868336	AA868336 FLAG pept
107	47	100.0	8	3	AAV70870	AAV70870 Peptide t	180	47	100.0	8	5	AA852698	AA852698 FLAG pept
108	47	100.0	8	3	AAV84889	AAV84889 Epitope r	181	47	100.0	8	5	AAE15822	AAE15822 FLAG tag
109	47	100.0	8	3	AAV92251	AAV92251 FLAG-tag	182	47	100.0	8	5	AB806583	AB806583 Beta-secr
110	47	100.0	8	3	AAV96309	AAV96309 FLAG pept	183	47	100.0	8	5	AAU77213	AAU77213 Synthetic
111	47	100.0	8	3	AAV99936	AAV99936 FLAG octa	184	47	100.0	8	5	AAE24638	AAE24638 Synthetic
112	47	100.0	8	3	AAV79315	AAV79315 FLAG tag	185	47	100.0	8	5	AB878473	AB878473 Bacteriop
113	47	100.0	8	3	AAV51945	AAV51945 FLAG pept	186	47	100.0	8	5	AB879204	AB879204 FLAG tag
114	47	100.0	8	3	AAV49275	AAV49275 FLAG pept	187	47	100.0	8	5	AB831625	AB831625 Human AUC
115	47	100.0	8	3	AAV94615	AAV94615 FLAG octa	188	47	100.0	8	5	AAE26099	AAE26099 Novel hum
116	47	100.0	8	3	AAV79579	AAV79579 FLAG octa	189	47	100.0	8	5	AB896490	AB896490 Novel hum
117	47	100.0	8	3	AAV93654	AAV93654 Amino aci	190	47	100.0	8	5	AAE14378	AAE14378 Hydrophil
118	47	100.0	8	3	AA826804	AA826804 N-terminu	191	47	100.0	8	5	AAU81015	AAU81015 FLAG pept
119	47	100.0	8	3	AA829272	AA829272 Human pro	192	47	100.0	8	5	AAE21825	AAE21825 Peptide #
120	47	100.0	8	3	AA804185	AA804185 FLAG pept	193	47	100.0	8	5	AB883168	AB883168 FLAG pept
121	47	100.0	8	3	AA801303	AA801303 FLAG pept	194	47	100.0	8	5	AB876872	AB876872 G-protein
122	47	100.0	8	3	AAV95774	AAV95774 FLAG affi	195	47	100.0	8	5	AA866037	AA866037 Amino aci
123	47	100.0	8	3	AAV95302	AAV95302 FLAG pept	196	47	100.0	8	5	AAU78504	AAU78504 FLAG pept
124	47	100.0	8	3	AAV96952	AAV96952 FLAG pept	197	47	100.0	8	5	AAU78429	AAU78429 FLAG pept
125	47	100.0	8	3	AA815375	AA815375 FLAG pept	198	47	100.0	8	5	AAU97725	AAU97725 Epitope t
126	47	100.0	8	3	AAV96883	AAV96883 C-termina	199	47	100.0	8	5	ABR52353	ABR52353 Peptide r
127	47	100.0	8	3	AA823545	AA823545 Delta1 fl	200	47	100.0	8	5	AAO19088	AAO19088 Human P51
128	47	100.0	8	3	AAV90317	AAV90317 BS325 pro	201	47	100.0	8	5	AAE13526	AAE13526 FLAG pept
129	47	100.0	8	4	AAE11238	AAE11238 Peptide #	202	47	100.0	8	5	AA847920	AA847920 M11-MMP r
130	47	100.0	8	4	AA878975	AA878975 FLAG pept	203	47	100.0	8	5	AA848738	AA848738 FLAG pept
131	47	100.0	8	4	AA813081	AA813081 Epitope t	204	47	100.0	8	5	AAO14438	AAO14438 Synthetic
132	47	100.0	8	4	AA804070	AA804070 C-termina	205	47	100.0	8	5	AAU78636	AAU78636 Synthetic
133	47	100.0	8	4	AA835432	AA835432 Epitope p	206	47	100.0	8	5	AAE22591	AAE22591 Peptide #
134	47	100.0	8	4	AA835440	AA835440 Nascent p	207	47	100.0	8	5	AAO21841	AAO21841 Breast t1
135	47	100.0	8	4	AA869180	AA869180 Murine ne	208	47	100.0	8	5	AB878099	AB878099 Amino aci
136	47	100.0	8	4	AA897013	AA897013 FLAG pept	209	47	100.0	8	5	AB894439	AB894439 Protease
137	47	100.0	8	4	AAE04422	AAE04422 FLAG pept	210	47	100.0	8	5	AAO19170	AAO19170 Human pro
138	47	100.0	8	4	AA819939	AA819939 FLAG pept	211	47	100.0	8	5	AAE18133	AAE18133 FLAG-pept
139	47	100.0	8	4	AA862061	AA862061 FLAG octa	212	47	100.0	8	5	AAO15234	AAO15234 FLAG pept
140	47	100.0	8	4	AA873089	AA873089 RXRalpha/	213	47	100.0	8	5	AB832027	AB832027 Synthetic
141	47	100.0	8	4	AA849752	AA849752 FLAG pept	214	47	100.0	8	5	AB877003	AB877003 Bacteriop
142	47	100.0	8	4	AAE07335	AAE07335 Peptide #	215	47	100.0	8	5	AB879221	AB879221 Bacteriop
143	47	100.0	8	4	AA882969	AA882969 FLAG pept	216	47	100.0	8	5	AB853979	AB853979 FLAG pept
144	47	100.0	8	4	AA850092	AA850092 FLAG pept	217	47	100.0	8	5	AA848731	AA848731 FLAG pept
145	47	100.0	8	4	AAV72749	AAV72749 FLAG octa	218	47	100.0	8	5	AB805641	AB805641 FLAG pept
146	47	100.0	8	4	AA882180	AA882180 FLAG-pept	219	47	100.0	8	5	AAE21834	AAE21834 Peptide #
147	47	100.0	8	4	AA835103	AA835103 FLAG pept	220	47	100.0	8	5	AAU79449	AAU79449 FLAG tag
148	47	100.0	8	4	AAE07158	AAE07158 Peptide t	221	47	100.0	8	5	ABU00725	ABU00725 B lymphoc
149	47	100.0	8	4	AA886312	AA886312 FLAG pept	222	47	100.0	8	5	AAU98374	AAU98374 Synthetic
150	47	100.0	8	4	AAE10443	AAE10443 Anti-DYKD	223	47	100.0	8	5	AB881599	AB881599 FLAG pept
151	47	100.0	8	4	AA852179	AA852179 Peptide t	224	47	100.0	8	5	AB879780	AB879780 FLAG tag
152	47	100.0	8	4	AAE00894	AAE00894 Synthetic	225	47	100.0	8	5	AB832759	AB832759 FLAG tag
153	47	100.0	8	4	AAE08051	AAE08051 Peptide #	226	47	100.0	8	5	ABP54337	ABP54337 FLAG octa
154	47	100.0	8	4	AAE03540	AAE03540 Peptide t	227	47	100.0	8	5	AAU79194	AAU79194 FLAG pept
155	47	100.0	8	4	AAE05046	AAE05046 C-termina	228	47	100.0	8	5	AAE23793	AAE23793 FLAG pept
156	47	100.0	8	4	AAE01989	AAE01989 FLAG pept	229	47	100.0	8	5	ABP68439	ABP68439 FLAG pept
157	47	100.0	8	4	AAU04209	AAU04209 FLAG pept	230	47	100.0	8	5	AB883455	AB883455 FLAG pept
158	47	100.0	8	4	AAE08231	AAE08231 Tag #5 fo	231	47	100.0	8	5	AAE13365	AAE13365 Peptide u
159	47	100.0	8	4	AAU00168	AAU00168 Peptide t	232	47	100.0	8	5	AB807133	AB807133 FLAG pept
160	47	100.0	8	4	AA862661	AA862661 C-termina	233	47	100.0	8	5	AA850571	AA850571 FLAG tag
161	47	100.0	8	4	AAU07188	AAU07188 M2 antibo	234	47	100.0	8	5	AAE18850	AAE18850 FLAG anti
162	47	100.0	8	4	AAV72632	AAV72632 FLAG tag	235	47	100.0	8	5	AAU88019	AAU88019 Tumour ne
163	47	100.0	8	4	AA868615	AA868615 FLAG pept	236	47	100.0	8	5	AAU76531	AAU76531 FLAG tag
164	47	100.0	8	4	AAE11034	AAE11034 FLAG tag	237	47	100.0	8	5	AAO15411	AAO15411 FLAG pept
165	47	100.0	8	4	AA851094	AA851094 FLAG tag	238	47	100.0	8	5	AAO19059	AAO19059 mutation
166	47	100.0	8	4	AA874234	AA874234 FLAG pept	239	47	100.0	8	5	AAE28605	AAE28605 FLAG pept
167	47	100.0	8	4	AA882480	AA882480 FLAG pept	240	47	100.0	8	5	ABJ10902	ABJ10902 K-beta M6
168	47	100.0	8	4	AA899939	AA899939 Human new	241	47	100.0	8	5	AB805002	AB805002 FLAG pept
169	47	100.0	8	4	AAE05400	AAE05400 Anti-DYKD	242	47	100.0	8	5	AB809934	AB809934 P10n pro

243	47	100.0	8	5	ABB07739	Abb07739 FLAG pep	316	47	100.0	8	6	ABP60044	Abp60044 FLAG pep
244	47	100.0	8	5	AAE14768	Aae14768 FLAG pep	317	47	100.0	8	6	ABP96701	Abp96701 FLAG pep
245	47	100.0	8	5	ABB81640	Abb81640 FLAG pep	318	47	100.0	8	6	ABU11922	Abu11922 FLAG pep
246	47	100.0	8	5	ABG97833	Abg97833 FLAG read	319	47	100.0	8	6	ABU38456	Abu38456 FLAG pep
247	47	100.0	8	5	ABG97824	Abg97824 FLAG tag	320	47	100.0	8	6	ADA03349	Ada03349 FLAG pep
248	47	100.0	8	5	AAE13735	Aae13735 FLAG pep	321	47	100.0	8	6	ABG74451	Abg74451 Endophil
249	47	100.0	8	5	AAE15570	Aae15570 Anti-DYK	322	47	100.0	8	6	ABU08631	Abu08631 LSI147-gpe
250	47	100.0	8	5	ABP47227	Abp47227 Human Bly	323	47	100.0	8	6	ABR56717	AbR56717 FLAG tag
251	47	100.0	8	5	ABG33586	Abg33586 Influenza	324	47	100.0	8	6	ABO01252	ABO01252 Zinc flng
252	47	100.0	8	5	ABB80696	Abb80696 Amino aci	325	47	100.0	8	6	ABG73775	Abg73775 Human CS
253	47	100.0	8	5	ABB76275	Abb76275 FLAG pep	326	47	100.0	8	6	ABU08455	ABU08455 FLAG tag
254	47	100.0	8	5	AAE24904	Aae24904 Synthetic	327	47	100.0	8	6	ABU62120	ABU62120 Immugen
255	47	100.0	8	5	ABU03956	Abu03956 FLAG pep	328	47	100.0	8	6	ABB99043	Abb99043 Peptide t
256	47	100.0	8	5	ABP52193	Abp52193 FLAG pep	329	47	100.0	8	6	AAE34694	AAE34694 FLAG tag
257	47	100.0	8	5	AAO22928	Aao22928 Human pap	330	47	100.0	8	6	ABU07887	ABU07887 Novel hum
258	47	100.0	8	5	AAU76908	Aau76908 C-termina	331	47	100.0	8	6	ADA08104	Ada08104 Epitope t
259	47	100.0	8	5	ABP75957	Abp75957 FLAG pep	332	47	100.0	8	6	ABG72134	Abg72134 FLAG pep
260	47	100.0	8	5	AAE25322	Aae25322 Bacteriop	333	47	100.0	8	6	AAE31706	AAE31706 Epitope t
261	47	100.0	8	5	ABB77917	Abb77917 Bacteriop	334	47	100.0	8	6	ABU55851	ABU55851 DYKDDDK
262	47	100.0	8	5	ABP52189	Abp52189 FLAG pep	335	47	100.0	8	6	ABP71104	ABP71104 Amino aci
263	47	100.0	8	5	AAU99567	Aau99567 FLAG pep	336	47	100.0	8	6	ABP72095	ABP72095 FLAG tag/
264	47	100.0	8	5	AAU87053	Aau87053 FLAG pep	337	47	100.0	8	6	ABU08796	ABU08796 C-termina
265	47	100.0	8	5	AAE21098	Aae21098 FLAG pep	338	47	100.0	8	6	ABP56844	ABP56844 FLAG pep
266	47	100.0	8	5	ABG35334	Abg35334 Thrombopo	339	47	100.0	8	6	AAE30830	AAE30830 FLAG tag
267	47	100.0	8	5	ABG35327	Abg35327 Thrombopo	340	47	100.0	8	6	ABG72367	ABG72367 FLAG tag
268	47	100.0	8	5	AAU98511	Aau98511 Matrix me	341	47	100.0	8	6	AAO19756	AAO19756 FLAG pep
269	47	100.0	8	5	ABG31282	Abg31282 FLAG-TAG	342	47	100.0	8	6	ABP58151	ABP58151 FLAG pep
270	47	100.0	8	5	AAE26118	Aae26118 Peptide #	343	47	100.0	8	6	ABP56483	ABP56483 FLAG pep
271	47	100.0	8	5	AAE28630	Aae28630 FLAG pep	344	47	100.0	8	6	ABU66326	ABU66326 FLAG pep
272	47	100.0	8	5	AAU11121	Aau11121 Flg epit	345	47	100.0	8	6	ABP60553	ABP60553 FLAG pep
273	47	100.0	8	5	AAU80474	Aau80474 Peptide F	346	47	100.0	8	6	AAE37228	AAE37228 FLAG tag
274	47	100.0	8	5	ABU07228	Abu07228 Amino aci	347	47	100.0	8	6	AAE32857	AAE32857 FLAG pep
275	47	100.0	8	5	AAE22696	Aae22696 Peptide #	348	47	100.0	8	6	AAE34830	AAE34830 FLAG pep
276	47	100.0	8	5	AAU79878	Aau79878 Novel fla	349	47	100.0	8	6	ABP72586	ABP72586 FLAG pep
277	47	100.0	8	5	ABG31041	Abg31041 Hepatitis	350	47	100.0	8	6	AAE33268	AAE33268 FLAG pep
278	47	100.0	8	5	AAE28944	Aae28944 Flg epit	351	47	100.0	8	6	ABG72477	ABG72477 FLAG mark
279	47	100.0	8	5	AAU11967	Aau11967 Zai1pha1	352	47	100.0	8	6	AAE32770	AAE32770 FLAG tag
280	47	100.0	8	5	ABU05629	Abu05629 Antigenic	353	47	100.0	8	6	ABG74757	ABG74757 H5V-2 HSV
281	47	100.0	8	5	AAU50814	Aau50814 FLAG pep	354	47	100.0	8	6	ABP97237	ABP97237 FLAG pep
282	47	100.0	8	5	AAU77640	Aau77640 FLAG tag	355	47	100.0	8	6	ABU08596	ABU08596 FLAG pep
283	47	100.0	8	5	ABB06981	Abb06981 FLAG pep	356	47	100.0	8	6	AAE37702	AAE37702 FLAG sequ
284	47	100.0	8	5	AAO18219	Aao18219 Synthetic	357	47	100.0	8	6	ABU62645	ABU62645 FLAG pep
285	47	100.0	8	5	ABG97970	Abg97970 Human leu	358	47	100.0	8	6	ADA26311	Ada26311 M2 antiBo
286	47	100.0	8	5	ABU05735	Abu05735 C-termina	359	47	100.0	8	6	ADA94909	Ada94909 Interfero
287	47	100.0	8	5	AAE21868	Aae21868 Peptide #	360	47	100.0	8	6	ADA00849	Ada00849 FLAG pep
288	47	100.0	8	5	AAO18986	Aao18986 FLAG pep	361	47	100.0	8	6	ADA27206	Ada27206 FLAG tag
289	47	100.0	8	5	AAO19214	Aao19214 FLAG pep	362	47	100.0	8	6	ADA00644	ADA00644 FLAG pep
290	47	100.0	8	5	ABG32858	Abg32858 Epitope t	363	47	100.0	8	6	ADA28170	Ada28170 FLAG pep
291	47	100.0	8	5	ABG71819	Abg71819 Peptide t	364	47	100.0	8	6	ADB25837	ADB25837 FLAG pep
292	47	100.0	8	5	ABG32887	Abg32887 FLAG tag	365	47	100.0	8	6	ABU63661	ABU63661 Antigenic
293	47	100.0	8	5	AAU76686	Aau76686 Synthetic	366	47	100.0	8	6	ABO42826	ABO42826 Human G-P
294	47	100.0	8	5	AAO17492	Aao17492 Antibody-	367	47	100.0	8	6	ABO14616	ABO14616 FLAG pep
295	47	100.0	8	5	ABU77484	Abu77484 AAV-he1pe	368	47	100.0	8	6	ADA26385	Ada26385 CS198 pur
296	47	100.0	8	5	AAU98812	Aau98812 C-termina	369	47	100.0	8	7	ABU62136	ABU62136 Epitope t
297	47	100.0	8	5	ABP51812	Abp51812 FLAG octa	370	47	100.0	8	7	ABU08853	ABU08853 C-termina
298	47	100.0	8	5	ABG71842	Abg71842 Peptide F	371	47	100.0	8	7	ADA09664	Ada09664 FLAG tag
299	47	100.0	8	5	ADP83590	Adp83590 Epitope P	372	47	100.0	8	7	ABU62402	ABU62402 FLAG pep
300	47	100.0	8	5	ADJ33315	Adj33315 Bacteriop	373	47	100.0	8	7	ADA09807	Ada09807 FLAG pep
301	47	100.0	8	6	ABU69593	Abu69593 FLAG pep	374	47	100.0	8	7	ADB16982	ADB16982 FLAG pep
302	47	100.0	8	6	ABG75693	Abg75693 FLAG pep	375	47	100.0	8	7	ADB85476	ADB85476 Epitope t
303	47	100.0	8	6	ADA05148	Ada05148 Peptide S	376	47	100.0	8	7	AAE38693	AAE38693 FLAG pep
304	47	100.0	8	6	ADA04916	Ada04916 FLAG pep	377	47	100.0	8	7	ABR62942	ABR62942 FLAG pep
305	47	100.0	8	6	AAE30393	Aae30393 FLAG tag	378	47	100.0	8	7	ADP72675	ADP72675 Human FGF
306	47	100.0	8	6	ABU03169	Abu03169 FLAG-pept	379	47	100.0	8	7	ADC51536	ADC51536 Potential
307	47	100.0	8	6	AAO16241	Aao16241 Synthetic	380	47	100.0	8	7	ADC39149	ADC39149 FLAG pep
308	47	100.0	8	6	ABP73008	Abp73008 Amino aci	381	47	100.0	8	7	AAE39550	AAE39550 Human and
309	47	100.0	8	6	AAAP5544	AAap5544 FLAG pep	382	47	100.0	8	7		
310	47	100.0	8	6	AAO16616	Aao16616 Synthetic	383	47	100.0	8	7		
311	47	100.0	8	6	ABU61985	Abu61985 FLAG pep	384	47	100.0	8	7		
312	47	100.0	8	6	ABU12327	Abu12327 Peptide t	385	47	100.0	8	7		
313	47	100.0	8	6	ABB99645	Abb99645 Amino aci	386	47	100.0	8	7		
314	47	100.0	8	6	ABP73041	Abp73041 Peptide u	387	47	100.0	8	7		
315	47	100.0	8	6	ABU08056	Abu08056 Synthetic	388	47	100.0	8	7		

389	47	100.0	8	7	ADC42904	Adc42904 FLAG epit	462	47	100.0	8	8	ADH76245	Adh76245 FLAG pep
390	47	100.0	8	7	ADC33452	Adc33452 FLAG epit	463	47	100.0	8	8	ADJ34693	Adj34693 FLAG pep
391	47	100.0	8	7	ADG39372	Adg39372 Bacteriop	464	47	100.0	8	8	ADJ23660	Adj23660 FLAG tag
392	47	100.0	8	7	ADC72996	Adc72996 FLAG epit	465	47	100.0	8	8	ADJ25159	Adj25159 FLAG-epit
393	47	100.0	8	7	ADC83638	Adc83638 FLAG pep	466	47	100.0	8	8	ADJ62546	Adj62546 FLAG tag
394	47	100.0	8	7	ADC78262	Adc78262 FLAG epit	467	47	100.0	8	8	ADJ36215	Adj36215 Self-coal
395	47	100.0	8	7	ABW00624	Abw00624 T125 tag	468	47	100.0	8	8	ADJ03828	Adj03828 Amino aci
396	47	100.0	8	7	ABW00757	Abw00757 Metallopr	469	47	100.0	8	8	ADJ36642	Adj36642 Protein P
397	47	100.0	8	7	ADD67235	Add67235 FLAG epit	470	47	100.0	8	8	ADJ41404	Adj41404 Human GPC
398	47	100.0	8	7	ADD68177	Add68177 C-termina	471	47	100.0	8	8	ADK67988	Adk67988 Synthetic
399	47	100.0	8	7	ABBB80306	Abbb80306 FLAG sequ	472	47	100.0	8	8	ADJ88089	Adj88089 Epitope-t
400	47	100.0	8	7	ABW01147	Abw01147 FLAG pep	473	47	100.0	8	8	ADJ57882	Adj57882 FLAG tag
401	47	100.0	8	7	ABW00602	Abw00602 Peptide #	474	47	100.0	8	8	ADJ29443	Adj29443 FLAG epit
402	47	100.0	8	7	ABW01400	Abw01400 Human HEA	475	47	100.0	8	8	ADJ16816	Adj16816 FLAG epit
403	47	100.0	8	7	ABW01459	Abw01459 FLAG epit	476	47	100.0	8	8	ADJ93454	Adj93454 Human BGS
404	47	100.0	8	7	ADG03552	Adg03552 FLAG pep	477	47	100.0	8	8	ADJ50914	Adj50914 IFN-beta-
405	47	100.0	8	7	ADD93432	Add93432 Octapepti	478	47	100.0	8	8	ADJ88258	Adj88258 FLAG pep
406	47	100.0	8	7	ADDE15841	Adde15841 FLAG pep	479	47	100.0	8	8	ADJ71859	Adj71859 FLAG pep
407	47	100.0	8	7	ADDE1578	Adde1578 FLAG epit	480	47	100.0	8	8	ADJ69052	Adj69052 IGF-1R/IR
408	47	100.0	8	7	ADDF71827	Adff71827 FLAG epit	481	47	100.0	8	8	ADJ68820	Adj68820 IGF-1R/IR
409	47	100.0	8	7	ADFF6666	Adff6666 FLAG tag	482	47	100.0	8	8	ADJ68121	Adj68121 FLAG epit
410	47	100.0	8	7	ABW02218	Abw02218 Bacteriop	483	47	100.0	8	8	ADJ27330	Adj27330 FLAG tag
411	47	100.0	8	7	ADFF69357	Adff69357 Goodpastu	484	47	100.0	8	8	ADK43172	Adk43172 FLAG pep
412	47	100.0	8	7	ADDE3708	Adde3708 Tag pep	485	47	100.0	8	8	ADM83503	Adm83503 FLAG pep
413	47	100.0	8	7	ADFE2087	Adfe2087 Human CCR	486	47	100.0	8	8	ADJ24296	Adj24296 FLAG pep
414	47	100.0	8	7	ADFF5337	Adff5337 Adeno-aa	487	47	100.0	8	8	ADK15503	Adk15503 FLAG tag
415	47	100.0	8	7	ADFF6626	Adff6626 FLAG epit	488	47	100.0	8	8	ADM38897	Adm38897 FLAG tag
416	47	100.0	8	7	ABRR83683	Abrr83683 C-termina	489	47	100.0	8	8	ADM38665	Adm38665 Insulin a
417	47	100.0	8	7	ADG24551	Adg24551 FLAG Tag	490	47	100.0	8	8	ADN06109	Adn06109 C-termina
418	47	100.0	8	7	ADFF83602	Adff83602 Cytokine	491	47	100.0	8	8	ADN17178	Adn17178 Peptide u
419	47	100.0	8	7	ADG30406	Adg30406 FLAG pep	492	47	100.0	8	8	ADM28629	Adm28629 FLAG epit
420	47	100.0	8	7	ADG25291	Adg25291 Methionin	493	47	100.0	8	8	ADO06950	Ado06950 FLAG tag
421	47	100.0	8	7	ADG16157	Adg16157 FLAG pep	494	47	100.0	8	8	ADJ60829	Adj60829 FLAG pep
422	47	100.0	8	7	ADG43833	Adg43833 FLAG pep	495	47	100.0	8	8	ADM28579	Adm28579 FLAG pep
423	47	100.0	8	7	ABU64397	Abu64397 Murine Se	496	47	100.0	8	8	ADN16201	Adn16201 FLAG pep
424	47	100.0	8	7	ADG98054	Adg98054 Peptide r	497	47	100.0	8	8	ADN75213	Adn75213 FLAG pep
425	47	100.0	8	7	ADG98834	Adg98834 FLAG epit	498	47	100.0	8	8	ADM97181	Adm97181 Anti-ADAM
426	47	100.0	8	7	ADH34359	Adh34359 FLAG pep	499	47	100.0	8	8	ADN48989	Adn48989 FLAG epit
427	47	100.0	8	7	ADG87507	Adg87507 FLAG pep	500	47	100.0	8	9	AEEO2117	Aee02117 Flag tag
428	47	100.0	8	7	ADG68023	Adg68023 Human TRP							
429	47	100.0	8	7	ADG46717	Adg46717 FLAG epit							
430	47	100.0	8	7	ADH69531	Adh69531 C-termina							
431	47	100.0	8	7	ADH50761	Adh50761 FLAG tag							
432	47	100.0	8	7	ADH53326	Adh53326 FLAG epit							
433	47	100.0	8	7	ADH44607	Adh44607 FLAG tag							
434	47	100.0	8	7	ADH62212	Adh62212 FLAG pep							
435	47	100.0	8	7	ADH63631	Adh63631 FLAG pep							
436	47	100.0	8	7	ADH96129	Adh96129 Insulin r							
437	47	100.0	8	7	ADH96129	Adh96129 Insulin r							
438	47	100.0	8	7	ADJ00943	Adj00943 Human zal							
439	47	100.0	8	7	ADJ26319	Adj26319 Chimeric							
440	47	100.0	8	7	ADJ59016	Adj59016 Amino aci							
441	47	100.0	8	7	ADJ74026	Adj74026 FLAG-1ike							
442	47	100.0	8	7	ADK41232	Adk41232 G-CSF rel							
443	47	100.0	8	7	ADJ64018	Adj64018 Epitope t							
444	47	100.0	8	7	ADJ58647	Adj58647 FLAG epit							
445	47	100.0	8	7	ADM31004	Adm31004 FLAG tag							
446	47	100.0	8	7	ADJ26600	Adj26600 Multimeri							
447	47	100.0	8	7	ADJ66798	Adj66798 Shg Prote							
448	47	100.0	8	7	ADM35466	Adm35466 Human LY1							
449	47	100.0	8	7	ADN62798	Adn62798 FLAG tag							
450	47	100.0	8	8	ADP51135	Adp51135 Human PS2							
451	47	100.0	8	8	ADG45053	Adg45053 Synthetic							
452	47	100.0	8	8	ADP78074	Adp78074 Peptide u							
453	47	100.0	8	8	ADG47239	Adg47239 FLAG pep							
454	47	100.0	8	8	ADG82594	Adg82594 FLAG pep							
455	47	100.0	8	8	ADG20761	Adg20761 FLAG epit							
456	47	100.0	8	8	ADG93200	Adg93200 Novel exp							
457	47	100.0	8	8	ADG71731	Adg71731 FLAG pep							
458	47	100.0	8	8	ADG75430	Adg75430 Human HLA							
459	47	100.0	8	8	ADH70791	Adh70791 Peptide t							
460	47	100.0	8	8	ADH53864	Adh53864 FLAG epit							
461	47	100.0	8	8	ADJ32464	Adj32464 Prostate							

## ALIGNMENTS

## RESULT 1

ID ABB99240 standard; peptide; 8 AA.

AC ABB99240;

DT 17-DEC-2002 (first entry)

DE Identification peptide.

KW Recombinant; protein production; identification peptide.

OS Unidentified.

PN EP150126-A.

PD 31-JUL-1985.

PF 23-JAN-1985; 85EP-00300432.

PR 24-JAN-1984; 84US-00573825.

PX 23-JUL-1987; 87US-00076811.

PA (IMMV ) IMMUNEX CORP.

PI Hopp TP, Bektesh SL, Conlon PJ, March CJ;

DR WPI; 1985-185385/31.

CC The sequence encodes a fusion construct which links a mutant sequence of  
CC human granulocyte-colony stimulating factor to a yeast alpha-factor  
CC leader sequence, fusion proteins capped with this peptide are resistant  
CC to intracellular degradation. See also AAN70029, AAN70031-35 and  
CC

The inventors claim a pharmaceutical compsn. which contains an effective amt. of a recombinant human interleukin-3 protein analogue, rhIL-3, (Asp15, Asp70). The rhIL-3 analogue has AA SEQ in AAR09326. The compsn. may also comprise the N-terminal octapeptide in AAR09327, and a diluent and 1 or more than 1 biological response modifier. The compsn. has a biological specific activity of equal to or more than  $4.0 \times 10$  to the 7 mcg/mg in a human bone marrow proliferation assay, and a binding affinity for human monocyte IL-3 receptors of equal to or more than  $4.0 \times 10$  to the 10 (M to the minus 1). (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)

QY 1 DYKDDDDK 8  
|||  
Db 1 DYKDDDDK 8

```

RESULT 4
AA844496
ID AA844496 standard; protein; 8 AA.
AC
XX
XX
XX
AA844496;
XX
XX
XX
25-MAR-2003 (revised)
DT 26-MAY-1994 (first entry)
DE
XX
XX
Sequence of the M2-FLAG epitope.
DE
XX
XX
Epitope; scFv; single chain antibody fragment; composite antibody.
XX
XX
XX
Synthetic.
XX
XX
WO9324630-A1.
XX
XX
09-DEC-1993.
XX
XX
19-MAY-1993; 93WO-AU000228.
XX
XX
22-MAY-1992; 92AU-0002551.
XX
XX
(AGEN-) AGEN LTD.
XX
XX
Lilley GG, Hudson PJ, Hillyard CJ;
PI
XX
WPI; 1993-405821/50.
DR
XX
XX
Bifunctional recombinant protein - contains particle and analyte binding
PT
XX
XX
moieties, used in agglutination assays pref. on whole blood.
PS
XX
XX
Example; Fig 7; 42pp; English.
XX
XX
Epitopes of the surface protein gp41 from HIV1 and HIV2 virus types may
CC
XX
XX
be combined with epitopes from gp120 surface protein or p24 core protein
CC
XX
XX
or substituted for the M2-FLAG epitope in scFv constructs or added to the
CC
XX
XX
scFv-M2 FLAG construct, thereby producing various bifunctional reagents
CC
XX
XX
capable of binding erythrocytes and serum antibodies which may be present
CC
XX
XX
in patient's serum. The sequences of M2-FLAG, HIV1 and HIV2 epitopes are
CC
XX
XX
given in AA844496, AA844497 and AA844498 respectively. (Updated on 25-MAR
CC
XX
XX
-2003 to correct PN field.)
SQ
XX
XX
Sequence 8 AA;
QY
XX
XX
Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB
XX
XX
1 DYKDDDDK 8
1 DYKDDDDK 8

```

```

PD 13-JUL-1995.
XX
XX
PF 06-JAN-1995; 95WO-US000362.
XX
XX
PR 07-JAN-1994; 94US-00179138.
XX
XX
PR 01-FEB-1994; 94US-00190559.
XX
XX
PA (IMMV ) IMMUNEX CORP.
XX
XX
PI Goodwin RG;
XX
XX
WPI; 1995-255032/33.
XX
XX
PT Human and murine DNA encoding ligand(s) binding to cell surface protein
PT
XX
XX
Fas - useful for studying auto-immune disorder(s) and development of self
PT
XX
XX
-tolerance.
XX
XX
PS Disclosure; Page 6; 38pp; English.
XX
XX
XX
The highly antigenic FLAG peptide is used to facilitate isolation of
CC
XX
XX
fusion proteins contg. Fas-L proteins. The epitope is reversibly bound by
CC
XX
XX
a specific MAb produced by hybridoma 4E1 (ATCC HB 9259), enabling rapid
CC
XX
XX
assay and purification. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
SQ
XX
XX
Sequence 8 AA;
QY
XX
XX
Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB
XX
XX
1 DYKDDDDK 8
1 DYKDDDDK 8

```

```

RESULT 6
AA87022
ID AA87022 standard; peptide; 8 AA.
AC
XX
XX
AA87022;
XX
XX
11-JUN-1996 (first entry)
DT
XX
XX
Flag octapeptide.
DE
XX
XX
B2LRF2; Epstein-Barr virus; EBV; C-type lectin; beta chain; MHC; antigen;
XX
XX
major histocompatibility complex; immunoglobulin; cytotoxic T cell;
XX
XX
autoimmune disease; myasthenia gravis; multiple sclerosis; allergy;
XX
XX
systemic lupus erythematosus; organ transplant rejection; asthma; IL-7;
XX
XX
tissue transplant rejection; therapy; cancer; viral disease; mouse;
XX
XX
interleukin-7.
XX
XX
OS
XX
XX
Synthetic.
XX
XX
WO9530015-A2.
XX
XX
09-NOV-1995.
XX
XX
PD
XX
XX
28-APR-1995; 95WO-US005348.
XX
XX
PF
XX
XX
28-APR-1994; 94US-00235397.
XX
XX
PR
XX
XX
(IMMV ) IMMUNEX CORP.
XX
XX
PA (UMOR ) UNIV MISSOURI
XX
XX
PA (USSH ) US NAT INST OF HEALTH.
XX
XX
PI Alderson M, Armitage RJ, Cohen JI, Comeau MR, Farrah TM,
XX
XX
PI Hutt-Fletcher LM, Spriggs MK;
XX
XX
DR
XX
XX
WPI; 1995-393086/50.
XX
XX
PT Epstein-Barr virus B2LRF2 fusion proteins - used for treating e.g. auto-
XX
XX
immune disease, transplant rejection, allergy, asthma, cancer or viral

```



PT infection.  
 XX  
 PS Example 1; Page 38; 51pp; English.  
 XX  
 CC This sequence represents the Flag octapeptide, and was used in creating a  
 CC BZLF2-immunoglobulin Fc fusion protein (BZLF2/Fc). BZLF2 is a Epstein-  
 CC Barr virus (EBV) protein. To create BZLF2/Fc, this sequence, a mouse  
 CC interleukin-7 (IL-7) leader sequence (see AAR87021), an immunoglobulin Fc  
 CC region (see AAR87023) and a flexible linker (see AAR87024) are joined to  
 CC the extracellular domain (residues 34 to 223) of the BZLF2 sequence (see  
 CC AAR87020). BZLF2 proteins are members of the C-type lectin family. The C-  
 CC type lectin domain is found in type II membrane proteins. The BZLF2  
 CC protein is capable of binding the beta chain of a major  
 CC histocompatibility complex (MHC) class II antigen. Fusion proteins with  
 CC an oligomerizing zipper domain (OZD), instead of an immunoglobulin Fc  
 CC region, can also be created. BZLF2 proteins inhibit antigen-specific  
 CC antibody formation, proliferation of blood mononuclear cells and  
 CC cytotoxic T cell responses. They also exhibit superantigen-like activity.  
 CC The proteins can be used for treating or preventing autoimmune diseases  
 CC such as myasthenia gravis, multiple sclerosis and systemic lupus  
 CC erythematosus. Also, for treating organ or tissue transplant rejection  
 CC and for treating or preventing allergy or asthma. They can be used for  
 CC treating cancer and viral disease, especially EBV infection  
 CC  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYKDDDDK 8  
 DB 1 DYKDDDDK 8  
 RESULT 7  
 AAR76469  
 ID AAR76469 standard; protein; 8 AA.  
 XX  
 AC AAR76469;  
 XX  
 DT 06-MAR-1996 (first entry)  
 XX  
 DE IBI FLAG epitope.  
 XX  
 KM Human: tyrosine kinase; receptor; non-differentiated; blood cell;  
 KW IBI FLAG epitope.  
 XX  
 OS Synthetic.  
 OS  
 PN WO9515386-A1.  
 XX  
 PD 08-JUN-1995.  
 XX  
 PF 02-DEC-1994; 94WO-JP002035.  
 XX  
 PR 02-DEC-1993; 93JP-00302704.  
 XX  
 PA (ASAH) ASAH KASEI KOGYO KK.  
 PI Sakano S, Oono M;  
 DR WPI; 1995-215266/28.  
 DR N-PSDB; AA092644.  
 XX  
 PT Polypeptide and modified versions having a receptor tyrosine kinase  
 PT activity - are expressed in a non-differentiated blood cell but undergo a  
 PT reduction in the expression level as the non-differentiated cell  
 PT differentiates.  
 XX  
 PS Example 8; Page 39; 73pp; Japanese.  
 XX  
 CC AA092644 encodes AAR76469 the IBI FLAG epitope, used in the prepn. of the

CC human non-differentiated blood cell tyrosine kinase receptor  
 XX  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYKDDDDK 8  
 DB 1 DYKDDDDK 8  
 RESULT 8  
 AA03656  
 ID AA03656 standard; peptide; 8 AA.  
 XX  
 AC AA03656;  
 XX  
 DT 22-FEB-1997 (first entry)  
 XX  
 DE FLAG-epitope tag.  
 XX  
 KM FLAG-epitope tag; affinity tag; Fas receptor; FADD; binding;  
 KM Fas-associating protein with novel death domain; apoptosis; gene therapy;  
 KW antibody; immunosay; drug screening; diagnostic; AIDS.  
 KW antitumour; antitumour; cerebroprotective; neuroprotective.  
 XX  
 OS Synthetic.  
 OS  
 PN WO9631603-A2.  
 XX  
 PD 10-OCT-1996.  
 XX  
 PF 28-FEB-1996; 96WO-US002857.  
 XX  
 PR 03-APR-1995; 95US-00416379.  
 PR 18-MAY-1995; 95US-00443982.  
 XX  
 PA (UNMT) UNIV MICHIGAN.  
 PI  
 PI Dixit VM, O'Rourke K;  
 XX  
 DR WPI; 1996-465026/46.  
 XX  
 PT FADD protein that binds to cytoplasmic region of Fas receptor - for  
 PT identifying inhibitors of Fas-associated apoptosis useful for treating  
 PT e.g. AIDS, leukaemia, stroke, etc.  
 XX  
 PS Example 1; Page 51; 96pp; English.  
 XX  
 CC This FLAG-epitope tag peptide has been fused to a Fas receptor, which  
 CC contains a cytoplasmic region binding a novel FADD protein (Fas-  
 CC associating protein with novel death domain, AAT93937), which modulates  
 CC apoptosis induced by activation of the receptor by ligand binding. DNA  
 CC encoding the tag is fused to the Fas gene and mutants by PCR, downstream  
 CC of a putative Fas signal peptide sequence, in a plasmid pcDNA3 vector,  
 CC using a 5'-FLAG PCR primer (AAT93938). The resulting fusion protein is  
 CC expressed in Escherichia coli and used in an assay to demonstrate in vivo  
 CC association of FADD protein and Fas receptor via death domains. FADD DNA  
 CC may be used in gene therapy, and FADD protein or a corresponding antibody  
 CC functions and Fas-associated apoptosis, for use in therapy of e.g. AIDS,  
 CC inflammation, leukaemia, myocardial infarction, degenerative disease, etc  
 XX  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYKDDDDK 8  
 DB 1 DYKDDDDK 8

Db 1 DYKDDDDK 8

RESULT 9  
 AAR91066  
 ID AAR91066 standard; peptide; 8 AA.  
 XX  
 AC AAR91066;  
 XX  
 DT 23-MAY-1996 (first entry)  
 XX  
 DE Affinity tag peptide.  
 XX  
 KM Interleukin-1 type-3 receptor; IL-1-2R; immune-associated disease;  
 KM vector; antibody; therapy; affinity tag.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9607739-A2.  
 XX  
 PD 14-MAR-1996.  
 XX  
 PF 11-SEP-1995; 95WO-US012037.  
 XX  
 PR 09-SEP-1994; 94US-00303957.  
 XX  
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 XX  
 PI Lovenberg TW, Oltersdorf T, Liaw CW, Clevenger W, Desouza EB;  
 DR WPI; 1996-171614/17.  
 XX  
 PT Interleukin-1 type 3 receptor proteins - useful for the treatment of  
 PT immune-associated diseases.  
 XX  
 PS Disclosure; Page 7; 64pp; English.  
 XX  
 CC An affinity tag (AAR91066) may be linked to interleukin-1 type-3  
 CC receptors (see e.g. AAR91064 and AAR91054) produced by recombinant DNA  
 CC technology. The peptide facilitates purification of the expressed  
 CC recombinant protein  
 CC  
 SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
 |||||  
 Db 1 DYKDDDDK 8

RESULT 10  
 AAR91045  
 ID AAR91045 standard; peptide; 8 AA.  
 XX  
 AC AAR91045;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 01-AUG-1996 (first entry)  
 XX  
 DE Antigenic N-terminal peptide for fusion to shuIL-1R.  
 XX  
 KM Interleukin-1 receptor; human; soluble; N-terminal peptide; antigen;  
 KM epitope; shuIL-1R; monoclonal antibody; bovine mucosal enterokinase;  
 KM interleukin-1; IL-1; immune response; mammal; diagnosis; therapy;  
 KM regulation; immune disease; inflammatory disease.  
 XX  
 OS Synthetic.  
 XX  
 PN US5492888-A.  
 XX

PD 20-FEB-1996.  
 XX  
 PF 17-JUN-1992; 92US-00904071.  
 XX  
 PR 25-NOV-1987; 87US-00125627.  
 PR 25-FEB-1988; 88US-00160550.  
 PR 13-OCT-1988; 88US-00258756.  
 PR 21-DEC-1989; 89US-00455488.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 XX  
 PI Sims JF, Dower SK, March CJ, Urdal DL;  
 XX  
 DR WPI; 1996-150236/15.  
 XX  
 PT Use of sol. IL-1 receptors to suppress IL-1-mediated immune responses -  
 PT e.g. for treatment of inflammation in mammals, esp. humans.  
 XX  
 PS Disclosure; Col 8; 22pp; English.  
 XX  
 CC This sequence represents an antigenic N-terminal peptide epitope. This  
 CC sequence can be fused to soluble human interleukin-1 receptor (shuIL-1R).  
 CC By using this sequence, recombinant shuIL-1R can be assayed and purified  
 CC easily, by using a monoclonal antibody that reversibly binds this  
 CC epitope. By using bovine mucosal enterokinase, this sequence can be  
 CC cleaved from the recombinant shuIL-1R. Proteins capped with this peptide  
 CC may also be resistant to intracellular digestion in E. coli. The shuIL-1R  
 CC can be used in a method for suppressing interleukin-1 (IL-1) mediated  
 CC immune responses in a mammal. The method comprises administering an  
 CC effective amount of shuIL-1R to the mammal, preferably in a dose of 500ng  
 CC -5mg/kg/day. The shuIL-1R is effective for use in assay, diagnosis or  
 CC therapy for regulation of immune or inflammatory activities, in contrast  
 CC to membrane-bound full-length mature IL-1 receptors. (Updated on 25-MAR-  
 CC 2003 to correct PF field.)  
 XX  
 SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
 |||||  
 Db 1 DYKDDDDK 8

RESULT 11  
 AAR89288  
 ID AAR89288 standard; peptide; 8 AA.  
 XX  
 AC AAR89288;  
 XX  
 DT 13-APR-1996 (first entry)  
 XX  
 DE FLAG affinity tail peptide.  
 XX  
 KM FLAG; affinity tail; immunoaffinity chromatography; purification;  
 KM affinity chromatography; immunoassay; monoclonal antibody;  
 KM fusion protein; cleavage; cattle mucosal enterokinase; LfERK-5; cytokine;  
 KM elk; hek; protein-tyrosine-kinase; receptor; human fetal brain; cloning;  
 KM drug delivery; cell targeting; cytostatic; leukaemia; therapy.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9601839-A1.  
 XX  
 PD 25-JAN-1996.  
 XX  
 PF 06-JUL-1995; 95WO-US008534.  
 XX  
 PR 08-JUL-1994; 94US-00271948.  
 XX  
 PA (IMMV ) IMMUNEX CORP.

XX Cereceti DP, Reddy P;  
 XX WPI; 1996-097585/10.  
 XX  
 PT DNA encoding LERK-5 cytokine capable of binding elk and hek - used as  
 PT carrier to deliver attached (anti-leukaemic) agents to cells bearing elk  
 PT or hek, i.e. human leukaemia cell lines JM and LK63.  
 XX  
 PS Disclosure; Page 8; 40pp; English.  
 XX  
 CC The sequence represents a FLAG affinity tail, which may be attached to  
 CC e.g. a full-length or soluble LERK-5 cytokine (AAR89287) to facilitate  
 CC purification. LERK-5 binds elk and hek receptor protein-tyrosine-kinases  
 CC (members of the eph/elk family), and may be isolated e.g. by expression  
 CC from a human fetal brain cell cDNA. The FLAG peptide is highly antigenic,  
 CC and provides an epitope reversibly bound by a specific monoclonal  
 CC antibody, enabling rapid immunoassay and purification by immunoadfinity  
 CC chromatography. The sequence is specifically cleaved by cattle mucosal  
 CC enterokinase at the residue immediately following the Asp-Lys pairing.  
 CC Purified LERK-5 may be used in binding assays to detect elk- or hek-  
 CC expressing cells, to measure elk or hek activity, as a drug delivery for  
 CC elk or hek receptor-specific cell targeting, e.g. for delivery of  
 CC cytostatic agents in leukaemia therapy  
 CC  
 SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYKDDDDK 8  
 |||||  
 Db 1 DYKDDDDK 8

RESULT 12  
 AAR94931  
 ID AAR94931 standard; peptide; 8 AA.  
 XX  
 AC AAR94931;  
 DT 23-OCT-1996 (first entry)  
 XX  
 DE FLAG peptide.  
 XX  
 KW Interleukin-4 receptor; IL-4; interleukin-2 gamma-c receptor; IL-2;  
 KW allergic rhinitis; asthma; atopic dermatitis; eczema; HIV; FLAG.  
 XX  
 OS Synthetic.  
 OS  
 PN WO9611213-A1.  
 PD 18-APR-1996.  
 XX  
 PF 05-OCT-1995; 95WO-US013101.  
 XX  
 PR 07-OCT-1994; 94US-00319496.  
 XX  
 PA (AMGE-) AMGEN BOULDER INC.  
 XX  
 PI Vanderslice RW, Cox GM;  
 XX  
 DR WPI; 1996-209810/21.  
 XX  
 PT Dimeric complex having affinity for interleukin-4 - comprises IL-4-  
 PT receptor homodimer or IL-4-IL2 gamma-c receptor heterodimer, used in  
 PT treatment of e.g. eczema, asthma and HIV.  
 XX  
 XX Example 4; Page 21; 53pp; English.  
 CC FLAG is an octapeptide (AAR94931) that is used to facilitate purification  
 CC of a protein using anti-FLAG monoclonal antibody. A DNA construct was

CC produced that coded for IL-2Rgamma-c FLAG comprising the 254-amino acid  
 CC extracellular domain of human interleukin-2 receptor gamma chain plus an  
 CC additional C-terminal cysteine and the FLAG peptide. The fusion was  
 CC expressed in Sf9 cells using a baculovirus expression system and purified  
 CC by affinity chromatography. IL-2Rgamma-c FLAG can be linked to  
 CC interleukin-4 via a polymeric (PEG) spacer. The resulting dimeric complex  
 CC has affinity for IL-4 and can be used to treat IL-4 mediated disease  
 CC involving elevated Ige levels  
 XX  
 SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYKDDDDK 8  
 |||||  
 Db 1 DYKDDDDK 8

RESULT 13  
 AAM18236  
 ID AAM18236 standard; peptide; 8 AA.  
 XX  
 AC AAM18236;  
 DT 01-OCT-1997 (first entry)  
 XX  
 DE FLAG epitope.  
 XX  
 KW Lysosomal enzyme; lysosome; transgenic plant; glucocerebrosidase;  
 KW alpha-L-iduronidase; IUDA; enzyme replacement therapy; Gaucher disease;  
 KW Hurler syndrome; FLAG.  
 XX  
 OS Synthetic.  
 OS  
 PN WO9710353-A1.  
 PD 20-MAR-1997.  
 XX  
 PF 13-SEP-1996; 96WO-US014730.  
 XX  
 PR 14-SEP-1995; 95US-0003737P.  
 XX  
 PA (VIRG ) VIRGINIA TECH INTELLECTUAL PTY INC.  
 PA (CROP-) CROPTTECH DBV CORP.  
 XX  
 PI Radin DN, Cramer CL, Oishi KK, Weissenborn DL;  
 XX  
 DR WPI; 1997-202248/18.  
 XX  
 PT Production of enzymatically active (modified) lysosomal enzyme in  
 PT transgenic plants - useful in treatment of lysosomal storage disorders.  
 XX  
 PS Claim 6; Page 37; 111pp; English.  
 XX  
 CC The FLAG epitope (AAM18236) is utilised in novel constructs for  
 CC expression of lysosomal enzymes, e.g. human glucocerebrosidase and alpha-  
 CC L-iduronidase in transgenic plants. The epitope coding sequence is fused  
 CC in-frame to the C-terminus of the lysosomal enzyme coding sequence (see  
 CC also AAT71753) in order to facilitate the detection and purification of  
 CC the gene product (see also AAM18237). It is designed to be a hydrophilic  
 CC marker peptide situated on a protein surface to facilitate antibody  
 CC interactions  
 XX  
 SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYKDDDDK 8  
 |||||

```
DB      1 DYKDDDDK 8

RESULT 14
AAM32484
XX      AAM32484 standard; peptide; 8 AA.
XX
AC      AAM32484;
XX
DT      27-MAR-1998 (first entry)
XX
DE      FLAG epitope.
XX
KM      Catalytic antibody; growth factor; B-cell mitogenesis; LHL; L protein;
KM      hen egg lysozyme; FLAG epitope.
XX
OS      Synthetic.
XX
PN      WO9735887-A1.
XX
PD      02-OCT-1997.
XX
PF      26-MAR-1997; 97WO-AU000194.
XX
PR      26-MAR-1996; 96AU-00008951.
XX
PR      27-FEB-1997; 97AU-00005375.
XX
PA      (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI      Koentgen F, Suesse GW, Tarlinton DM, Treutlein HR;
XX
DR      WPI; 1997-489572/45.
XX
PT      New catalytic antibody precursors - comprising a B-cell surface molecule
PT      binding portion which can induce B-cell mitogenesis.
XX
PS      Example 3; Page 40; 109pp; English.
XX
CC      This peptide comprises the FLAG epitope that is recognised by anti-FLAG
CC      monoclonal antibodies. A form of novel growth factor LHL (see AAM32479)
CC      was generated by PCR that contains the FLAG epitope at its N-terminus and
CC      a strep-tag (see AAM32485) at its C-terminus. The construct is designated
CC      LHL.seq (see AAM32481), where L is the immunoglobulin binding entity from
CC      Streptococcus magnum and H is residues 42-62 of hen egg lysozyme.
CC      The FLAG-epitope was added to facilitate the secretion of LHL.seq into
CC      the periplasmic space of host cells. However, this was unsuccessful and
CC      LHL.seq needed to be purified from total bacterial lysate. As a result of
CC      this, the ompA signal peptide was not removed, leading to the formation
CC      of LHL.seq multimers. LHL.seq has identical activity to that of LHL, and
CC      can be used in novel methods for the generation of catalytic antibodies
XX
SQ      Sequence 8 AA;

Query Match      100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYKDDDDK 8
       |||||||
DB      1 DYKDDDDK 8

RESULT 15
AAM00971
ID      AAM00971 standard; peptide; 8 AA.
XX
AC      AAM00971;
XX
DT      12-NOV-1997 (first entry)
XX
DE      FLAG epitope.
XX
KM      DNA binding protein; RNA binding protein; amphipathic peptide;
```

```
KM      acidic extension peptide; gene control; gene regulation; transcription;
KM      dominant negative protein; cancer; drug therapy; drug design;
KM      leucine zipper; FLAG.
XX
OS      Synthetic.
XX
PN      WO9705249-A2.
XX
PD      13-FEB-1997.
XX
PF      31-JUL-1996; 96WO-US012590.
XX
PR      31-JUL-1995; 95US-0001654P.
PR      29-MAY-1996; 96US-0018496P.
XX
PR      31-JUL-1996; 96US-00690011.
XX
PA      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI      Vinson CR, Kcylow D;
XX
DR      WPI; 1997-145687/13.
XX
PT      New nucleic acid binding proteins - having an acidic amino acid sequence
PT      extension at the amino-terminus, to increase ability to regulate gene
PT      transcription, useful e.g. in cancer therapeutics.
XX
PS      Claim 16; Page 58; 144pp; English.
XX
CC      This peptide sequence comprises a FLAG epitope that can be attached to
CC      the N-terminus of a nucleic acid binding protein (NABP) such as a leucine
CC      zipper bZIP protein or bHLH protein. Claimed NABPs having an appended
CC      acidic extension peptide (see AAM00958-65) can regulate the function of a
CC      target nucleic acid or gene to which they are bound, and act as potent
CC      dominant-negative regulators of gene transcription, cell growth and cell
CC      proliferation. They can be used in cancer therapeutics, to treat diseases
CC      caused by eukaryotic microorganisms or by viruses, and as tools for drug
CC      development, rational drug design, and drug and gene therapies
XX
SQ      Sequence 8 AA;

Query Match      100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYKDDDDK 8
       |||||||
DB      1 DYKDDDDK 8

RESULT 16
AAM09824
ID      AAM09824 standard; peptide; 8 AA.
XX
AC      AAM09824;
XX
DT      15-JUL-1997 (first entry)
XX
DE      FLAG epitope tag.
XX
KM      NR4; haemoprotein receptor; interleukin-13 receptor; cytokine; allergy;
KM      asthma; therapy; FLAG.
XX
OS      Synthetic.
XX
PN      WO9715663-A1.
XX
PD      01-MAY-1997.
XX
PF      23-OCT-1996; 96WO-AU000668.
XX
PR      23-OCT-1995; 95AU-00006135.
PR      22-DEC-1995; 95AU-00007276.
PR      09-SEP-1996; 96AU-00002208.
```

XX (AMRA-) AMRAD OPERATIONS PTY LTD.  
 XX  
 XX  
 PI Willson T, Nicola NA, Hilton DJ, Metcalf D, Zhang JG;  
 XX  
 DR WPI; 1997-259018/23.  
 XX  
 PT DNA encoding animal haemopoietin receptor which interacts with  
 PT interleukin-13 - useful to treat asthma, allergy or condition exacerbated  
 PT by IGE production.  
 XX  
 PS Example 2; Page 56; 93pp; English.  
 XX  
 CC Using PCR, a derivative of novel haemoprotein receptor NR4 cDNA was  
 CC generated which encoded the interleukin-3 signal peptide (AAW09823) and  
 CC an N-terminal FLAG epitope tag (AAW09824) preceding the mature coding  
 CC region (Thr27-Pro424) of murine NR4 (see also AAW09821). The PCR product  
 CC was cloned into the mammalian expression vector pBF-BOS  
 XX  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYKDDDDK 8  
 DB 1 DYKDDDDK 8  
 RESULT 17  
 AAW6330  
 ID AAW6330 standard; peptide; 8 AA.  
 XX  
 AC AAW6330;  
 XX  
 DT 08-MAY-1998 (first entry)  
 XX  
 DE Binding domain of chimeric adenovirus penton base protein.  
 XX  
 KM Integrin; cell surface receptor; penton base protein; adenovirus;  
 KM binding site; binding domain; cell surface binding site; gene therapy;  
 KM bispecific molecule; antibody; adenoviral transfer vector; PAT.  
 XX  
 OS Synthetic.  
 XX  
 PN US5712136-A.  
 XX  
 PD 27-JAN-1998.  
 XX  
 PF 17-APR-1996; 96US-00634060.  
 XX  
 PR 08-SEP-1994; 94US-00303162.  
 XX  
 PA (GENV-) GENVEC INC.  
 XX  
 PI Bruder JT, Mcvey DL, Wickham TJ, Roelvink PW, Kovessi I;  
 PI Brough DE;  
 XX  
 DR WPI; 1998-119984/11.  
 XX  
 PT Methods for introducing adenovirus into cells - used for genetic  
 PT engineering and gene therapy.  
 XX  
 PS Claim 14; Col 16; 56pp; English.  
 XX  
 CC The present sequence represents a binding domain of a chimeric adenovirus  
 CC penton base protein. The present sequence contains an epitope for an  
 CC antibody that is preferably not present in wild type adenovirus protein.  
 CC The penton base protein binds to cell surface receptors called integrins.  
 CC The integrins not only provide a binding site for the adenoviral penton  
 CC base protein, but also mediate cellular adhesion to the extracellular  
 CC matrix molecules. The specification describes a method of introducing an

CC adenovirus into a cell in vitro having a particular cell surface binding  
 CC site. The adenovirus is contacted with a bispecific molecule (e.g.  
 CC bispecific antibody) comprising a component that selectively binds a  
 CC binding domain of the penton base protein of the adenovirus and a second  
 CC component that selectively binds the cell surface binding site. A complex  
 CC of the adenovirus and the bispecific molecule is formed, and the cell is  
 CC contacted with it to allow entry of the adenovirus into the cell. The  
 CC methods can be used for research and the vectors can be used for gene  
 CC therapy  
 XX  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYKDDDDK 8  
 DB 1 DYKDDDDK 8  
 RESULT 18  
 AAW80476  
 ID AAW80476 standard; peptide; 8 AA.  
 XX  
 AC AAW80476;  
 XX  
 DT 28-JAN-1999 (first entry)  
 XX  
 DE Peptide sequence encoded by an antisense primer.  
 XX  
 KM EST sequence; CS141; gastrointestinal tract; cancer; Barrett's esophagus;  
 KM gastric ulcer; gastritis; leiomyoma; polyps; Crohn's disease;  
 KM ulcerative colitis; pancreatitis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9844133-A1.  
 XX  
 PD 08-OCT-1998.  
 XX  
 PF 31-MAR-1998; 98WO-US006337.  
 XX  
 PR 31-MAR-1997; 97US-00826489.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;  
 PI Granados EN, Hayden M, Hodges SC, Klass MR, Kratochvil JD;  
 PI Roberts-Rapp L, Russell JC, Stroupe SD;  
 XX  
 DR WPI; 1998-568280/48.  
 XX  
 PT New gastrointestinal tract specific polynucleotides, CS141 - used to  
 PT develop products for the diagnosis and treatment of e.g. cancers, gastric  
 PT ulcer, gastritis, Crohn's disease, ulcerative colitis or pancreatitis.  
 XX  
 PS Example 10; Page 67; 116pp; English.  
 XX  
 CC The present sequence represents a peptide sequence encoded by an  
 CC antisense primer of the invention. The sequence incorporates a  
 CC recognition site to aid in analysis and purification of the CS141  
 CC protein. A set of contiguous and partially overlapping EST sequences  
 CC (AAV63504-15) are designated CS141. The sequences are isolated from a  
 CC cDNA library made from gastrointestinal tract tumour and normal tissues.  
 CC The CS141 gene is useful as a marker for gastrointestinal tract  
 CC disorders. The methods and products can be used in detecting, diagnosing,  
 CC staging, monitoring, prognosticating, preventing or determining the  
 CC predisposition to diseases and conditions of the gastrointestinal tract,  
 CC such as gastrointestinal tract cancers, Barrett's esophagus, gastric  
 CC ulcer, gastritis, leiomyoma, polyps, Crohn's disease, ulcerative colitis,  
 CC pancreatitis  
 XX

SQ Sequence 8 AA;  
 Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYKDDDDK 8  
 |||||  
 DB 1 DYKDDDDK 8  
 |||||  
 RESULT 19  
 AAW54166  
 ID AAW54166 standard; peptide; 8 AA.  
 XX  
 AC AAW54166;  
 XX  
 DT 17-AUG-1998 (first entry)  
 XX  
 DE FLAG-epitope.  
 XX  
 KM Protein targeting to glycogen; PTG; PPIC; mouse; diabetes; animal model;  
 KW knockout mouse; FLAG epitope.  
 KM  
 XX Synthetic.  
 OS  
 XX WO9808948-A1.  
 PN  
 XX 05-MAR-1998.  
 PD  
 XX 22-AUG-1997; 97WO-US014142.  
 PF  
 XX 30-AUG-1996; 96US-0025107P.  
 PR 12-AUG-1997; 97US-0055243P.  
 PS  
 XX (WARREN) WARNER LAMBERT CO.  
 PA  
 XX Brady MJ, Printen JA, Saltiel AR;  
 PI  
 XX WPI; 1998-230264/20.  
 DR  
 XX  
 PT Isolated protein targeting to glycogen genes - used to develop products  
 for increasing glycogen levels in cells and to develop animal models for  
 the study of e.g. diabetes.  
 PT  
 XX  
 PS Disclosure; Page 24; 71pp; English.  
 XX  
 CC This FLAG epitope was introduced into pCI-neo by ligating complementary  
 CC oligonucleotides into NheI/EcoRI digested vector. An EcoRI fragment from  
 CC murine clone B1-1, which codes for novel protein targeting to glycogen  
 CC (PTG) protein (see AAW54166), was cloned at the EcoRI site of the  
 CC resulting plasmid. The FLAG epitope-tagged PTG construct was transiently  
 CC transfected into CHO cells over-expressing the insulin receptor. Results  
 CC showed that PTG can direct PPIC localisation to glycogen both in vivo and  
 CC in vitro. PTG can be used to develop products for increasing glycogen  
 CC levels in cells and to develop animal models for the study of e.g.  
 CC diabetes  
 CC  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYKDDDDK 8  
 |||||  
 DB 1 DYKDDDDK 8  
 |||||  
 RESULT 20  
 AAW64456  
 ID AAW64456 standard; protein; 8 AA.  
 XX

AC AAW64456;  
 XX  
 DT 16-OCT-1998 (first entry)  
 XX  
 DE Human CHK protein flag epitope.  
 XX  
 DE Breast; cancer; matK; CSK homologous kinase; CHK; detection; diagnosis;  
 KM cytoplasmic protein; tyrosine kinase; ErbB-2; negative regulator;  
 KM mitogenic signalling.  
 KM  
 XX Homo sapiens.  
 OS  
 XX WO9830704-A1.  
 PN  
 XX 16-JUL-1998.  
 PD  
 XX 07-JAN-1998; 98WO-US000420.  
 PF  
 XX 08-JAN-1997; 97US-0035228P.  
 PR 16-JUN-1997; 97US-00876882.  
 PS  
 XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
 PA  
 XX Abraham H, Groopman JE;  
 PI  
 XX WPI; 1998-399149/34.  
 DR  
 XX  
 PT Detecting breast cancer by detecting Csk homologous kinase expression -  
 especially in humans and use of Csk homologous kinase in treatment or  
 PT prophylaxis of breast cancer and for producing medicaments.  
 PT  
 XX  
 PS Example 3; Page 26; 54pp; English.  
 XX  
 CC This sequence represents a CSK homologous kinase (CHK) derived flag  
 CC epitope which is used in a method of detecting cancer in breast tissue.  
 CC The method allows diagnosis of breast cancer in mammals, especially  
 CC humans. It is based on the discovery that a cytoplasmic protein tyrosine  
 CC kinase, CHK, is expressed in human breast tissue, but not in adjacent  
 CC tissue. This protein can be used to raise antibodies which can be  
 CC included in compositions and diagnostic kits for diagnosis of breast  
 CC cancer. The presence of CHK in breast tissue can also be determined using  
 CC other standard methods (e.g. Northern blotting) or by detecting nucleic  
 CC acid sequences encoding all/a portion of the protein (e.g. using  
 CC hybridisation probes). Over-expression of the receptor tyrosine kinase  
 CC ErbB-2 has previously been associated with the development of breast  
 CC cancer, and CHK specifically interacts with activated ErbB-2, and may  
 CC function as a negative regulator of ErbB-2 mediated mitogenic signalling.  
 CC The compositions may also be used to design drugs (e.g. which incorporate  
 CC CHK analogues with greater biological activity than CHK) and to identify  
 CC CHK antagonists and agonists for therapeutic use  
 CC  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYKDDDDK 8  
 |||||  
 DB 1 DYKDDDDK 8  
 |||||  
 RESULT 21  
 AAW56763  
 ID AAW56763 standard; peptide; 8 AA.  
 XX  
 AC AAW56763;  
 XX  
 DT 05-AUG-1998 (first entry)  
 XX  
 DE FLAG peptide epitope used for producing soluble TRAIL polypeptide.  
 XX  
 KM Tumour necrosis factor related apoptosis ligand; TRAIL; research; human;  
 XX



XX Example 11; Page 98; 123pp; English.

PS This peptide is used in the construction of a plasmid expressing LUI05

CC polypeptides. Sequences shown in AAV54616 to AAV54621 represent LUI05

CC specific polynucleotide sequences which are used in the method of the

CC invention for detecting target LUI05 nucleic acid. The method comprises

CC treating a sample with at least one LUI05 specific nucleic acid, or its

CC complement which is at least 50 percent identical with the LUI05 specific

CC nucleic acid sequences. LUI05 is a lung disease marker. Cells transformed

CC with a recombinant expression system that contains LUI05 specific nucleic

CC acid fragments, are used to express recombinant LUI05 polypeptides which

CC are used to raise antibodies. The antibodies are used to detect the LUI05

CC antigen, and correspondingly this antigen is used to detect specific

CC antibodies, in usual immunoassays. The LUI05 polypeptides and nucleic

CC acid sequences are used for diagnosis, staging, monitoring, prognosis,

CC prevention, treatment and determination of susceptibility to, lung

CC disease, specifically cancer. The LUI05 polypeptides are also used to

CC screen for specific binding agents, useful therapeutically. LUI05 is a

CC marker for lung disease (present at high concentration. In altered form

CC or in an unusual body compartment). LUI05 can be detected in blood

CC plasma or serum in an inexpensive, non-invasive test. (Updated on 25-MAR-

CC 2003 to correct PI field.)

XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.1e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8

1 | | | | |

Db 1 DYKDDDDK 8

RESULT 24

AAB99286

ID AAB99286 standard; peptide; 8 AA.

XX

AC AAB99286;

DT 12-SEP-2001 (first entry)

XX

DE FLAG peptide.

XX

KM TRAIL receptor; TRAIL-R; thrombotic thrombocytopenic purpura;

KW tumour necrosis factor-related apoptosis-inducing ligand; HIV infection;

KW haemolytic-uraemic syndrome; systemic lupus erythematosus; apoptosis;

XX FLAG peptide.

OS Synthetic.

XX

PN WO9835986-A1.

XX

PD 20-AUG-1998.

XX

PF 11-FEB-1998; 98WO-US002239.

XX

PR 13-FEB-1997; 97US-00799861.

XX

PR 12-MAR-1997; 97US-00815255.

XX

PR 28-MAR-1997; 97US-00829536.

XX

PR 04-JUN-1997; 97US-00869852.

XX

PR 26-JUN-1997; 97US-00883036.

XX

PA (IMMV ) IMMUNEX CORP.

XX

PI Rauch C, Walczak H;

XX

DR WPI; 1998-480767/41.

XX

PT New TRAIL receptor protein and related oligomers, nucleic acid, vectors -

PT used to inhibit TRAIL activity, e.g. in cases of thrombocytic purpura,

PT clotting in small blood vessels etc., also for diagnosis.

XX Example 1; Page 31; 53pp; English.

PS The present invention relates to human TRAIL-receptor polypeptide and

CC coding sequence (TRAIL-R; where TRAIL is tumour necrosis factor-related

CC apoptosis-inducing ligand, see AA46372 and AAB99284). TRAIL-R protein

CC and coding sequence can be used to treat conditions involving defective

CC or inadequate TRAIL-R, e.g. thrombotic thrombocytopenic purpura,

CC haemolytic-uraemic syndrome, clotting of small blood vessels, systemic

CC lupus erythematosus and TRAIL-mediated apoptosis of T cells in human

CC immune deficiency virus infections. The present sequence is the FLAG

CC peptide, which was used in an example from the present invention

XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.1e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8

1 | | | | |

Db 1 DYKDDDDK 8

RESULT 25

AAW54280

ID AAW54280 standard; peptide; 8 AA.

XX

AC AAW54280;

DT 25-MAR-2003 (revised)

XX

DT 29-JUL-1998 (first entry)

XX

DE Peptide sequence used in constructing a BU101 expression plasmid.

XX

KM BU101; breast cancer; diagnosis; prevention; treatment; gene therapy;

KW immunisation; drug screening.

XX

OS Homo sapiens.

XX

PN WO9807857-A1.

XX

PD 26-FEB-1998.

XX

PF 19-AUG-1997; 97WO-US014665.

XX

PR 19-AUG-1996; 96US-00697105.

XX

PR 15-AUG-1997; 97US-00912276.

XX

PA (ABBO ) ABBOTT LAB.

XX

PI Billings-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;

PI Grando EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;

PI Russell JC, Stroupe SD;

XX

DR WPI; 1998-169161/15.

XX

PT New BU101 protein over-expressed in breast cancer - useful for, e.g.

PT diagnosis, treatment and prevention of breast cancer.

XX

XX Example 11; Page 66; 105pp; English.

XX The sequence encoding this peptide is incorporated into a primer for

CC constructing a BU101 protein expression plasmid. BU101 is a member of the

CC uteroglobin family of proteins and is over-expressed in breast cancer.

CC Cells transformed with a recombinant expression system comprising a

CC sequence derived from the BU101 open reading frame and with at least 50

CC percent identity to the sequences shown in AAV26458 to AAV26461 are used

CC to produce BU101 polypeptides containing at least 1 epitope. These are

CC used to detect BU101-specific antibodies which are used correspondingly

CC to detect BU101 antigens. The BU101 polynucleotide sequences can be used

CC in a method for detecting the presence of a target BU101 polynucleotide.

CC The various assays are used for diagnosis, prognosis, staging,



CC monitoring, treating and preventing diseases of the breast (especially  
 CC cancer and its metastases), and also for determining susceptibility. The  
 CC BUI01 polypeptides are also useful in drug screening, e.g. to identify  
 CC antagonists of BUI01, potentially useful therapeutically and as targets  
 CC for therapy. The antibodies are also useful for targeted drug delivery  
 CC and therapeutically to neutralise BUI01 polypeptides. Fragments of the  
 CC BUI01 nucleic acid are useful as probes and primers, e.g. for detection  
 CC of altered gene expression or in fluorescent in situ hybridisation, also  
 CC in gene therapy to generate antisense or ribozyme molecules or for  
 CC genetic immunisation. (Updated on 25-MAR-2003 to correct PI field.)

XX  
 SQ .Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
 |||||  
 DB 1 DYKDDDDK 8

RESULT 26

ID AAW44300 standard; peptide; 8 AA.  
 XX  
 AC AAW44300;

DT 19-JUN-1998 (first entry)  
 XX  
 DE Human serrate 2 FLAG peptide.

XX  
 KM Human; serrate 2; regulation; stem cell; differentiation; neoplasm;  
 KM leukemia; endothelial cell; tumour; FLAG.

OS Synthetic.

OS Homo sapiens.

PN WO9802458-A1.

XX  
 PD 22-JUN-1998.

PF 11-JUL-1997; 97WO-JP002414.

XX  
 PR 16-JUL-1996; 96JP-00186220.

XX  
 PR 14-MAY-1997; 97JP-00124063.

PA (ASAH) ASAH1 KASEI KOGYO KK.

XX  
 PI Sakano S, Itoh A;

XX  
 DR WPI; 1998-110528/10.

DR N-PSDB; AAV15195.

PT Human serrate-2 gene expression products - used to regulate stem cell  
 PT differentiation, useful in treating neoplasms, e.g. leukaemia.

XX  
 PS Example 4; Page 92; 103pp; Japanese.

XX  
 CC The present sequence represents a FLAG peptide for human serrate 2, used  
 CC in an example of the present invention which describes human serrate 2.  
 CC The present invention also describes a method for the preparation of the  
 CC polypeptides, and antibodies binding to the polypeptide and its  
 CC fragments. The polypeptide and its fragments expressed by the serrate-2  
 CC gene can be used to inhibit stem (especially blood stem) cell  
 CC differentiation and to inhibit endothelial cell growth. They may be  
 CC incorporated in a cell culture media for culturing undifferentiated stem  
 CC cells. They can also be used for treatment of neoplasms such as  
 CC leukemia. The antibodies can be used for the diagnosis of malignant  
 CC tumours

XX  
 SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
 |||||  
 DB 1 DYKDDDDK 8

RESULT 27

AAW59269  
 ID AAW59269 standard; protein; 8 AA.

XX  
 AC AAW59269;

DT 27-AUG-1998 (first entry)

XX  
 DE Type II IL-1R protein antigenic motif.

XX  
 KM Type II interleukin-1 receptor; IL-1R; immune response; inflammation;  
 KM regulation; soluble; cell surface receptor; treatment; alloantigen;  
 KM tissue; organ; rejection; transplant; graft-versus-host disease;  
 KM autoimmune dysfunction; T-cell activation; self antigen;  
 KM rheumatoid arthritis; diabetes mellitus; multiple sclerosis.

XX  
 OS Homo sapiens.

XX  
 PN US5767064-A.

XX  
 PD 16-JUN-1998.

PF 16-MAY-1995; 95US-00442043.

XX  
 PR 05-JUN-1990; 90US-00534193.

XX  
 PR 24-AUG-1990; 90US-00573576.

XX  
 PR 13-DEC-1990; 90US-00627071.

XX  
 PR 16-MAY-1991; 91US-00701415.

XX  
 PR 12-JUL-1993; 93US-00091519.

XX  
 PR 13-MAY-1994; 94US-00242211.

XX  
 PA (IMMV) IMMUNEX CORP.

XX  
 PI Cosman DJ, Lupton SD, Mosley BA, Dower SK, Sims JE;

XX  
 DR WPI; 1998-361746/31.

XX  
 PT Regulation of interleukin-1 mediated immune or inflammatory response in

XX  
 PT mammal - comprises administering soluble IL-1 receptor protein, used in

XX  
 PT treatment of e.g. graft versus host disease and multiple sclerosis.

XX  
 PS Disclosure; Col 8; 33pp; English.

XX  
 PS This sequence represents an antigenic motif found in human and mouse type

XX  
 CC II interleukin-1 receptor (IL-1R). This receptor is used in a method to

XX  
 CC investigate the regulation of the immune or inflammatory response in a

XX  
 CC mammal. This method involves administering a soluble type-II IL-1

XX  
 CC receptor protein in an amount effective to bind to IL-1 and prevent its

XX  
 CC binding to cell-surface IL-1 receptors. The process can be used for

XX  
 CC treating alloantigen-induced rejection of transplanted tissues or organs,  
 CC graft-versus-host disease and autoimmune dysfunction dependent upon the  
 CC activation of T cells against self antigens, selected from rheumatoid  
 CC arthritis, diabetes mellitus or multiple sclerosis

XX  
 SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
 |||||  
 DB 1 DYKDDDDK 8

```

RESULT 28
AAW54434
ID AAW54434 standard; peptide; 8 AA.
XX
XX AAW54434;
AC
XX 15-SEP-1998 (first entry)
DT
XX Human PS112 expression plasmid peptide fragment.
DE
XX Prostate; disease; PS112 gene; detection; diagnosis; cancer; treatment;
XX antibody.
XX Homo sapiens.
OS
XX Synthetic.
OS
XX WO9815657-A1.
XX
XX 16-APR-1998.
XX
XX 08-OCT-1997; 97WO-US018290.
XX
XX 08-OCT-1996; 96US-00727688.
XX
XX (ABRO ) ABBOTT LAB.
XX
XX Cohen M, Friedman PN, Gordon J, Hodges SC, Klaas MR;
PI Kratochvil JD, Roberts-Rapp L, Russell JC, Stroupe SD;
XX WPI; 1998-240838/21.
XX
XX Detecting a target PS112 polynucleotide - used for diagnosing prostate
XX cancer.
XX
XX Example 11a; Page 92; 104pp; English.
XX
XX This sequence is a protein fragment used in the design of an antisense
XX PCR primer used in the isolation of a human PS112 protein from a prostate
XX library. This protein is used in a novel method of detecting the presence
XX of a target PS112 polynucleotide in a test sample. The method can also be
XX used to detect mRNA of PS112 in a test sample. The method can be used for
XX diagnosis of prostate cancer, as the presence of PS112 is an indicator of
XX prostate cancer. Antibodies against the polypeptides may be used as
XX markers, or to treat prostate cancer
XX
XX Sequence 8 AA;
SQ
Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

```

```

PN WO9823760-A1.
XX
XX 04-JUN-1998.
XX
XX 25-NOV-1997; 97WO-US021655.
XX
XX 25-NOV-1996; 96US-00777405.
XX
XX (ICOS-) ICOS CORP.
XX
XX Chantry DH, Hoekstra MF, Holtzman DA;
PI WPI; 1998-322736/28.
XX
XX New phosphatidylinositol 3-kinase catalytic sub-unit - used to develop
XX products for modulating kinase activity in immune system signalling and
XX in carcinogenesis.
XX
XX Example 1; Page 12; 53pp; English.
XX
XX This FLAG peptide is recognised by the M2 anti-FLAG monoclonal antibody.
XX PCR amplification of cDNA (see AAV31340) coding for human
XX phosphatidylinositol 3-kinase (PI 3-kinase) p110 delta subunit (see
XX AAW58570) using a primer (see AAV31349) including a FLAG sequence yielded
XX a FLAG-tagged PI 3-kinase construct. This was ligated into mammalian
XX expression vector pCDNA3, and FLAG-tagged p110 delta was expressed in
XX transfected COS cells. p110 delta can be used to develop products for
XX modulating PI 3-kinase activity in immune system signalling and in
XX carcinogenesis
XX
XX Sequence 8 AA;
SQ
Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

```

```

RESULT 30
AAW76424
ID AAW76424 standard; peptide; 8 AA.
XX
XX AAW76424;
AC
XX 20-JAN-1999 (first entry)
XX
XX FLAG affinity label used in the course of the invention.
DE
XX TAK2 protein; cytoplasmic domain; betac subunit; screening; asthma;
XX interleukin; granulocyte macrophage-colony stimulating factor; GM-CSF;
XX IL-3; IL-5; human; FLAG.
XX
XX Synthetic.
XX
XX WO9843087-A1.
XX
XX 01-OCT-1998.
XX
XX 23-MAR-1998; 98WO-US005387.
XX
XX 24-MAR-1997; 97US-0041511P.
XX
XX (PHAA ) PHARMACIA & UPJOHN CO.
XX
XX Roberds SL, Kayes PS;
PI WPI; 1998-532151/45.
XX
XX Screening for compounds useful for preventing or treating asthma - by
XX determining if compounds inhibit binding of the JAK2 protein to e.g. IL-
XX PT

```

PT 3, IL-5 or GM-CSF.  
 XX  
 PS Example 8; Page 48; 112pp; English.  
 XX  
 CC This represents a FLAG affinity label contained in a recombinant JAK2  
 CC protein used in the course of the invention. The invention provides a  
 CC method of screening for compounds useful for treating or preventing  
 CC asthma. The method comprises contacting a molecule comprising at least  
 CC the N-terminal 294 amino acid residues of the JAK2 protein, with another  
 CC molecule comprising at least 13 membrane-proximal cytoplasmic amino acids  
 CC of interleukin (IL)-3, IL-5 or granulocyte macrophage-colony stimulating  
 CC factor (GM-CSF) proteins in the presence of the candidate compound, and  
 CC determining whether the first and the second molecules form a complex. If  
 CC the compound inhibits complex formation, it can be used to treat asthma  
 XX  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DYKDDDK 8  
 Db 1 DYKDDDK 8  
 RESULT 31  
 AAW81752  
 ID AAW81752 standard; protein; 8 AA.  
 XX  
 AC AAW81752;  
 XX  
 DT 27-JAN-1999 (first entry)  
 XX  
 DE Synthetic FLAG peptide.  
 XX  
 KW US6; immunomodulator; therapeutic; prophylactic; inhibitor; cell surface;  
 KW antigen presentation; major histocompatibility complex; MHC Class I;  
 KW immunogenicity; gene therapy.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9847914-A2.  
 XX  
 PD 29-OCT-1998.  
 XX  
 PF 16-APR-1998; 98WO-EP002225.  
 XX  
 PR 18-APR-1997; 97EP-00106470.  
 XX  
 PA (BOE) BOEHRINGER MANNHEIM GMBH.  
 XX  
 PI Hengel H, Kozminski U;  
 XX  
 DR WPI; 1998-583601/49.  
 XX  
 PT New US6 gene of cytomegalovirus - useful for diagnosis and therapeutic or  
 PT prophylactic immunomodulation, e.g. to reduce immunogenicity of gene  
 PT therapy vectors.  
 XX  
 PS Example 1; Page 15; 34pp; German.  
 XX  
 CC This sequence is a FLAG peptide used in a method resulting in the  
 CC isolation of a US6 protein from human cytomegalovirus which can be used  
 CC as therapeutic or prophylactic immunomodulators, in particular inhibitors  
 CC of antigen presentation by MHC Class I on the surface of cells. A  
 CC particularly application of this protein is to reduce immunogenicity of  
 CC cells being transfected for gene therapy. Fragments of US6 nucleic acid  
 CC and is analogues are useful diagnostically as probes and primers, and  
 CC also as antisense sequences and ribozymes. US6 proteins are used to raise  
 CC antibodies. The US6 protein inhibits a later stage of antigen  
 CC presentation than known inhibitors

SQ Sequence 8 AA;  
 Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DYKDDDK 8  
 Db 1 DYKDDDK 8  
 RESULT 32  
 AAW79682  
 ID AAW79682 standard; protein; 8 AA.  
 XX  
 AC AAW79682;  
 XX  
 DT 11-JAN-1999 (first entry)  
 XX  
 DE Human CS198 C-terminal peptide fragment.  
 XX  
 KW Gastrointestinal tract; GI tract; cancer; disease; detection; CS198;  
 KW human; predisposition; treatment; Barrett's oesophagus; gastric ulcer;  
 KW gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis;  
 KW pancreatitis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9844159-A1.  
 XX  
 PD 08-OCT-1998.  
 XX  
 PF 30-MAR-1998; 98WO-US006251.  
 XX  
 PR 31-MAR-1997; 97US-00828855.  
 XX  
 PA (ABBOTT) ABBOTT LAB.  
 XX  
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;  
 PI Grados EN, Hayden M, Hodges SC, Klass MR, Kratochvil JD;  
 PI Roberts-Rapp L, Russell JC, Stroupe SD;  
 XX  
 DR WPI; 1998-542714/46.  
 XX  
 PT New gastrointestinal polynucleotides, CS198, and their detection - used  
 PT for developing products for the diagnosis and treatment of  
 PT gastrointestinal disorders, e.g. cancers, gastric ulcer or gastritis.  
 XX  
 PS Example 11a; Page 104; 127pp; English.  
 XX  
 CC This sequence represents a C-terminal fragment of the human CS198 protein  
 CC which is used in a method to detect the presence of a target CS198  
 CC polynucleotide in a test sample. The CS198 gene is useful as a marker for  
 CC gastrointestinal (GI) tract disorders. The methods and products can be  
 CC used in detecting, diagnosing, staging, monitoring, prognosticating,  
 CC preventing or treating, or determining the predisposition to diseases and  
 CC conditions of the GI tract, such as GI tract cancer, Barrett's oesophagus,  
 CC gastric ulcer, gastritis, leiomyoma, polyps, Crohn's disease, ulcerative  
 CC colitis, and pancreatitis  
 XX  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DYKDDDK 8  
 Db 1 DYKDDDK 8  
 RESULT 33  
 AAW79770

ID AAM79770 standard; peptide; 8 AA.  
 AC AAM79770;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 02-MAR-1999 (first entry)  
 XX  
 DE FLAG epitope tag for human presenilin 2 protein.  
 XX  
 KW proteolytic processing; human; presenilin 2; inhibitor; apoptosis;  
 KW cell death; early onset familial Alzheimer's disease; FAD; diagnosis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9847917-A2.  
 XX  
 PD 29-OCT-1998.  
 XX  
 PP 24-APR-1998; 98WO-US008260.  
 XX  
 PR 24-APR-1997; 97US-0044262P.  
 XX  
 PA (TANZ/) TANZI R E.  
 PA (KIMT/) KIM T.  
 PI Tanzi RE, Kim T;  
 DR WPI; 1998-583602/49.  
 XX  
 PT 20 kDa presenilin 2 C-terminal fragment, PS2-CTF - useful to screen for  
 PT compounds inhibiting proteolysis of presenilin 2 and to produce  
 PT antibodies used in diagnosis of familial Alzheimer's.  
 XX  
 PS Disclosure; Page 38; 84pp; English.  
 XX  
 CC The invention relates to a C-terminal fragment from the human 20 kD  
 CC presenilin 2 protein (PS2-CTF) which is useful in screening for compounds  
 CC that inhibit proteolytic processing of PS2 in cells and in screening of  
 CC presenilin 2 or PS2-CTF, when expressed in cells and in screening assays,  
 CC is done by linking a FLAG epitope peptide (this sequence) to the N- or C-  
 CC termini of the PS2 protein. The inhibitory compounds can be administered  
 CC to prevent proteolytic cleavage of presenilin 2 at a cleavage site which  
 CC generates PS2-CTF, and therefore to inhibit apoptotic cell death.  
 CC Mutations in the presenilin genes presenilin 1 and presenilin 2 (PS1 and  
 CC PS2) cause a major portion (at least 50%) of early onset familial  
 CC Alzheimer's disease (FAD), and detection of abnormal PS2-CTF levels can  
 CC be indicative of a specific disease, e.g. FAD. (Updated on 25-MAR-2003 to  
 CC correct PA field.)  
 CC  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYKDDDDK 8  
 |||||  
 Db 1 DYKDDDDK 8  
 |||||  
 RESULT 34  
 AAM56033  
 ID AAM56033 standard; peptide; 8 AA.  
 AC AAM56033;  
 XX  
 DT 29-JUL-1998 (first entry)  
 XX  
 DE Chimeric adenovirus fiber protein non-native amino acid sequence 2.  
 XX  
 KW Chimeric; adenovirus; fiber protein; binding; targeting; coat protein;  
 KW constrained peptide motif; gene therapy; cancer; heart disease;  
 KW autoimmune disorder.  
 XX  
 PA

XX  
 OS Synthetic.  
 OS Mastadenovirus.  
 XX  
 PN WO9807865-A1.  
 XX  
 PD 26-FEB-1998.  
 XX  
 PP 21-AUG-1997; 97WO-US014719.  
 XX  
 PR 21-AUG-1996; 96US-00701124.  
 XX  
 PA (GENVE-) GENVEEC INC.  
 XX  
 PI Wickham TJ, Roelvink PW, Kovacs I;  
 DR WPI; 1998-169169/15.  
 XX  
 PT Chimeric adenovirus fibre proteins - containing non-native amino acid  
 PT sequence to provide for binding and entry into cells, especially for gene  
 PT therapy.  
 XX  
 PS Claim 7; Page 68; 124pp; English.  
 XX  
 CC The present sequence represents a specifically claimed non-native amino  
 CC acid sequence from a chimeric adenovirus fibre protein (AFP) of the  
 CC present invention. The non-native amino acid sequence allows the chimeric  
 CC fibre (or a vector comprising the chimeric fibre) to more efficiently  
 CC bind to and enter cells. The products can be used for gene therapy, for  
 CC treating cancer, e.g. melanoma, glioma and lung cancers as well as  
 CC genetic disorders, e.g. cystic fibrosis, haemophilia and muscular  
 CC dystrophy as well as pathogenic infections, e.g. HIV, tuberculosis and  
 CC hepatitis and also for heart disease, to e.g. prevent restenosis  
 CC following angioplasty or to promote angiogenesis to reperfuse necrotic  
 CC tissue, and in autoimmune disorders, e.g. Crohn's disease, colitis,  
 CC rheumatoid arthritis, and Alzheimer's disease  
 CC  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYKDDDDK 8  
 |||||  
 Db 1 DYKDDDDK 8  
 |||||  
 RESULT 35  
 AAM30566  
 ID AAM30566 standard; peptide; 8 AA.  
 AC AAM30566;  
 XX  
 DT 02-FEB-1999 (first entry)  
 XX  
 DE FLAG tag.  
 XX  
 KW ZSIG-35; beta-chemokine; human; ligand; lymphocyte migration;  
 KW inflammation; ischaemia; reperfusion injury; FLAG.  
 XX  
 OS Synthetic.  
 OS  
 PN WO9844117-A1.  
 XX  
 PD 08-OCT-1998.  
 XX  
 PP 27-MAR-1998; 98WO-US006115.  
 XX  
 PR 28-MAR-1997; 97US-0042862P.  
 PR 09-MAY-1997; 97US-0046083P.  
 XX  
 PA (ZYMO) ZYMOGENETICS INC.

XX Shepard PO;  
 PI  
 XX  
 DR WPI; 1998-557114/47.  
 XX  
 PT New human chemokine ZSIG-35 - used for, e.g. treating inflammatory  
 PT disease, lymphocyte migration and ischemia/reperfusion injury.  
 XX  
 PS Example 4; Page 88; 105pp; English.  
 XX  
 CC This FLAG peptide can be used as a N- or C-terminal tag of novel human  
 CC chemokine ZSIG-35 polypeptides (see AAW30565) of the invention. Vectors  
 CC have been designed for expression of FLAG-tagged ZSIG-35 in mammalian  
 CC host cells. The FLAG peptide acts as a purification aid. ZSIG-35  
 CC polypeptides are useful in the regulation of acute and chronic  
 CC inflammatory disease conditions, lymphocyte migration and  
 CC ischemia/reperfusion injury  
 CC  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYKDDDDK 8  
 Db 1 DYKDDDDK 8  
 RESULT 36  
 AAW75806  
 ID AAW75806 standard; peptide; 8 AA.  
 AC AAW75806;  
 XX  
 DT 27-OCT-1998 (first entry)  
 XX  
 DE FLAG peptide epitope sequence.  
 XX  
 KM Mast cell protease; MCP; mouse; inhibitor; peptide substrate; asthma;  
 KM tryptase-6 protein; inflammatory disorder; allergic rhinitis; urticaria;  
 KM antioedema; eczematous dermatitis; atopic dermatitis; anaphylaxis;  
 KM hyperproliferative skin disease; peptic ulcer; hyperresponsiveness;  
 KM inflammatory skin condition; FLAG.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9833812-A1.  
 XX  
 PD 06-AUG-1998.  
 XX  
 PF 30-JUN-1998; 98WO-US001865.  
 XX  
 PR 05-FEB-1997; 97US-0037090P.  
 XX  
 PA (BGMH) BRIGHAM & WOMENS HOSPITAL.  
 XX  
 PI Stevens RL, Huang C;  
 DR WPI; 1998-437390/37.  
 XX  
 PT Tryptase-6 complex inhibitory peptides - used to treat mast cell-mediated  
 PT inflammatory disorders e.g. asthma.  
 XX  
 PS Example; Page 18; 69pp; English.  
 CC This represents a FLAG peptide epitope sequence. The invention provides  
 CC sequences shown in AAW63160 to AAW63169 that are inhibitors of mouse mast  
 CC cell protease (mMCP-6). These peptides which are tryptase-6 complex  
 CC inhibitors, can be used for treating a mast cell-mediated inflammatory  
 CC disorder. The inhibitors can be used to treat inflammatory disorders  
 CC including asthma, allergic rhinitis, urticaria and antioedema, eczematous  
 CC dermatitis (atopic dermatitis), anaphylaxis, hyperproliferative skin

CC disease, peptic ulcers, inflammatory bowel disorder, hyperresponsiveness  
 CC and inflammatory skin conditions  
 CC  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYKDDDDK 8  
 Db 1 DYKDDDDK 8  
 RESULT 37  
 AAW54266  
 ID AAW54266 standard; peptide; 8 AA.  
 AC AAW54266;  
 XX  
 DT 30-JUL-1998 (first entry)  
 XX  
 DE FLAG peptide.  
 XX  
 KM Peptide tag; purification; identification; mutation; breast cancer;  
 KM BRCA1; BRCA2; PCR; amplification; primer.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9811249-A1.  
 XX  
 PD 19-MAR-1998.  
 XX  
 PF 13-SEP-1996; 96WO-US014708.  
 XX  
 PR 13-SEP-1996; 96WO-US014708.  
 XX  
 PA (GARV/) GARVIN A M.  
 XX  
 PI Garvin AM;  
 XX  
 DR WPI; 1998-207407/18.  
 DR N-PSDB; AAV26454.  
 XX  
 PT Mutation detection using peptide tagged in vitro synthesised proteins -  
 PT useful for identification of mutations in disease causing genes, e.g.  
 PT breast cancer susceptibility genes BRCA1 and 2.  
 XX  
 PS Disclosure; Page 3; 13pp; English.  
 XX  
 CC The DNA sequences (AAV26452-V26455) are examples of 4 elements which are  
 CC present in a unique oligonucleotide sequence. The Flag peptide is an  
 CC example of a tag which can be encoded by a region of the unique  
 CC oligonucleotide sequence. The unique oligonucleotide sequence is used to  
 CC amplify desired mutated sequences and to tag the encoded peptide at the N  
 CC -terminus. Ligands recognising the peptide can be used to purify the  
 CC proteins for further analysis. The method is capable of detecting  
 CC mutations that qualitatively alter the protein product or any protein  
 CC encoding gene, using genomic DNA or cDNA as the starting material. The  
 CC method is useful for identification of mutations in certain disease  
 CC causing genes, e.g. the breast cancer susceptibility genes BRCA1 and 2  
 CC  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYKDDDDK 8  
 Db 1 DYKDDDDK 8

```

RESULT 38
AAW29748
ID AAW29748 standard; peptide; 8 AA.
XX
XX AAW29748;
XX
XX AC
XX
XX DT 27-OCT-1998 (first entry)
XX
XX DE Synthetic octapeptide recognised by anti-FLAG M2.
XX
XX KM TNF; endothelium proliferative agent; TREPA; wound healing; cancer;
XX tissue grafting; vascularisation; apoptosis; autoimmune; birth control.
XX
XX OS Synthetic.
XX
XX PN WO9835061-A2.
XX
XX PD 13-AUG-1998.
XX
XX PF 12-FEB-1998; 98WO-US002859.
XX
XX PR 12-FEB-1997; 97US-00798692.
XX
XX PR 10-FEB-1998; 98US-00021706.
XX
XX PA (ABBO ) ABBOTT LAB.
XX
XX PI Wiley SR;
XX
XX DR WPI; 1998-447255/38.
XX
XX PR Detecting nucleic acid encoding TREPA - useful for diagnosis and
XX treatment of autoimmune disease, tumours and inflammation.
XX
XX PS Claim 43; Page 126; 142pp; English.
XX
XX CC The synthetic octapeptide recognised by anti-FLAG M2 was used in the
XX creation of a plasmid for the expression of secretable TNF-related
XX endothelium proliferative agent (TREPA). TREPA, or its activators or
XX agonists, are used to treat a deficit of TREPA, e.g. to promote wound
XX healing or tissue grafting, by promoting vascularisation, also to induce
XX apoptosis for treating cancer and eliminating autoreactive T cells, as an
XX adjunct to cancer chemotherapy or antiviral treatment. TREPA peptides can
XX also be used to target cytotoxic agents or for affinity isolation of the
XX corresponding receptor, the nucleic acid for which can be used to
XX transform tumour cells to render them more responsive to TREPA and to
XX screen for TREPA mimics. Ribozymes, antisense RNA, antibodies or
XX peptides, are used to treat TREPA-associated diseases, e.g. tumours and
XX metastases (by inhibiting vascularisation), inflammation or a wide range
XX of autoimmune conditions, conditions involving abnormal stimulation of
XX epithelial cells (e.g. atherosclerosis), for birth control (inhibiting
XX ovulation and placental formation) or other angiogenic conditions (e.g.
XX ulcers)
XX
XX SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
   |||||
   1 DYKDDDDK 8
Db

```

```

XX
XX KM Adenovirus serotype 2; Ad2; hexon; coat protein; gene therapy; vector;
XX FLAG.
XX
XX OS Synthetic.
XX
XX PN WO9840509-A1.
XX
XX PD 17-SEP-1998.
XX
XX PF 13-MAR-1998; 98WO-US005033.
XX
XX PR 13-MAR-1997; 97US-00816346.
XX
XX PA (CORR ) CORNELL RES FOUND INC.
XX (GENV-) GENVEEC INC.
XX
XX PI Crystal RG, Falck-Pedersen E, Gall J, Kovsed I, Wickham TJ;
XX
XX DR WPI; 1998-506738/43.
XX
XX DR N-PSDB; AAV61524.
XX
XX PT Chimeric adenovirus coat protein - useful in, e.g. vector for gene
XX transfer to treat inherited genetic diseases.
XX
XX PS Example 4; Page 87; 112pp; English.
XX
XX CC This is the amino acid sequence of a FLAG peptide. DNA encoding FLAG (see
XX AAV61524) can be introduced into an adenovirus vector. The invention
XX provides a chimeric adenoviral coat protein, particularly a chimeric
XX CC adenovirus hexon protein (see AAW79538-39), that has a decreased ability
XX or inability to be recognised by a neutralising antibody directed against
XX the corresponding wild-type adenovirus coat protein. The chimeric
XX CC adenoviral coat protein has a non-native amino acid sequence, especially
XX comprising a deletion of one or more regions of the hexon protein. A
XX vector that comprises the chimeric adenovirus coat protein is claimed,
XX CC and can be used for gene transfer, for the treatment of inherited
XX diseases
XX
XX SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
   |||||
   1 DYKDDDDK 8
Db

```







QY 1 DYKDDDDK 8  
 XX |||||  
 Db 1 DYKDDDDK 8

## RESULT 45

AAW46969  
 ID AAW46969 standard; protein; 8 AA.  
 XX

AC AAW46969;  
 XX

DT 06-JUL-1998 (first entry)  
 XX

DE Peptide sequence of the specification.  
 XX

KM S11c-like protein; human; diagnosis; treatment; brain-specific disease;  
 cancer; antibody.  
 XX

OS Unidentified.  
 XX

PN JP10087699-A.  
 XX

PD 07-APR-1998.  
 XX

PF 15-JUL-1997; 97JP-00205351.  
 XX

PR 16-JUL-1996; 96JP-00186219.  
 XX

PA (ASAH ) ASAH KASEI KOGYO KK.  
 XX

DR WPI; 1998-267127/24.  
 XX

PT Human S11c-like protein - useful for diagnosis and treatment of brain-  
 specific diseases and cancers.  
 XX

PS Disclosure; Page 39; 45pp; Japanese.  
 XX

CC The present sequence appears in the specification. The specification  
 describes a novel human s11c-like protein (the mature protein is claimed  
 in Claim 1). The s11c-like polypeptide is useful for diagnosis and  
 treatment of brain-specific diseases and cancers. Antibodies directed  
 against the protein, or its fragments can also be used for diagnosing  
 cancer  
 CC  
 CC

SQ Sequence 8 AA;  
 XX

Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
 XX |||||  
 Db 1 DYKDDDDK 8

## RESULT 46

AAW68289  
 ID AAW68289 standard; peptide; 8 AA.  
 XX

AC AAW68289;  
 XX

DT 08-OCT-1998 (first entry)  
 XX

DE FLAG peptide epitope for constructing RANK/Fc fusion protein.  
 XX

KM RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;  
 immune response; inflammatory response; toxic shock; sepsis; TNF; RANKL;  
 RANK ligand; tumour necrosis factor; FLAG peptide epitope.  
 XX

OS Synthetic.  
 OS Homo sapiens.  
 XX

PN W09828424-A2.  
 XX

PD 02-JUL-1998.  
 XX

PF 22-DEC-1997; 97WO-US023866.  
 XX

PR 23-DEC-1996; 96US-0059978P.  
 XX

PR 07-MAR-1997; 97US-00813509.  
 XX

PR 14-OCT-1997; 97US-0064671P.  
 XX

PA (IMMV ) IMMUNEX CORP.  
 XX

PI Anderson DM, Galibert LJ, Maraskovsky E;  
 XX

DR WPI; 1998-377655/32.  
 XX

PT New isolated receptor activator of necrosis factor-kappa B - useful for,  
 e.g. developing products for regulating an immune or inflammatory  
 response, treating toxic shock or sepsis.  
 XX

PS Example 6; Page 53; 80pp; English.  
 XX

CC This represents a FLAG peptide epitope used in the construction of a  
 RANK/FC fusion protein. RANK (receptor activator of necrosis factor-  
 kappaB (NF-kB)) is a member of the tumour necrosis factor (TNF) family.  
 CC Host cells transformed or transfected with an expression vector  
 comprising the RANK encoding nucleic acid can be used to produce  
 recombinant RANK protein. A soluble form of RANK is fused to the FC  
 region of human IgG1. The soluble RANK may be used for inhibiting  
 activation of NF-kB, by contacting a cell expressing membrane-associated  
 RANK with a soluble RANK which binds to RANK ligand (RANKL). The soluble  
 RANK polypeptide composition may also be used for regulating an immune or  
 inflammatory response. Inhibition of NF-kB by RANK antagonists may be  
 useful in ameliorating negative effects of an inflammatory response that  
 result from triggering of RANK, e.g. in treating toxic shock or sepsis,  
 CC graft-versus-host reactions, or acute inflammatory reactions. They can  
 also be used in adjunct therapy for disease characterised by neoplastic  
 CC cells that express RANK. The products can also be used for detection and  
 drug screening  
 CC  
 CC

SQ Sequence 8 AA;  
 XX

Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
 XX |||||  
 Db 1 DYKDDDDK 8

## RESULT 47

AAW44008  
 ID AAW44008 standard; peptide; 8 AA.  
 XX

AC AAW44008;  
 XX

DT 05-JUN-1998 (first entry)  
 XX

DE FLAG peptide i used in an epitope tagged prion protein construct.  
 XX

KM Prion; epitope; FLAG; Strept; poly-histidine; haemagglutinin; recombinant;  
 transgenic animal; scrapie; Creutzfeldt-Jakob disease; CJD;  
 KM bovine spongiform encephalopathy; BSE.  
 XX

OS Synthetic.  
 XX

PN W09746572-A1.  
 XX

PD 11-DEC-1997.  
 XX

PF 29-MAY-1997; 97WO-US009289.  
 XX

```

PR 06-JUN-1996; 96US-00660626.
XX (RESC ) UNIV CALIFORNIA.
PA Prusiner SB, Telling GC, Cohen FE, Scott MR;
XX WPI; 1998-042112/04.
XX
XX Nucleic acid construct encoding biologically active protein and epitope -
PT especially epitope-tagged prion protein.
XX
XX Claim 4; Page 48; 62pp; English.
XX
XX This sequence represents an artificial FLAG peptide epitope. It is used
CC in a recombinant nucleic acid construct encoding an epitope-tagged prion
CC protein (PrP). The construct comprises a first nucleic acid sequence
CC encoding an amino acid sequence of a biologically active protein fragment
CC and a second nucleic acid sequence encoding a heterologous epitope
CC domain. The heterologous epitope domain is a peptide selected from a
CC peptide group of FLAG, Strep, poly-histidine, human c-myc peptide
CC recognised by monoclonal antibody 9E10 and haemagglutinin peptide
CC synthetic or chimeric PrP molecule. The protein has two different three -
CC dimensional conformations and the epitope domain is spatially positioned
CC relative to the protein such that the epitope domain is more exposed in a
CC first conformation relative to a second conformation. The nucleic acid
CC construct may be used for the production of transgenic animals or cells
CC that are useful in a method for distinguishing between different
CC conformational shapes of a protein. These methods are particularly useful
CC in studying diseases caused by prion proteins, e.g. Creutzfeldt-Jakob
CC disease (CJD), scrapie and bovine spongiform encephalopathy (BSE)
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 48
AAW80478 standard; peptide; 8 AA.
XX
AC AAW80478;
XX
XX 28-JAN-1999 (first entry)
XX
XX Peptide sequence encoded by an antisense primer.
XX
XX EST sequence; CS110; gastrointestinal tract; cancer; adenocarcinoma;
XX lymphoma.
XX
XX Synthetic.
XX
XX WO9844160-A1.
XX
XX 08-OCT-1998.
XX
XX 31-MAR-1998; 98WO-US006338.
XX
XX 31-MAR-1997; 97US-00829755.
XX
XX (ABBO ) ABBOTT LAB.
XX
XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
XX Grados EN, Hayden M, Hodges SC, Klass MR, Kratochvil JD;
XX Roberts-Rapp L, Russell JC, Stroupe SD;
XX WPI; 1998-557139/47.

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XX New CS110 polypeptide(s) - useful for detecting gastrointestinal tract
PT diseases, e.g. gastrointestinal tract cancers and to produce antibodies.
XX
XX Example 11a; Page 67; 116pp; English.
XX
XX The present sequence represents a peptide sequence encoded by an
CC antisense primer of the invention. The sequence incorporates a
CC recognition site to aid in analysis and purification of the CS110
CC protein. A set of contiguous and partially overlapping EST sequences
CC (AAV63521-27) are designated CS110. The sequences are isolated from a
CC cDNA library made from gastrointestinal tract tumour and normal tissues.
CC The polypeptides are useful diagnostically to detect CS110 antigen/anti-
CC CS110 antibody in samples, e.g. to detect diseases and conditions of the
CC gastrointestinal tract, especially cancers, e.g. adenocarcinoma and
CC lymphoma
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 49
AAW70592 standard; peptide; 8 AA.
XX
AC AAW70592;
XX
XX 21-JAN-1999 (first entry)
XX
XX Flag sequence used in the course of the invention.
XX
XX zsig25; adhesion-modulating protein; prostate cell; prostatic carcinoma;
XX B-cell cancer; infertility; Wolf-Hirschhorn syndrome;
XX chromosome 4 (p16.3).
XX
XX Synthetic.
XX
XX WO9845442-A2.
XX
XX 15-OCT-1998.
XX
XX 10-APR-1998; 98WO-US007117.
XX
XX 10-APR-1997; 97US-0043421P.
XX
XX 11-JUN-1997; 97US-0049288P.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Sheppard PO;
XX
XX WPI; 1998-557522/47.
XX
XX New zsig25 protein - and antibodies, involved in modulation of adhesion,
PT used for diagnosis and treatment of prostatic and B-cell tumours,
PT stimulation of haematopoietic cells, treatment of immune deficiency etc.
XX
XX Claim 10; Page 120; 161pp; English.
XX
XX The present sequence represents a Flag sequence used in the course of the
CC invention. The specification describes zsig25 protein, an adhesion-
CC modulating protein expressed at very high level in prostatic cells. The
CC protein is useful as a diagnostic marker for prostatic carcinoma and B-
CC cell cancers, possibly also for infertility, and as a reagent for
CC separating cancerous and non-cancerous cells. The products may also be
CC used to diagnose or treat Wolf-Hirschhorn syndrome, associated with a
CC deletion in the region of chromosome 4 (p16.3) where the zsig25 gene is

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CC located  
 XX  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DYKDDDK 8  
 1 DYKDDDK 8  
 1 DYKDDDK 8  
 RESULT 50  
 ID AAE08734 standard; peptide; 8 AA.  
 AC AAE08734;  
 DT 15-NOV-2001 (first entry)  
 XX FLAG tag, used to determine the association of TRAF with RANK.  
 DE  
 XX Human; receptor activator of nuclear factor kappaB; RANK; NF;  
 KM tumour necrosis factor; TNF; TNF receptor associated factor; TRAF;  
 KM immune response; inflammatory response; graft-versus-host reaction;  
 KM toxic shock; sepsis; acute inflammatory reaction; bone resorption;  
 KM anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory.  
 OS Synthetic.  
 PN US6271349-B1.  
 PD 07-AUG-2001.  
 XX 17-DEC-1998; 98US-00215649.  
 XX 23-DEC-1996; 96US-0059978P.  
 PR 23-DEC-1996; 96US-00772330.  
 PR 07-MAR-1997; 97US-0077281P.  
 PR 07-MAR-1997; 97US-00813509.  
 PR 14-OCT-1997; 97US-0064671P.  
 PR 22-DEC-1997; 97US-00996139.  
 XX (IMMV ) IMMUNEX CORP.  
 PI Dougall WC, Galibert L;  
 DR WPI; 1998-377655/32.  
 XX  
 PT New isolated receptor activator of necrosis factor-kappa B - useful for,  
 PT e.g. developing products for regulating an immune or inflammatory  
 PT response, treating toxic shock or sepsis.  
 XX  
 PS Example 6; Col 59; 47bp; English.  
 CC The patent discloses novel receptor activator of nuclear factor (NF) -  
 CC kappaB (RANK) proteins and their corresponding DNAs. RANK is a member of  
 CC the tumour necrosis factor (TNF) receptor superfamily and associates with  
 CC TNF receptor associated factor (TRAF) 2 and 3 which are important in the  
 CC regulation of immune and inflammatory response. The receptors are useful  
 CC for regulating immune response and in screening for inhibitors of these  
 CC receptors. The cytoplasmic domain of RANK is used in developing assays  
 CC for inhibitors of signal transduction, e.g. for screening the molecules  
 CC that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3, TRAF5 and  
 CC particularly TRAF6. NF-kappaB inhibition by RANK antagonists are useful  
 CC in ameliorating the negative effects of an inflammatory response that  
 CC result from triggering of RANK, e.g. in treating toxic shock or sepsis,  
 CC graft-versus-host reactions, acute inflammatory reactions and the effects  
 CC of bone resorption. RANK acts as an anti-apoptotic signal and rescue the  
 CC cells that express RANK from apoptosis. Soluble forms of the receptor are  
 CC used in vivo or in vitro based screening tests for agonists or  
 CC antagonists of RANK activity, as antagonists of RANK-mediated NF-kappa B

CC activation, or to inhibit transduction of a signal via RANK. RANK  
 CC compositions are used in the development of both agonistic and  
 CC antagonistic antibodies, or as an adjunct therapy for disease  
 CC characterised by neoplastic cells that express RANK. Compounds that  
 CC interfere with RANK/TRAF6 interactions are useful for modulating the  
 CC formation of osteoclasts from osteoclast precursors and for modulating  
 CC osteoclast function and activities. They are used as inhibitors of  
 CC diseases associated with excess bone resorption and as immunosuppressants  
 CC or anti-inflammatory agents. The RANK DNAs are useful for the expression  
 CC of recombinant proteins, as probes for analysis of the presence or  
 CC distribution of RANK transcripts, while the proteins are useful in  
 CC preparing kits for the detection of soluble RANK, or monitor RANK-related  
 CC activity. The present sequence is a FLAG tag which is used in the  
 CC exemplification of the invention to determine the association of TRAF  
 CC with RANK  
 XX  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DYKDDDK 8  
 1 DYKDDDK 8  
 1 DYKDDDK 8  
 RESULT 51  
 ID AAW94672 standard; peptide; 8 AA.  
 AC AAW94672;  
 DT 04-MAY-1999 (first entry)  
 XX Human TRAIL-BP Flag peptide.  
 DE  
 XX Human; TNF-related apoptosis-inducing ligand binding protein; clotting;  
 KM TRAIL-BP; tumour necrosis factor; T cell death; HIV; gene therapy;  
 KM thrombotic microangiopathy; thrombotic thrombocytopenic purpura;  
 KM haemolytic-uraemic syndrome; systemic lupus erythematosus.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 PN WO9900423-A1.  
 PD 07-JAN-1999.  
 XX 25-JUN-1998; 98WO-US013491.  
 PR 26-JUN-1997; 97US-00893529.  
 XX (IMMV ) IMMUNEX CORP.  
 PI Walczak H, Smith CA;  
 DR WPI; 1999-095685/08.  
 XX  
 PT New isolated TRAIL binding protein - which binds to a tumour necrosis  
 PT factor-related apoptosis inducing ligand, used in the diagnosis and  
 PT treatment of TRAIL-mediated disorders.  
 XX  
 PS Disclosure; Page 3; 47bp; English.  
 CC The present sequence represents a flag peptide from the present  
 CC invention. The present invention describes human tumour necrosis factor  
 CC (TNF)-related apoptosis-inducing ligand (TRAIL) binding protein (BP)  
 CC TRAIL-BP can be used for inhibiting the biological activities of TRAIL or  
 CC for purifying TRAIL. TRAIL-BP proteins can be used for treating a TRAIL-  
 CC mediated disorder such as T cell death in HIV-infected patients. They can  
 CC be used for treating thrombotic microangiopathies such as thrombotic  
 CC thrombocytopenic purpura, haemolytic-uraemic syndrome, clotting of small

CC blood vessels or systemic lupus erythematosus. The TRAIL-BP nucleic acids  
CC can also be used for gene therapy. They can also be used as carriers for  
CC delivering attached agents to cells bearing TRAIL

SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDDK 8  
DB 1 DYKDDDDK 8

RESULT 52

AAV06471  
ID AAV06471 standard; peptide; 8 AA.

AC AAV06471;

DT 27-SEP-1999 (first entry)

DE Epitope tag.

KW Epitope tag; antibody engineering; yeast; surface display;

KM protein library; peptide library.

OS Synthetic.

PN WO9336569-A1.

PD 22-JUL-1999.

PF 20-JAN-1999; 99WO-US001188.

PR 20-JAN-1998; 98US-0009388.

PR 26-AUG-1998; 98US-00140084.

PA (UNIT 1) UNIT ILLINOIS FOUND.

PI Witterup KD, Kieke MC, Kranz DM, Shusta E, Boder ET;

DR WPI; 1999-430619/36.

PT Selecting proteins with enhanced phenotypic properties than wild-type  
PT proteins, is useful for highly specific cancer diagnosis and therapy.

PS Disclosure; Page 7; 116pp; English.

CC This peptide comprises an epitope tag that can be used in methods of the  
CC invention. The invention discloses a powerful new system for engineering  
CC antibody affinity and specificity, by constructing a microbial analogue  
CC of the mammalian system's B cell repertoire. Antibodies are displayed on  
CC the surface of yeast cells by genetic fusion with yeast cell wall  
CC proteins, especially agglutinin proteins. After mutation, variants are  
CC selected on the basis of improved binding characteristics with  
CC fluorescently labeled targets. The selection method also identifies  
CC proteins with enhanced phenotypic characteristics; proteins that are  
CC displayed at higher levels; proteins that are secreted at higher  
CC efficiency and proteins of improved stability

SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDDK 8  
DB 1 DYKDDDDK 8

RESULT 53

AAW99020  
ID AAW99020 standard; peptide; 8 AA.

AC AAW99020;

DT 12-MAY-1999 (first entry)

DE Flag peptide.

KW Human; TRAIL; TRAIL receptor; immunoreactive; thrombotic microangiopathy;  
KW HIV infection; tumour necrosis factor related apoptosis inducing ligand;  
KW TNF related apoptosis inducing ligand; systemic lupus erythematosus;  
KW multiple sclerosis.

OS Synthetic.

PN WO9903992-A1.

PD 28-JAN-1999.

PF 10-JUL-1998; 98WO-US014410.

PR 15-JUL-1997; 97US-00892119.

PA (IMMUNEX ) IMMUNEX CORP.

PI Degli-Esposti M;

DR WPI; 1999-132236/11.

PT New isolated TRAIL receptor polypeptides - used to develop products for  
PT treating e.g. thrombotic microangiopathy, multiple sclerosis, systemic  
PT lupus erythematosus or HIV infection.

PS Disclosure; Page 13; 51pp; English.

CC The present invention describes human tumour necrosis factor (TNF) -  
CC related apoptosis-inducing ligand (TRAIL) receptors (TRAILR). TRAILR  
CC proteins can be used for binding TRAIL, e.g. to measure or inhibit the  
CC biological activity of TRAIL. TRAILR proteins can be used for treating  
CC thrombotic microangiopathies, e.g. thrombotic thrombocytopenic purpura  
CC (TTP) or haemolytic-uraemic syndrome (HUS), clotting of small blood  
CC vessels in e.g. AIDS, multiple sclerosis or systemic lupus erythematosus  
CC or for reducing TRAIL-mediated death of T cells in HIV-infected patients.  
CC They can also be used to purify TRAIL or TRAIL-expressing cells or as  
CC carriers for delivering agents to cells bearing TRAIL. The present  
CC sequence represents a flag peptide form the present invention

SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDDK 8  
DB 1 DYKDDDDK 8

RESULT 54

AAW88371  
ID AAW88371 standard; peptide; 8 AA.

AC AAW88371;

DT 26-APR-1999 (first entry)

DE FLAG peptide.

KW Tumour necrosis factor-gamma; TNF-gamma; human; inflammation; cancer;  
KW tumour; metastasis; graft versus host disease; drug screening; therapy;  
KW diagnosis; FLAG.

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XX OS Synthetic.
XX XX WO9900518-A1.
XX PN 07-JAN-1999.
XX PD 12-JUN-1998; 98WO-US012101.
XX PF 26-JUN-1997; 97US-00883086.
XX PR (ABBO ) ABBOTT LAB.
XX PA Wiley SR;
XX PI WPI; 1999-095761/08.
XX DR Tumour necrosis factor gamma detects target polynucleotides - useful for,
XX PT e.g. treating inflammation, cancer and graft versus host disease.
XX PS Claim 43; Page 70; 106pp; English.
XX CC This is a FLAG peptide recognised by monoclonal antibody anti-FLAG M2.
XX CC DNA encoding the FLAG peptide can be ligated to DNA encoding a human
XX CC serum albumin leader sequence (see AAW88370) and the C-terminal portion
XX CC (see AAW88369) of novel human tumour necrosis factor gamma (TNFG, see
XX CC AAW88368) in order to provide a construct for the expression of
XX CC secretable TNFG proteins in mammalian host cells. Such soluble
XX CC polypeptides can be used to treat deficiencies of TNFG and disease
XX CC conditions ameliorated by TNFG. Antibodies, antagonists and inhibitors of
XX CC the polypeptide may be used to treat TNFG-associated diseases, tumours or
XX CC metastases, and to screen for, diagnose and monitor conditions
XX CC attributable to TNFG, especially inflammation, cancer and graft versus
XX CC host disease
XX SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 55
AAW97660
ID AAW97660 standard; peptide; 8 AA.
XX AC AAW97660;
XX DT 10-MAY-1999 (first entry)
XX DE FLAG epitope.
XX KW BL210; urinary tract; cancer; tumour; metastasis; diagnosis; therapy;
XX KM human; epitope; antigen; antibody; FLAG.
XX OS Synthetic.
XX PN WO9902734-A1.
XX PD 21-JAN-1999.
XX PF 08-JUL-1998; 98WO-US014210.
XX PR 08-JUL-1997; 97US-00889866.
XX PA (ABBO ) ABBOTT LAB.
XX PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
XX PI Granados EN, Hodges SC, Klass MR, Kratochvyl JD, Russell JC;

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PI Stroupe SD, Yu H;
XX WPI; 1999-120934/10.
XX DR Nucleic acid derived from the BL210 gene - used for diagnosis and
XX PT treatment of urinary tract disease, particularly cancer.
XX PS Example 11a; Page 70; 120pp; English.
XX CC This peptide comprises a FLAG epitope. An antisense primer incorporating
XX CC a sequence encoding FLAG has been used in the PCR amplification of human
XX CC urinary tract specific BL210 cDNA clones (see also AAX07044-57) for the
XX CC production of a BL210 expression plasmid. The BL210 protein product (see
XX CC also AAW97655) was recovered from transfected mammalian cells using anti-
XX CC FLAG monoclonal antibody M2. The invention provides BL210 cDNA clones and
XX CC polypeptides useful for developing products for detecting, diagnosing,
XX CC staging, in vivo imaging, preventing or treating diseases or conditions
XX CC of the urinary tract, including cancer
XX SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 56
AAV08479
ID AAV08479 standard; protein; 8 AA.
XX AC AAV08479;
XX DT 29-JUL-1999 (first entry)
XX DE Human BS274 protein fragment 1.
XX KW Human; breast tissue; BS274; detection; disease; marker; antitumour;
XX KM breast cancer; metastases; atypical hyperplasia; fibroadenoma; cyst;
XX KM diagnosis; therapy; antagonist; cytotoxin; immunosassay; drug screen;
XX KM chromosomal anomaly; immunisation; antisense; triplex; ribozyme.
XX OS Homo sapiens.
XX PN WO9925850-A1;
XX PD 27-MAY-1999.
XX PF 17-NOV-1998; 98WO-US024562.
XX PR 17-NOV-1997; 97US-00971772.
XX PA (ABBO ) ABBOTT LAB.
XX PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
XX PI Granados EN, Hodges SC, Klass MR, Kratochvyl JD, Roberts-Rapp L;
XX PI Russell JC, Stroupe SD;
XX DR WPI; 1999-347484/29.
XX PT New BS274 nucleic acid as a marker for breast disease.
XX PS Example 11a; Page 102; 105pp; English.
XX CC This invention describes novel human BS274 protein clones which can be
XX CC used as markers for breast cancer and have antitumour activity. BS274 can
XX CC also be used as a marker of cancer and its metastases, atypical
XX CC hyperplasia, fibroadenoma and cysts, so detection/quantification of BS274
XX CC encoded polypeptides and BS274-specific antibodies are used for
XX CC diagnosis, staging, monitoring, prognosis, in vivo imaging of, and

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CC determining predisposition to these diseases. Antibodies are useful as  
 CC therapeutic antagonists (optionally coupled to a cytotoxicin), as  
 CC immunoassay reagents and in competitive drug screens. BS274 nucleic acid  
 CC and its fragments, are used as probes and primers (in diagnostic assays,  
 CC for quantifying gene expression, for detecting chromosomal anomalies and  
 CC to isolate related sequences), for genetic immunization, as a source of  
 CC therapeutic antisense, triplex-forming and ribozyme sequences, and for  
 CC recombinant production of BS274 polypeptides. BS274 polypeptides are used  
 CC as immunoassay reagents, for generating antibodies, in drug screens for  
 CC specific binding agents (i.e. antagonists and inhibitors, potentially  
 CC useful as therapeutic agents) and for rational drug design

XX Sequence 8 AA;

Qy Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 DYKDDDDK 8  
 1 DYKDDDDK 8

RESULT 57

AAW81534 standard; peptide; 8 AA.

XX AAW81534;

DT 01-MAR-1999 (first entry)

XX FLAG peptide epitope.

XX JIP-1; JNK-interacting protein; c-Jun NH2-terminal kinase;  
 KW signal transduction; inhibitor; mouse; neurodegenerative disease;  
 KW Parkinson's disease; Alzheimer's disease; blood clot; stroke; malignancy;  
 KW cancer; leukaemia; autoimmune disease; inflammation; apoptosis; therapy;  
 KW diagnosis; FLAG.

XX Synthetic.

XX WO9849188-A1.

XX 05-NOV-1998.

XX 28-APR-1998; 98WO-US008513.

XX 28-APR-1997; 97US-00819177.

XX (UYMA-) UNTV MASSACHUSETTS.

XX Davis RJ, Dickens M,

XX WPI; 1999-024042/02.

PT c-Jun NH2-terminal kinase (JNK)-interacting protein 1 - used to treat  
 PT neurodegenerative disease, blood clot, leukaemia, autoimmune disease, and  
 PT inflammation.

XX Example 2; Page 48; 95pp; English.

CC This peptide comprises a FLAG epitope. DNA encoding this epitope has been  
 CC inserted into murine JIP-1 cDNA (see AAV69289) between the first 2 codons  
 CC of the coding region. Recombinant JIP-1 was expressed in bacterial host  
 CC cells as GST fusion proteins. Experiments demonstrate that JIP-1 (see  
 CC also AAW81525) specifically binds JNK (c-Jun NH2-terminal kinase) in  
 CC vivo. JIP-1 polypeptides and nucleic acids are used in the manufacture of  
 CC medicaments for treating a pathological condition associated with  
 CC abnormal expression or activity of JNK, such as a neurodegenerative  
 CC disease (selected from Parkinson's disease and Alzheimer's disease), a  
 CC blood clot, stroke, malignancy, leukaemia, an autoimmune disease or  
 CC inflammation

SO Sequence 8 AA;

Qy Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 DYKDDDDK 8  
 1 DYKDDDDK 8

RESULT 58

AAW6792 standard; peptide; 8 AA.

XX AAW6792;

DT 22-JUN-1999 (first entry)

XX FLAG peptide epitope.

XX Urinary tract; detection; diagnosis in vivo imaging; cancer; keratin;  
 KW cyokeratin; cellular apoptosis susceptibility; CAS; mat-8; FLAG.

XX Synthetic.

XX WO914372-A1.

XX 25-MAR-1999.

XX 15-SEP-1998; 98WO-US019362.

XX 15-SEP-1997; 97US-0058925P.

XX (ABBO) ABBOTT LAB.

XX Billing-Medel PA, Cohen M, Friedman PN, Gordon J, Hodges SC;

PI Klasse MR, Kratochvil JD, Russell E, Stroupe SD;

XX WPI; 1999-229552/19.

PT Detection and treatment of urinary tract disease, particularly cancer.  
 PS Example 12a; Page 69; 109pp; English.

CC The invention relates to novel methods for detecting, diagnosing,  
 CC staging, monitoring, prognosticating, in vivo imaging, preventing,  
 CC treating or determining a predisposition to diseases or conditions of  
 CC the urinary tract, particularly cancer. The methods use products derived  
 CC from keratin/cyokeratin, cellular apoptosis susceptibility (CAS) or mat-  
 CC 8-specific polynucleotides (AAW32486 to AAW32498). These polynucleotide  
 CC sequences are used in the methods for detecting diseases of the urinary  
 CC tract, especially cancer

XX Sequence 8 AA;

Qy Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 DYKDDDDK 8  
 1 DYKDDDDK 8

RESULT 59

AAW9670 standard; peptide; 8 AA.

XX AAW9670;

DT 07-JUN-1999 (first entry)

DE FLAG tag sequence SEQ ID NO:6.  
 XX Human; lipocalin; testis; mammary gland; breast tumour; zlipol;  
 KM breast cancer; emphysema; skin disease; reproduction; anti-inflammatory;  
 KM antimicrobial.  
 XX Synthetic.  
 OS  
 XX MO9907740-A2.  
 XX  
 XX  
 PD 18-FEB-1999.  
 XX  
 PF 06-AUG-1998; 98WO-US016425.  
 XX  
 PR 06-AUG-1997; 97US-0054867P.  
 XX  
 PA (ZYMO ) ZYMOGENETICS INC.  
 XX  
 PI Conklin DC;  
 PI  
 DR WPI; 1999-167367/14.  
 XX  
 PT New lipocalin homologue designated zlipol - whose expression is  
 PT restricted to testis and mammary gland tissues, particularly breast  
 PT tumour tissue, used to, e.g. predict tumour aggressiveness.  
 XX  
 PS Example 5; Page 61; 94pp; English.  
 XX  
 CC The present invention describes a lipocalin homologue, designated zlipol.  
 CC The lipocalin homologue, zlipol, is specifically expressed in testis and  
 CC mammary gland, particularly breast tumour tissue. Based on this tissue  
 CC distribution, zlipol may be used as a diagnostic for breast carcinomas  
 CC and as a tool for predicting tumour aggressiveness. Agonists can be used  
 CC for transportation of small hydrophobic molecules either in vivo or in  
 CC vitro, and so are useful in specifically promoting the growth and/or  
 CC development of testis-specific cell lineages in culture. Zlipol can be  
 CC used to identify inhibitors. Zlipol proteins can also be used to prepare  
 CC antibodies (which can be linked to toxins), and can serve as immunogens.  
 CC Zlipol proteins can be used as a delivery and encapsulation system to  
 CC transport and/or stabilise small lipophilic molecules, e.g. to protect  
 CC from gut pH and digestive enzymes. They can also be used to bind small  
 CC fatty acids in blood or tissues to modulate their biological function,  
 CC e.g. to transport retinoids or steroids to receptors, in particular as  
 CC therapy for breast cancer, emphysema and diseases of the skin. They may  
 CC also play an important role in reproduction. Other uses include anti-  
 CC inflammatory responses, and antimicrobial activities. Zlipol nucleic acid  
 CC sequences may be used for gene therapy to increase or inhibit zlipol  
 CC activity, to derive probes and primers, to derive antisense sequences,  
 CC and to detect genetic abnormalities. The present sequence represents a  
 CC FLAG tag sequence which is used in an example from the present invention  
 XX  
 XX  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYKDDDDK 8  
 |||||  
 Db 1 DYKDDDDK 8  
 RESULT 60  
 AAM95645  
 ID AAM95645 standard; protein; 8 AA.  
 XX  
 XX AAM95645;  
 AC  
 XX  
 DT 08-JUN-1999 (first entry)  
 XX  
 DE Human BS124 peptide fragment.  
 XX  
 KM BS124; breast; cancer; detection; diagnosis; prevention; treatment;

KW peptide; fragment.  
 XX  
 OS Homo sapiens.  
 XX  
 FN MO9859049-A1.  
 XX  
 PD 30-DEC-1998.  
 XX  
 PF 19-JUN-1998; 98WO-US012862.  
 XX  
 PR 20-JUN-1997; 97US-00879354.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;  
 PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Russell UC;  
 PI Scheffel CP, Stroupe SD, Yu H;  
 XX  
 DR WPI; 1999-105623/09.  
 XX  
 PT New isolated BS124 polynucleotides and polypeptides - used for detecting,  
 PT diagnosing, preventing or treating diseases or conditions of the breast,  
 PT such as breast cancer.  
 XX  
 PS Example 11a; Page 100; 125pp; English.  
 XX  
 CC The sequence is that of a BS124 peptide fragment. It is useful for  
 CC detecting, diagnosing, staging, preventing or treating, or determining  
 CC predisposition to diseases or conditions of the breast, such as breast  
 CC cancer  
 XX  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYKDDDDK 8  
 |||||  
 Db 1 DYKDDDDK 8  
 RESULT 61  
 AAY31721  
 ID AAY31721 standard; peptide; 8 AA.  
 XX  
 AC AAY31721;  
 XX  
 DT 22-NOV-1999 (first entry)  
 XX  
 DE Flag epitope.  
 XX  
 KW Fibrinogen domain related protein; FDRG; TANGO 115; angiogenesis;  
 KW adipocyte; diabetes; obesity; inflammation; gene therapy; diagnosis;  
 KW human; Flag epitope.  
 XX  
 OS Synthetic.  
 XX  
 PN WO945135-A1.  
 XX  
 PD 10-SEP-1999.  
 XX  
 PF 02-MAR-1999; 99WO-US004548.  
 XX  
 PR 02-MAR-1998; 98US-00033539.  
 XX  
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
 PA (DAND ) DANA FARBER CANCER INST INC.  
 XX  
 PI Holtzman DA, Spiegelman BM, Yoon CH;  
 XX  
 DR WPI; 1999-540859/45.

PT New isolated Fibrinogen Domain Related polypeptides, used to develop  
PR products for treating e.g. obesity, diabetes, cancers, angiogenesis or  
PI inflammation.  
PS Example 6; Page 93; 152pp; English.  
XX  
XX  
CC The present sequence represents the FLAG epitope. A human FDRG FLAG  
CC epitope-tagged protein was constructed by PCR amplification of FDRG cDNA  
CC (see AAX87858) using a primer that includes the epitope sequence.  
CC ligation into expression vector pMT2 stop, and expression in HEK 293T  
CC cells. FDRG is a secreted molecule that is believed to modulate  
CC angiogenesis and to mediate the contribution of adipocytes to various  
CC metabolic processes. The invention provides FDRG proteins, antibodies,  
CC nucleic acid, and transgenic animals. Also provided are methods for  
CC identifying compounds that modulate FDRG activity or which modulate a  
CC metabolic disorder involving FDRG. Claimed methods of treating obesity or  
CC diabetes, and of regulating angiogenesis, involve administering a small  
CC molecule modulator of FDRG, a FDRG nucleic acid molecule or FDRG antibody  
XX  
SQ Sequence 8 AA:  
  
Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DYKDDDDK 8  
DB 1 DYKDDDDK 8  
  
RESULT 62  
AAY31944  
ID AAY31944 standard; peptide; 8 AA.  
XX  
XX AAY31944;  
XX  
DT 21-DEC-1999 (first entry)  
XX  
XX FLAG epitope tag.  
DE  
XX Rad17; cell cycle checkpoint; human; modulator; screening; cancer;  
XX cell proliferation; immune disorder; cirrhosis; rheumatoid arthritis;  
XX therapy; diagnosis; FLAG epitope.  
XX  
OS Synthetic.  
XX  
XX WO9949043-A2.  
XX  
XX 30-SEP-1999.  
XX  
XX 29-MAR-1999; 99WO-US006782.  
XX  
XX 27-MAR-1998; 98US-00049760.  
XX  
XX (ICOS-) ICOS CORP.  
XX (MEDI-) MEDICAL RES COUNCIL.  
XX  
XX Carr AM, Herendeen DR;  
XX  
XX WPI; 1999-591096/50.  
XX  
XX Novel human RAD17 gene and protein useful for identifying factors  
XX involved in cell cycle checkpoint control, e.g. for treatment of cell  
XX cycle control disorders such as cancer.  
XX  
XX Example 3; Page 28; 75pp; English.  
XX  
XX This peptide represents the FLAG epitope tag that was used in fusion  
XX proteins with human Rad17 (see AAY31937) for expression in mammalian host  
XX cells, permitting immuno-detection and immuno-purification. Rad17 is a  
XX novel cell cycle checkpoint control protein. The invention provides rad17  
XX polynucleotides and polypeptides, expression constructs, host cells,  
XX methods for producing Rad17 polypeptides, antibodies, methods for

CC identifying binding partners of the polypeptides, and methods of  
CC screening for modulators of Rad17 activity. Modulators may be  
CC therapeutically useful in treatment of a wide range of diseases, such as  
CC cancer, in which rad17 activity is involved. They may also be useful as  
CC chemotherapy and radiotherapy adjuvants  
XX  
XX  
SQ Sequence 8 AA:  
  
Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DYKDDDDK 8  
DB 1 DYKDDDDK 8  
  
RESULT 63  
AAW92256  
ID AAW92256 standard; peptide; 8 AA.  
XX  
XX AAW92256;  
XX  
XX 21-APR-1999 (first entry)  
XX  
XX FLAG peptide epitope.  
DE  
XX BL172; urinary tract; marker; cancer; recombinant; human; FLAG.  
XX  
XX Synthetic.  
XX  
XX WO9855656-A1.  
XX  
XX 10-DEC-1998.  
XX  
XX 05-JUN-1998; 98WO-US011693.  
XX  
XX 05-JUN-1997; 97US-00869579.  
XX  
XX (ABBOTT LAB.  
XX  
XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;  
XX Pi Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;  
XX Pi Russell JC, Stroupe SD, Yu H;  
XX  
XX WPI; 1999-045802/04.  
XX  
XX New purified polynucleotide BL172 derivatives and encoded polypeptides -  
XX useful in the identification of markers, which are indicative of urinary  
XX tract diseases or conditions.  
XX  
XX Example 11a; Page 68; 114pp; English.  
XX  
XX The invention provides polynucleotide sequences from urinary tract tissue  
XX library BL172. The BL172 polynucleotides (AAX01683-87) are used to detect  
XX target BL172 polynucleotides and BL172 mRNA and the BL172 polypeptides  
XX are used to detect BL172 antigens/antibodies in a test sample. The  
XX identification of certain markers in these methods are indicative of the  
XX presence of urinary tract disease, especially cancer. Additionally, the  
XX polypeptides are used to detect antibodies that bind specifically to a  
XX BL172 epitope derived from a BL172 polypeptide. Host cells containing a  
XX recombinant expression vector comprising the BL172 polynucleotide  
XX sequences are used to produce the polypeptides containing BL172 epitopes.  
XX The methods aid in diagnosis, detection, staging, monitoring,  
XX prognostication, in vivo imaging, prevention and treatment of diseases or  
XX conditions associated with BL172, especially urinary tract cancer. The  
XX present sequences represents a FLAG peptide epitope used in a BL172  
XX expression plasmid  
XX  
SQ Sequence 8 AA:  
  
Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.1e+06;



Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
 |||||  
 Db 1 DYKDDDK 8

RESULT 64  
 AAY07740  
 ID AAY07740 standard; protein; 8 AA.

XX AAY07740;

XX 05-JUL-1999 (first entry)

DE Human breast-specific BS200 derived protein fragment 1.

KW Breast; cancer; BS200; EST; expressed sequence tag; human; detection;  
 KW diagnosis; prevention; treatment; disease predisposition.

XX Synthetic.

OS Homo sapiens.

XX WO9902714-A1.

XX 21-JAN-1999.

PF 07-JUL-1998; 98WO-US013908.

PR 07-JUL-1997; 97US-00889127.

PA (ABBO ) ABBOTT LAB.

PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;  
 PI Granados EN, Hodges SC, Klasse MR, Kratochvili JD, Russell JC;  
 PI Stroupe SD, Yu H;

DR WPI; 1999-120915/10.

PT New breast specific gene BS200 - used to develop products for detecting,  
 PT diagnosing, staging, preventing or treating diseases or conditions of the  
 PT breast, e.g. Breast cancer.

PS Example 11a; Page 119; 124pp; English.

CC This invention describes a novel human breast-specific protein BS200.

CC This protein and its encoding nucleic acids are useful for detecting,  
 CC diagnosing, staging, monitoring, prognosticating, preventing or treating,  
 CC or determining predisposition to diseases or conditions of the breast,  
 CC such as breast cancer

XX Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
 |||||  
 Db 1 DYKDDDDK 8

RESULT 65

AAW94250  
 ID AAW94250 standard; peptide; 8 AA.

XX AAW94250;

XX 15-APR-1999 (first entry)

DE FLAG peptide epitope.

KW p35 protein; cowpox; vaccinia; variola; secreted protein; chemokine;

KW chemotaxis; cytokine; monocyte chemotactic protein; MCP-1; MCP-3; MIP-1;  
 KW Rantes; Botaxin; macrophage inflammatory protein; inflammation; asthma;  
 KW lung; allergy; influenza; psoriasis; arthritis; autoimmune disorder.

XX Synthetic.

OS US5871740-A.

XX 16-FEB-1999.

PF 26-SEP-1996; 96US-00720258.

PR 29-SEP-1995; 95US-00537324.

PR 20-DEC-1995; 95US-00575715.

PA (IMMV ) IMMUNEX CORP.

PI Smith CA;

DR WPI; 1999-166574/14.

PT Use of poxvirus p35 polypeptides - for binding to chemokines and treating  
 PT conditions mediated by chemokines, e.g. inflammation, asthma, allergy,  
 PT influenza or autoimmune disorders.

PS Disclosure; Col 31; 20pp; English.

CC The invention provides nucleic acid sequences (AAW06698-700) encoding p35  
 CC proteins of cowpox, vaccinia and variola viruses (AAW94242-44)

CC respectively. p35 is a secreted protein that can be produced by usual  
 CC recombinant techniques. These p35 proteins can bind to a number of

CC chemotaxis-stimulating cytokines (chemokines). The p35 proteins can be  
 CC used to treat conditions mediated by chemokines such as monocyte

CC chemotactic protein (MCP)-1, MCP-3, Rantes, Botaxin, macrophage  
 CC inflammatory protein (MIP)-1 alpha, and MIP-1 beta. They can be used to

CC treat inflammation such as inflammation of the lung, e.g. associated with  
 CC allergy or asthma. They can also be used to treat influenza, skin

CC inflammation, e.g. psoriasis, or arthritis or autoimmune disorders. The  
 CC p35 polypeptides can also be used as reagents in assays and for purifying

CC chemokines. The present sequence represents a FLAG peptide epitope used  
 CC during the course of the invention

XX Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
 |||||  
 Db 1 DYKDDDDK 8

RESULT 66  
 AAW82735  
 ID AAW82735 standard; peptide; 8 AA.

XX AAW82735;

XX 29-MAR-1999 (first entry)

DE Adenovirus chimeric protein FLAG-peptide.

KW Chimeric protein; adenoviral fibre protein; monomer; infection;  
 KW trimerisation domain; affinity; substrate; gene therapy vector;  
 KW attachment; interaction assay.

XX Mastadenovirus.

OS WO9854346-A1.

XX 03-DEC-1998.

XX

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PF 28-MAY-1998; 98WO-US011024.
XX
XX 28-MAY-1997; 97US-0047849P.
PR 16-JAN-1998; 98US-0071668P.
XX
PA (GENV-) GENVEC INC.
XX
XX Wickham TJ, Kovacsdi I, Roelwink PW, Einfeld D, Brough DE;
PI Lizanova A, Yonehito G;
DR WPI; 1999-059848/05.
XX
XX New adenoviral fibre trimer with reduced binding to native substrate -
PT useful for, e.g. preparing gene therapy vector with minimal ectopic
PI infection for in vitro applications.
XX
XX Example 14; Page 65; 103pp; English.
XX
XX This sequence represents a FLAG peptide used in a method to construct
CC novel monomers having an N-terminus of an adenoviral fibre protein and a
CC trimerisation domain. Such monomers have lower affinity for native
CC substrate than the native adenoviral fibre trimer. Cell lines containing
CC such monomers are used (i) to propagate adenovirus for use as gene
CC therapy vectors (for in vitro or in vivo applications), (ii) as reagents
CC for studying adenoviral attachment and infection, and (iii) in receptor-
CC ligand interaction assays. The new viruses produce minimal ectopic
CC infection (they can not infect native host cells) so are safer as vectors
CC and can be engineered for selective targeting to other cells
XX
XX Sequence 8 AA;
SQ

```

```

Query Match          100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 DYKDDDDK 8
   |||||
Db 1 DYKDDDDK 8

```

```

RESULT 67
AAV42254
ID AAV42254 standard; peptide; 8 AA.
XX
XX AAV42254;
AC
XX
XX 01-DEC-1999 (first entry)
DT
XX
XX Synthetic FLAG octapeptide.
DE
XX
XX Adenovirus; gene therapy; coxsackievirus adenovirus receptor; CAR;
KM cancer; cystic fibrosis; muscular dystrophy.
XX
XX Synthetic.
OS
XX
XX WO9939734-A1.
XX
XX 12-AUG-1999.
PD
XX
XX 05-FEB-1999; 99WO-US002549.
PF
XX
XX 06-FEB-1998; 98US-0073947P.
PR 10-SEP-1998; 98US-0099801P.
XX
XX (UABR-) UAB RES FOUND.
PA
XX Curiel DT, Krasnykh VN, Dmitriev I;
PI
XX WPI; 1999-539951/45.
DR
XX
XX Recombinant adenovirus vectors with modified fiber knob loops, useful in
PT gene therapy.
XX

```

```

PS Example 14; Page 39; 126pp; English.
XX

```

```

CC This sequence represents a synthetic FLAG octapeptide. DNA encoding this
CC sequence was cloned into the sequence encoding the HI loop of the
CC adenovirus fibre protein knob domain, which was then used in the
CC construction of plasmids encoding a fibre protein. Recombinant adenovirus
CC genomes were generated by homologous DNA recombination in E. coli, before
CC excision of the newly generated genome for virus rescue. The knob domain
CC of the adenovirus fibre protein mediates the initial binding and
CC recognition of the coxsackievirus and adenovirus receptor (CAR) on the
CC cell surface. The HI loop protrudes from the knob domain and connects
CC beta-strands involved in the formation of the cell binding site.
CC Recombinant adenovirus vectors are used in a number of gene therapy
CC applications; however, the reliance on the CAR means that in certain
CC situations, recombinant viruses are sequestered by high CAR-expressing
CC non-target cells while the true target cells, if low in CAR, receive
CC little of the therapeutic gene. Studies of fibre proteins with an HI loop
CC modified by insertion of the FLAG octapeptide (a widely used detection
CC and purification tag) suggested that a heterologous peptide sequence at
CC this location would not affect the structure of the protein and that the
CC HI loop was still accessible for binding. The infectivity of recombinant
CC viruses carrying this modified fibre protein was unaffected
XX

```

```

SQ Sequence 8 AA;
Query Match          100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 DYKDDDDK 8
   |||||
Db 1 DYKDDDDK 8

```

```

RESULT 68
AAV49544
ID AAV49544 standard; peptide; 8 AA.
XX
XX AAV49544;
AC
XX
XX 12-JAN-2000 (first entry)
DT
XX
XX FLAG epitope for insertion into the N-terminus of Nsp1.
DE
XX
XX Human; PRO201; PRO308; PRO309; Nsp1; Nsp2; Nsp3; SH2 domain; EST;
KM expressed sequence tag; tumour; tumorigenesis; diagnosis; cancer;
KM identification; proliferation; neoplastic cell growth.
XX
XX Synthetic.
OS
XX
XX WO9954467-A1.
XX
XX 28-OCT-1999.
PD
XX
XX 23-APR-1999; 99WO-US008847.
PF
XX
XX 23-APR-1998; 98US-0082767P.
PR 22-DEC-1998; 98US-0113296P.
XX
XX (GETH ) GENENTECH INC.
PA
XX Stewart TA, Lu Y;
PI
XX WPI; 1999-620728/53.
DR
XX
XX New human polypeptides useful to screen for antagonists and produce
PT antibodies useful to diagnose and treat tumors, e.g. cancers.
XX
XX Example 3; Page 54; 152pp; English.
PS
XX
XX The present invention describes human proteins designated PRO201, PRO308
CC and PRO309, (also designated Nsp1, Nsp2 and Nsp3 respectively) which are
CC encoded by cDNA clones DNA30676, DNA40575 and DNA61601. The proteins were

```

Query Match	100.0%;	Score 47;	DB 2;	Length 8;
Best Local Similarity	100.0%;	Pred. No. 2.1e+06;		
Matches	8;	Conservative	0;	Mismatches 0;
			Indels	0;
Gaps				
QY	1	DYKDDDDK	8	
Db	1	DYKDDDDK	8	

DT	26-OCT-1999	(first entry)
XX		
DE	FLAG peptide.	

KW islet cell antigen; I $\alpha$ 2; human; epitope; autoantigen; autoantibody;  
KM insulin-dependent diabetes mellitus; IDDM; immunoassay; diagnosis; FLAG  
XX Synthetic.  
OS  
X

XX	29-DEC-1998;	98EP-00660149
PF		
XX	29-JAN-1998;	98US-00015399;
PR		

XX  
PI Hinkkanen A;  
XX  
DR WPI; 1999-481070/41.  
XX

PT New fusion protein, useful for diagnosing insulin-dependent diabetes mellitus.

PS Disclosure; Page 4; 27pp; English  
XX

This peptide represents a FLAG peptide that is recognised by monoclonal antibody M1 (ATCC HB 9259). FLAG has been used in novel fusion proteins of the invention. Such fusion proteins have epitopes of at least 2 of the autogenyins glutamate decarboxylase (GAD65 (see AY006607), islet cell antigen (IICA (see AY006606)) and preproinsulin (PPINS, see AY006608), the epitopes being connected via linker peptides. The invention also provides the cDNA encoding the fusion protein, a vector and an Escherichia coli cell encompassing the cDNA. The fusion protein is used in an immunoassay for the simultaneous detection of autoantibodies related to insulin-

CC	dependent diabetes mellitus (IDDM)	
xx		
sq	Sequence 8 AA;	
Query Match	100.0%	Score 47; DB 2; Length 8;
Best Local Similarity	100.0%	Pred. No. 2.1e+06;
Matches	8; Conservative	0; Mismatches 0; Indels 0; Gaps 0

Qy	1	DYKDDDDK	8
Db	1	DYKDDDDK	8

RESULT 70	
AAW92410	.
ID AAW92410	standard; peptide; 8 AA
xy	

DT	21-APR-1999 (first entry)
XX	
DE	Human IL-17R FLAG peptide
XX	

X  
 B cell proliferation; immunoglobulin secretion; immunogen.  
 KM  
 autoimmune disease; allergy; asthma; treatment; inflammatory disease  
 KM  
 T cell proliferation; T cell activation; organ; graft; rejection;  
 KM  
 IL-1/ $\alpha$  human; interleukin-1 receptor; immunoregulator; inhibitor  
 KM  
 X

AA	US5869286-A.
PN	
XX	
PD	09-FEB-1999.
XX	

23-MAR-1995; 95US-00410535  
07-AUG-1995; 95US-00538765  
(IMMV ) IMMUNEX CORP.

PPI Spriggs MK, Fanslow WC, Yao Z, XXX  
DR WPI; 1999-152766/13.

Example 3, Col 29-30; 25pp; English.  
PS Isolated interleukin-17 receptor DNA - used to develop products for  
PT treating e.g. organ or graft rejection, autoimmune disease, allergy  
PT asthma or inflammatory disease.  
XXX

This sequence represents a human interleukin-17 receptor (IL-17R) FLAG peptide. IL-17R polypeptides have immunoregulatory activity. They can be used for inhibiting T cell proliferation, or for inhibiting T cell activation. In particular they can be used for preventing or treating organ or graft rejection, autoimmune disease, allergy or asthma. They can also be used for the prevention or treatment of inflammatory disease in which activated T cells play a role or for inhibiting B cell proliferation or immunoglobulin secretion. The IL-17 polypeptides can also be used as immunogens, reagents in *in vitro* assays, or as binding agents for affinity purification procedures

Sequence 8 AA;

```
Query Match      100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0
```

2y	1	DYKDDDDK	8
db	1	DYKDDDDK	8

```

RESULT 71
AAV06911
ID AAV06911 standard; peptide; 8 AA.
XX
XX
AC AAV06911;
XX
XX 01-JUL-1999 (first entry)
XX
XX FLAG peptide epitope.
DE
XX
XX Growth factor precursor; B-cell surface; T cell surface; Cab; hepatitis;
XX catalytic antibody; immunoglobulin; tumour necrosis factor; influenza;
XX rheumatoid arthritis; toxic shock syndrome; viral docking receptor;
XX human immune virus; tumour-specific antigen; amyloid plaque; myeloma;
XX Alzheimer's disease; IGE; allergy; asthma; drug detoxification;
XX autoimmune; inflammatory disease; gene therapy; FLAG.
XX
XX Synthetic.
XX
XX WO915563-A1.
XX
XX 01-APR-1999.
XX
XX 18-SEP-1998; 98WO-AU000783.
XX
XX 19-SEP-1997; 97AU-00009306.
XX
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX Koentgen F, Suesse GM, Tarlinton DM, Treutlein HR,
XX
XX WPI; 1999-244394/20.
XX
XX Growth factor precursor cleaved by antigen-specific catalytic antibody.
XX
XX Example 3; Page 42; 101pp; English.
XX
XX The invention relates to a growth factor precursor that comprises B-cell
XX surface binding part, T cell surface binding part, antigen cleavable by a
XX catalytic antibody (CAB); and a peptide comprising heavy and light chains
XX of immunoglobulin. When the antigen is cleaved the B cell surface part
XX can interact with its target. The growth factor precursors are used to
XX select B cells that produce Ag-specific Cab, and to generate Cab from
XX such cells (by inducing mitogenesis, caused by the growth factor released
XX by specific cleavage). The Ag-specific Cab can be directed against, e.g.
XX tumour necrosis factor (treatment of rheumatoid arthritis or toxic shock
XX syndrome); viral docking receptors (treatment of human immune virus,
XX hepatitis and influenza infections); tumour-specific antigens; amyloid
XX plaque (treatment of Alzheimer's disease or myeloma) or IGE (treatment of
XX allergies such as asthma). Cab may also be used for drug detoxification,
XX to treat autoimmune or inflammatory diseases and to eliminate
XX environmental or industrial pollutants, such as plastics and petroleum.
XX Particularly the growth factor precursors are produced by delivering the
XX corresponding nucleic acid in a viral or other gene therapy vector. The
XX present sequence represents a FLAG peptide epitope
XX
XX Sequence 8 AA:
SQ

```

```

Query Match          100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 DYKDDDDK 8
   |||||
Db 1 DYKDDDDK 8

```

```

RESULT 72
AAV23636
ID AAV23636 standard; peptide; 8 AA.
XX
XX
AC AAV23636;
XX
XX

```

```

DT 06-SEP-1999 (first entry)
XX
XX Octapeptide used to make BZLF2 fusion proteins.
DE
XX
XX BZLF2 protein; beta chain; blood mononuclear mononuclear cell;
XX Class II major histocompatibility complex antigen; proliferation;
XX cytotoxic T cell response; antigen specific response; asthma;
XX autoimmune disease; transplant rejection.
XX
XX Synthetic.
XX
XX US5925734-A.
XX
XX 20-JUL-1999.
XX
XX 24-SEP-1997; 97US-00936854.
XX
XX 28-APR-1994; 94US-00235397.
XX
XX 28-APR-1995; 95US-00430633.
XX
XX (IMNV ) IMMUNEX CORP.
XX
XX Comeau MR, Hutt-Fletcher LM, Armitage RJ, Farrar TM, Alderson M;
XX Spriggs MK, Cohen UI;
XX
XX WPI; 1999-418295/35.
XX
XX Epstein-Barr virus BZLF2 proteins.
XX
XX Example 1; Col 31-32; 25pp; English.
XX
XX The present sequence represents a peptide used to create fusion proteins
XX with the Epstein-Barr virus BZLF2 proteins of the invention. The BZLF2
XX protein is capable of binding to a beta chain of a Class II major
XX histocompatibility complex antigen to inhibit an antigen-specific
XX response. BZLF2 is useful for inhibiting antigen-specific antibody
XX formation, the proliferation of blood mononuclear mononuclear cells, and
XX cytotoxic T cell responses. BZLF2 is also useful for inhibiting
XX undesirable antigen specific responses, e.g. in the treatment or
XX prevention of asthma; for preventing or treating autoimmune disease; and
XX for preventing tissue or organ transplant rejection
XX
XX Sequence 8 AA:
SQ

```

```

Query Match          100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 DYKDDDDK 8
   |||||
Db 1 DYKDDDDK 8

```

```

RESULT 73
AAW86029
ID AAW86029 standard; peptide; 8 AA.
XX
XX
AC AAW86029;
XX
XX 23-FEB-1999 (first entry)
XX
XX FLAG peptide epitope.
DE
XX
XX UTI16; urinary tract; epitope; antigen; detection; diagnosing;
XX monitoring; in vivo imaging; cancer; agonist; antibody; tumour;
XX metastasis.
XX
XX Synthetic.
XX
XX MO9851824-A1.
XX
XX 19-NOV-1998.
XX
XX

```



SO Sequence 8 AA; 100.0%; Score 47; DB 2; Length 8;  
 Query Match Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDK 8  
 |||||  
 1 DYKDDDK 8

Db 1 DYKDDDK 8

RESULT 76  
 AAW96302  
 ID AAW96302 standard; peptide; 8 AA.  
 AC AAW96302;  
 DT 28-JUN-1999 (first entry)  
 DE C-terminal tagging peptide.  
 XX  
 XX TANGO-69; herpesvirus entry mediator; HVEM; glycoprotein D; LIGHT;  
 KW lymphotoxin; tumour necrosis factor receptor; TNFR; cell proliferation;  
 KW programmed cell death; apoptosis; immune response; probe; primer;  
 KW antibody; signal transduction; cytokine; leukocyte; cell differentiation;  
 KW coagulation.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9911662-A1.  
 XX  
 PD 11-MAR-1999.  
 XX  
 PF 03-SEP-1998; 98MO-US018533.  
 XX  
 PR 05-SEP-1997; 97US-0057936P.  
 XX  
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
 XX  
 PI Busfield SJ;  
 DR WPI; 1999-205132/17.  
 XX  
 PT Newly isolated murine polynucleotide encoding a TANGO-69 polypeptide -  
 PT useful for regulating cell proliferation and differentiation, and cell  
 PT survival.  
 XX  
 PS Example 4(b); Page 104; 125pp; English.

The murine TANGO-69 cDNA encodes a type II membrane protein, which is the murine homolog of the human herpesvirus entry mediator (HVEM) ligand, LIGHT. LIGHT is a novel cytokine and is termed LIGHT because it shows homology to lymphotoxins, exhibits inducible expression and competes with HSV Glycoprotein D for HVEM, a receptor expressed by T-lymphocytes. HVEM and TANGO-69 are members of the tumour necrosis factor receptor (TNFR) ligand superfamily. The TANGO-69 protein regulates a variety of cellular processes including cell proliferation, programmed cell death and immune responses by binding to a membrane-bound form of HVEM (mHVEM) to inhibit mHVEM activity. The protein plays an essential role in inhibiting inflammation. Probes or primers derived from the TANGO-69 coding sequence are useful for detecting the polynucleotide in samples (especially mRNA) and antibodies directed against the TANGO-69 polypeptide are useful for detecting the polypeptide. Compounds which bind to the TANGO-69 polypeptide are useful for modulating the activity of the polypeptide and TANGO-69 protein variants are useful as (ant)agonists. TANGO-69 polypeptides are useful for interacting with proteins in the TANGO-69 signalling pathway, binding the TANGO-69 receptor, interacting with mHVEM and mast cells, and for modulating inflammation, cytokine production, leukocyte activation, MHC I induction, allergic reactions, cellular differentiation, viral proliferation, cell death adhesion molecule induction on endothelial cells and coagulation. Two primers (AA08401, AA08402) were used to amplify the TANGO-69 sequence for its subcloning into the expression vector pPicAlpha A for expression in Pichia

CC pastoris. The resulting plasmid fused the Pichia pastoris alpha-factor  
 CC signal sequence to the mature form of TANGO-69 also comprising this C-  
 CC terminal tag

SO Sequence 8 AA; 100.0%; Score 47; DB 2; Length 8;  
 Query Match Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDK 8  
 |||||  
 1 DYKDDDK 8

Db 1 DYKDDDK 8

RESULT 77  
 AAW95562  
 ID AAW95562 standard; peptide; 8 AA.  
 AC AAW95562;  
 DT 29-MAR-1999 (first entry)  
 DE FLAG peptide epitope used in a Ls170 expression plasmid.  
 XX  
 XX Ls170 gene; in vivo imaging; lung disease; cancer; drug screening; FLAG.  
 KW  
 OS Synthetic.  
 XX  
 PN WO9856951-A1.  
 XX  
 PD 17-DEC-1998.  
 XX  
 PF 11-JUN-1998; 98MO-US011601.  
 XX  
 PR 11-JUN-1997; 97US-0049183P.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;  
 PI Granados EM, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;  
 PI Russell JC, Stroupe SD;  
 XX  
 DR WPI; 1999-060335/05.  
 XX  
 PT New Ls170 nucleic acid from lung tissue - useful for detecting,  
 PT monitoring, preventing and treating lung disease, particularly cancer.  
 XX  
 PS Example 11; Page 70; 120pp; English.

The present invention relates to the detection of a target Ls170 polynucleotide that comprises treating a test sample with at least one Ls170-specific nucleic acid that has at least 50 percent identity with any of the sequences (AA00801-809) which are fragments derived from Ls170 gene. These Ls170 nucleic acid fragments represent a set of contiguous, partially overlapping sequences transcribed from lung tissue. They are used for diagnosis, staging, monitoring, in vivo imaging, prevention and treatment of lung disease, specifically cancer, and to indicate predisposition to such disease. Particularly detection of Ls170 polynucleotide, Ls170 antigens, or anti-Ls170 antibodies is indicative of disease. Cells transformed with an expression system comprising the Ls170 nucleic acid sequences are used to express recombinant polypeptides. The Ls170 polypeptides containing at least one epitope in their sequences, are used to raise Ab and for drug screening. Ls170-related nucleic acid can be used to isolate related sequences; as standards and reagents in assays; as targets for drug screening, and as components or targets for therapy, e.g. as antisense, ribozyme or triplex-forming agents. Ab can be used to deliver therapeutic agents to Ls170-expressing cells; directly as therapeutic agents (by neutralising Ls170 polypeptides); in competitive binding drug screens, and to generate anti-idiotypic antibodies for use in rational drug design. The present sequence represents a FLAG peptide epitope used in the Ls170 expression plasmids

SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.1e+06; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
| | | | |  
Db 1 DYKDDDK 8

RESULT 78

AAV09543

ID AAV09543 standard; peptide; 8 AA.

XX AAV09543;

XX 21-JUL-1999 (first entry)

XX Human TAB1 FLAG peptide.

XX Human; TAB1; TAK1; screening; inhibition; TGF-beta;  
XX transforming growth factor beta.

XX Homo sapiens.

XX MO9921010-A1.

XX 29-APR-1999.

XX 22-OCT-1998; 98MO-JF004796.

XX 22-OCT-1997; 97JP-00290188.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Ono K, Ohtomo T, Tsuchiya M;

XX WPI; 1999-312645/26.

PT Screening for TGF-beta inhibitory substances, which are useful as drugs  
PT for treatment of diseases relating to its disorder.

XX Example 1; Page 58; 195pp; Japanese.

XX A method has been developed for screening for substances which inhibit  
 CC the binding of TAK1 polypeptide to TAB1 polypeptide. The method  
 CC comprises: (a) contacting the polypeptide in the presence of a sample;  
 CC and (b) detecting the amount of bound polypeptide, in which the sample  
 CC can be pre-mixed with TAK1 or TAB1 polypeptide first. The transforming  
 CC growth factor (TGF)-beta inhibitory substances can be used in drugs for  
 CC indications e.g. as TGF-beta signal transduction inhibitors or  
 CC activators, or extracellular matrix protein production enhancement  
 CC inhibitors, or monocycle migration inhibitors or activators, or  
 CC physiological activity induction inhibitors or activators, or  
 CC immunosuppression inhibitors or activators, or amyloid beta protein  
 CC precipitation inhibitors or activators, and such substances can also be  
 CC inhibitors of the TAK1 polypeptide function, particularly kinase  
 CC activity. The present sequence represents a peptide from an example of  
 CC the present invention

SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.1e+06; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
| | | | |  
Db 1 DYKDDDK 8

RESULT 79

AAW82718

ID AAW82718 standard; protein; 8 AA.

XX AAW82718;

XX 15-MAR-1999 (first entry)

XX Human ZCHEMO-8 C/N terminal FLAG peptide.

XX Chemokine; ZCHEMO-8; human; pathological condition; infection; cancer;  
 XX autoimmune disorder; immunodeficiency; myelopietic; wound healing;  
 XX transplant; progenitor cell; HIV infection; AIDS; chemotherapy;  
 XX radiation therapy; T cell; macrophage activation inhibitor; B lymphocyte;  
 XX chronic inflammatory disease; infective disease; diagnosis; detection;  
 XX drug screening; gene therapy; FLAG peptide.

XX Synthetic.

XX MO9854326-A1.

XX 03-DEC-1998.

XX 19-MAY-1998; 98MO-US010329.

XX 29-MAY-1997; 97US-0047860P.

XX (ZYMO) ZYMOGENETICS INC.

XX Shepard PO;

XX WPI; 1999-059841/05.

PT New isolated human beta-chemokine, ZCHEMO-8 - used to develop products  
 PT for treating e.g. ischaemia, reperfusion, wound healing, autoimmune  
 PT diseases, inflammation, asthma or infections.

PS Claim 10; Page 94; 131pp; English.

XX This sequence represents a FLAG peptide used in the isolation of a  
 CC novel human beta chemokine, ZCHEMO-8. Altered levels of ZCHEMO-8 may be  
 CC indicative of pathological conditions, including infections, cancer,  
 CC myelopietic disorders, autoimmune disorders and immunodeficiencies. The  
 CC ZCHEMO-8 polypeptides can be used, e.g. to reduce the damage in ischemic  
 CC and reperfusion injuries, in a wound healing regime to stimulate an  
 CC infiltration of immune cells (e.g. monocytes, neutrophils, T lymphocytes  
 CC or basophils) to a wound site to facilitate healing. ZCHEMO-8 may be used  
 CC to mobilise progenitor cells from the marrow into the peripheral blood  
 CC for transplants. ZCHEMO-8 polypeptides could be used to further define  
 CC the role of chemokines in mediating suppression of HIV replication in  
 CC CD4+ T-cells and limiting progression of HIV infection to AIDS. Use may  
 CC be made of ZCHEMO-8 polypeptides during chemotherapy or radiation  
 CC therapy, to protect haematopoietic cells. ZCHEMO-8 antagonists may have a  
 CC beneficial therapeutic effect in diseases where the inhibition of  
 CC activation of certain macrophages, neutrophils, basophils, B lymphocytes  
 CC and/or T cells may be effective. Such diseases include autoimmune  
 CC diseases e.g. multiple sclerosis, insulin-dependent diabetes and systemic  
 CC lupus erythematosus, rheumatoid arthritis, allergies, asthma or  
 CC atherosclerosis. Also benefit may be derived from using ZCHEMO-8  
 CC antagonists for chronic inflammatory and infective diseases. Antagonists  
 CC may be used to dampen or inactivate ZCHEMO-8 during activated immune  
 CC response. The products can also be used for detection, diagnosis, drug  
 CC screening or gene therapy

SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.1e+06; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
| | | | |  
Db 1 DYKDDDK 8

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RESULT 80
AAV06900
ID AAV06900 standard; peptide; 8 AA.
XX
XX
AC AAV06900;
XX
DT 06-JUL-1999 (first entry)
XX
DE FLAG affinity peptide sequence.
XX
KM Secretory protein; ZSIG-11; ligand polypeptide; testis; endoprotease;
KM prohormone convertase; fertility; therapeutic; human; FLAG.
OS Synthetic.
XX
PN WO916870-A1.
XX
PD 08-APR-1999.
XX
PF 29-SEP-1998; 98WO-US020449.
XX
PR 29-SEP-1997; 97US-0060327P.
PR 29-SEP-1997; 97US-00939897.
PR 19-MAY-1998; 98US-00081310.
PR 19-MAY-1998; 98US-0085966P.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Sheppard PO;
XX
DR WPI; 1999-263692/22.
XX
PT Polynucleotide encoding a human secretory protein, ZSIG-11.
XX
PS Example 4; Page 107; 113pp; English.
XX
CC The invention relates to a human secretory protein, ZSIG-11. Host cells
CC containing a vector comprising the ZSIG-11 nucleic acid are used for the
CC recombinant expression of the protein. ZSIG-11 is a novel ligand
CC polypeptide and specific antibodies can be used to detect its presence in
CC a biological sample. Probes derived from ZSIG-11 nucleotide sequences can
CC also be used in detection of ZSIG-11 RNA. ZSIG-11 is expressed at high
CC levels in testis, and could be used to identify/study prohormone
CC convertases or endoproteases that exhibit testis specificity.
CC Antagonists, including antibodies, are useful for inhibiting or
CC eliminating the function of ZSIG-11. It is possible that ZSIG-11 and its
CC antagonists will be useful as fertility inducing therapeutics
XX
SQ Sequence 8 AA:
Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

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KW gene therapy.
XX
XX
OS Homo sapiens.
XX
PN WO9931274-A2.
XX
PD 24-JUN-1999.
XX
PF 11-DEC-1998; 98WO-US026441.
XX
PR 15-DEC-1997; 97US-00990568.
XX
PA (ABBOTT ) ABBOTT LAB.
XX
PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados EM, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;
PI Russell JC, Stroupe SD;
XX
DR WPI; 1999-405041/34.
XX
PT PA153 cDNA transcribed from pancreatic tissue.
XX
PS Example 11a; Page 123; 123pp; English.
XX
CC This invention describes novel contiguous and partially overlapping cDNA
CC sequences and their encoded polypeptides, designated PA153, transcribed
CC from human pancreatic tissue and which have cytostatic activity. The
CC PA153 polynucleotides, proteins and antibodies are all useful in methods
CC of detection. Detection of PA153 polynucleotide, antigens or anti-PA153
CC antibodies in a sample is indicative of pancreatic disease. PA153
CC antibodies (antagonists) can also be used in vivo for therapeutic use,
CC e.g. treatment of pancreatic disease, tumours or metastases. Antisense
CC PA153 polynucleotides can be used in gene therapy of pancreatic diseases
XX
SQ Sequence 8 AA:
Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

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```

RESULT 81
AAV25328
ID AAV25328 standard; protein; 8 AA.
XX
XX
AC AAV25328;
XX
DT 03-SEP-1999 (first entry)
XX
DE Human pancreatic PA153 derived peptide.
XX
KW Pancreatic disease; PA153; human; cytostatic; detection; antigen;
KW anti-PA153; antagonist; therapy; treatment; tumour; metastasis;
XX

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```

RESULT 82
AAV13471
ID AAV13471 standard; peptide; 8 AA.
XX
XX
AC AAV13471;
XX
DT 26-JUL-1999 (first entry)
XX
DE FLAG peptide sequence.
XX
KW BSI06; breast; marker; detection; diagnosis; breast cancer.
XX
OS Synthetic.
XX
PN WO9923230-A1.
XX
PD 14-MAY-1999.
XX
PF 19-OCT-1998; 98WO-US022020.
XX
PR 31-OCT-1997; 97US-00962094.
XX
PA (ABBOTT ) ABBOTT LAB.
XX
PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados E, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;
PI Russell JC, Stroupe SD;
XX

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DR WPI; 1999-326991/27.  
 XX New isolated BS106 nucleic acids.  
 XX  
 PS Example 11a; Page 93; 105pp; English.  
 CC The invention provides BS106 polynucleotides (AAK55578-82) and  
 CC polypeptides (AAV13466-470). The BS106 nucleic acids correspond to a  
 CC breast tissue gene and can be used as markers for breast tissue disease.  
 CC The products can be used for detecting, diagnosing, staging, monitoring,  
 CC prognosticating, preventing or treating, or determining diseases or  
 CC conditions associated with BS106, especially breast cancer  
 XX  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYKDDDDK 8  
 Db 1 DYKDDDDK 8  
 RESULT 83  
 ID AAY04141 standard; peptide; 8 AA.  
 XX AAY04141;  
 AC  
 XX 15-JUN-1999 (first entry)  
 DT  
 XX Human slit 3 peptide.  
 DE  
 XX Human; slit-like protein; slit 3; slit 1; prevention; treatment; disease;  
 KW spinal cord; thyroid gland; ovary; prostate; renal gland;  
 KW small intestine; heart; trachea; thymus; lymph node; muscular system;  
 KW colon.  
 XX  
 OS Homo sapiens.  
 XX  
 PN JP11075846-A.  
 PD 23-MAR-1999.  
 PF 02-SEP-1997; 97JP-00236994.  
 PR 02-SEP-1997; 97JP-00236994.  
 XX (ASAH ) ASAH KASEI KOGYO KK.  
 PA  
 XX WPI; 1999-257695/22.  
 DR  
 XX New slit-like polypeptide - useful for prevention and treatment of  
 PT diseases in spinal cord, thyroid gland, ovary, prostate, renal gland,  
 PT small intestine, heart, trachea, thymus, lymph node, muscular system and  
 PT colon.  
 XX  
 PS Example 4; Page 47; 48pp; Japanese.  
 CC The present sequence represents a peptide from a human slit-like protein.  
 CC Slit-like proteins can be used for the prevention and the treatment of  
 CC diseases in spinal cord, thyroid gland, ovary, prostate, renal gland,  
 CC small intestine, heart, trachea, thymus, lymph node, muscular system and  
 CC colon  
 XX  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYKDDDDK 8

Db 1 DYKDDDDK 8  
 RESULT 84  
 ID AAY49750 standard; peptide; 8 AA.  
 XX AAY49750;  
 AC AAY49750;  
 XX 19-JAN-2000 (first entry)  
 DT  
 XX Compact structure forming exemplification peptide #43.  
 DE  
 XX Compact structure forming peptide; dimerisation; stability; scaffold;  
 KW library screening; drug screening; gene therapy.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9951625-A2.  
 PD 14-OCT-1999.  
 PF 02-APR-1999; 99WO-US007374.  
 PR 02-APR-1998; 98US-0080444P.  
 XX (RIGE-) RIGEL PHARM INC.  
 PA  
 XX Anderson D;  
 PI  
 DR WPI; 1999-620191/53.  
 XX  
 PT Novel dimerization peptides which self-associate are used with other  
 PT proteins to effect the formation of compact structures.  
 XX  
 PS Disclosure; Page 13; 75pp; English.  
 XX  
 CC The present invention describes peptides which have a moderate or high  
 CC affinity for each other, when added as extensions to both the N-terminus  
 CC and C-terminus of a protein, can be used to help fold the protein into a  
 CC compact structure. This compact structure is more stable to proteases. A  
 CC composition (A) comprises at least a first dimerisation peptide (I)  
 CC comprising the sequence (SI) that is no more than 8 amino acids long,  
 CC where the composition optionally comprises a second dimerisation peptide  
 CC (II): NH2-X1-X2-X3-X4-X5-COOH (SI) where X1 to X4 = Ala, Val, Ile, Leu,  
 CC Trp, Phe, Met, or Tyr, and X5 = Lys, Arg, Asp or Glu; NH2-X1-X2-X3-X4-X5-  
 CC COOH (II). The compositions of the invention are displayed  
 CC intracellularly or extracellularly and are useful to identify binding  
 CC proteins and molecules, and to modulate intracellular signalling  
 CC pathways. A library of constrained proteins may be evaluated in vivo for  
 CC its bioactive potential. The invention can be used to access molecules or  
 CC targets within living cells, and then provide for the isolation of the  
 CC constrained protein which has a phenotypic effect on the living cells.  
 CC The methods are also useful to identify in vitro binding partners of the  
 CC constrained protein. The compositions of the invention are useful as a  
 CC scaffold for gene therapy and for potential use as a therapeutic in  
 CC physiological fluids. The present sequence is used in the exemplification  
 CC of the present invention  
 XX  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYKDDDDK 8  
 Db 1 DYKDDDDK 8  
 RESULT 85  
 AAE16563

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ID  AA616563 standard; peptide; 8 AA.
XX
AC  AA616563;
XX
DT  09-APR-2002 (first entry)
XX
DE  Epitope tag #7 fused to yeast cell wall protein AGA2.
XX
KW  Yeast cell wall protein; AGA2, T cell receptor; multiple sclerosis;
KW  cancer; sepsis; autoimmune disease; arthritis; diabetes.
XX
OS  Synthetic.
XX
PN  US6331391-B1.
XX
PD  18-DEC-2001.
XX
PF  20-JAN-1998; 98US-00009388.
XX
PR  31-MAY-1996; 96US-0018741P.
XX  30-MAY-1997; 97US-00866398.
XX
PA  (UNII ) UNIV ILLINOIS FOUNO.
XX
PI  Wittrup KD, Kranz DM, Kieke M, Boder ET;
XX  WPI; 1999-430619/36.
XX
PT  Selecting proteins with enhanced phenotypic properties than wild-type
PS  proteins, is useful for highly specific cancer diagnosis and therapy.
XX
XX  Claim 40; Col 60; 59pp; English.
XX
CC  The present invention relates to a method for selecting proteins for
CC  displayability on a yeast cell surface. The method comprises transforming
CC  yeast cells with a vector that expresses a test protein fused to a yeast
CC  cell wall protein (AGA2), contacting the cells with a label that binds to
CC  proteins displayed on the cell wall, and isolating label-bound cells,
CC  where the test protein is from a variegated population generated by
CC  mutagenesis. The invention is also directed to new processes for
CC  engineering T cell receptor for improved binding properties. Improved T
CC  cell receptor molecules are useful in therapies for cancer, sepsis,
CC  autoimmune diseases such as arthritis, diabetes or multiple sclerosis.
CC  The methods are useful to select proteins with altered affinity, altered
CC  specificity or conditional binding. The present sequence is an epitope
CC  tag fused between protein of interest and yeast cell wall protein AGA2
XX
SQ  Sequence 8 AA;

Query Match      100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 DYKDDDDK 8
    |||||
    1 DYKDDDDK 8
Db

RESULT 86
AAW97673
ID  AAW97673 standard; peptide; 8 AA.
XX
AC  AAW97673;
XX
DT  10-MAY-1999 (first entry)
XX
DE  FLAG epitope.
XX
KW  MKK3, human; mitogen activated protein kinase kinase; MAP kinase kinase;
KW  signal transduction; inflammation; psoriasis; AIDS; cancer; apoptosis;
XX  therapy; FLAG; epitope.
XX
OS  Synthetic.

```

```

XX
PN  WO9902547-A1.
XX
PD  21-JAN-1999.
XX
PF  07-JUL-1998; 98WO-US014101.
XX
PR  07-JUL-1997; 97US-00888429.
XX
PA  (UTMA-) UNIV MASSACHUSETTS.
XX
PI  Davis RJ, Whitmarsh A, Tournier C;
XX  WPI; 1999-120771/10.
XX
PT  New isolated mitogen-activated protein kinase kinase isoforms - used to
PS  develop products for treating e.g. inflammatory disorders, oxidative
XX  damage, proliferative disorders or autoimmune disorders.
XX
XX  Example 3; Page 31; 168pp; English.
XX
CC  This peptide comprises a FLAG epitope. DNA coding for the epitope was
CC  inserted between codons 1 and 2 of cDNA clones (see AAX07065 and AAX07067
CC  -69) encoding human mitogen activated protein (MAP) kinase kinase 3 (see
CC  AAW97668) and MKK4 (see AAW97670-72) by insertional overlapping PCR.
CC  Recombinant MKK3 polypeptides were used in in vitro phosphorylation
CC  experiments. MKK3 phosphorylated p38 MAP kinase but not JNK1 or ERK2.
CC  Human MKK3, MKK4, MKK6 and MKK7 (see AAW97664 and AAW97668-72) mediate
CC  the transduction of specific signals from the cell surface to the nucleus
CC  along specific pathways. They are useful for screening reagents which
CC  modulate MKK activity. Such agents can be used to prevent or treat MKK-
CC  mediated disorders, e.g. inflammation, oxidative damage or stress-related
CC  proliferative disorders, e.g. psoriasis, AIDS, malignancies of e.g. the
CC  skin, bone marrow, lung, liver, breast, gastrointestinal system and
CC  genito-urinary tract. Agents which inhibit the activity or expression of
CC  MKK inhibit cell growth or cause apoptosis. MKK7 polynucleotides (see
XX  AAX07059-64) and polypeptides (see AAW97662-67) are claimed

SQ  Sequence 8 AA;

Query Match      100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 DYKDDDDK 8
    |||||
    1 DYKDDDDK 8
Db

RESULT 87
AAW77538
ID  AAW77538 standard; peptide; 8 AA.
XX
AC  AAW77538;
XX
DT  03-MAY-2000 (first entry)
XX
DE  FLAG peptide epitope tag sequence.
XX
KW  Neurotactin; multiple sclerosis; chemokine; inflammation; brain; human;
KW  neuroprotective; antiinflammatory, cyostatic; antibacterial; FLAG.
XX
OS  Synthetic.
XX
PN  US6013257-A.
XX
PD  11-JAN-2000.
XX
PF  16-DEC-1997; 97US-00991426.
XX
PR  07-MAY-1996; 96US-00643798.
XX  05-MAY-1997; 97US-00851160.
XX

```

PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
 XX Pan Y;  
 XX WPI; 2000-146535/13.  
 DR  
 XX Treating multiple sclerosis by administering an antibody that binds the  
 PT proinflammatory chemokine neurotactin.  
 XX  
 XX Example 2; Col 29; 36pp; English.  
 CC The invention provides a method of treatment of multiple sclerosis that  
 CC comprises administering an antibody that binds to human chemokine  
 CC neurotactin. The antibodies inhibit neurotactin, a chemokine that is  
 CC associated with inflammation, particularly in the brain. The antibodies  
 CC are useful for treatment of multiple sclerosis. The present sequence  
 CC represents a FLAG peptide epitope tag  
 CC  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 47; DB 3; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYKDDDDK 8  
 DB 1 DYKDDDDK 8  
 RESULT 89  
 AAB03362 standard; peptide; 8 AA.  
 ID AAB03362;  
 AC AAB03362;  
 XX  
 XX 05-OCT-2000 (first entry)  
 DT  
 XX N-terminal sequence of a soluble human IL-1R fusion protein.  
 DE  
 XX Surgical irrigation solution; anti-inflammatory; anti-pain; anti-spasm;  
 KM anti-restenosis; analgesic; human; IL-1R fusion protein; Interleukin-1.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO200025745-A2.  
 PD 11-MAY-2000.  
 PF 05-NOV-1999; 99WO-US026330.  
 PR 05-NOV-1998; 98US-0107256P.  
 XX  
 PA (OMER-) OMEROS MEDICAL SYSTEMS INC.  
 PI Demopulos GA, Palmer PP, Herz JM;  
 XX  
 XX WPI; 2000-365358/31.  
 DR  
 XX Preemptive inhibition of pain and inflammation in surgical procedures  
 PT comprising application of soluble receptors, e.g. TNF, optionally with  
 PT pain and inflammation inhibitor, directly at the wound site, useful e.g.  
 PT in arthroscopy, dentistry.  
 XX  
 PS Disclosure; Page 70; 122pp; English.  
 CC Various mediators are known to cause pain and inflammation e.g.  
 CC prostaglandins, histamine, bradykinin and serotonin. The present  
 CC invention relates to inhibition of pain and inflammation at a wound  
 CC during surgery by delivering locally and peroperatively to the site a  
 CC solution containing at least one soluble receptor antagonist. The  
 CC solution would inhibit locally the mediators of pain, inflammation, spasm  
 CC and restenosis. The present sequence is the N-terminal sequence of a  
 CC soluble human interleukin-1 receptor (IL-1R) fusion protein. IL-1 is

CC proinflammatory and it is thought that IL-1 effects would be prevented by  
 CC blocking IL-1 binding to IL-1R, e.g. IL-1 induced inflammation and  
 CC cartilage destruction within joints. The IL-1R fusion protein consists of  
 CC the IL-1R binding domain and binds to IL-1 with high affinity. Local  
 CC delivery of an IL-1R soluble receptor, such as the IL-1R fusion protein  
 CC in an irrigation solution during joint surgery may be useful as a  
 CC cartilage protective agent  
 CC  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 47; DB 3; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYKDDDDK 8  
 DB 1 DYKDDDDK 8  
 RESULT 89  
 AAY9877 standard; protein; 8 AA.  
 ID AAY9877  
 AC AAY9877;  
 XX  
 XX 16-OCT-2000 (first entry)  
 DT  
 XX FLAG epitope antibody label.  
 DE  
 XX Human; hepatitis C virus; HCV; envelope glycoprotein E2; antiviral;  
 KM vaccine; immunotherapy; antibody; CBH.  
 XX  
 OS Synthetic.  
 OS  
 PN WO200026418-A1.  
 PD 11-MAY-2000.  
 PF 29-OCT-1999; 99WO-US025711.  
 PR 05-NOV-1998; 98US-00187057.  
 XX  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Fong SKI, Hadlock KG;  
 XX  
 XX WPI; 2000-451625/39.  
 DR  
 XX Detection of hepatitis C virus (HCV) infection comprises using monoclonal  
 PT antibodies binding to conformational epitope of an envelope protein from  
 PT more than one HCV genotype, the monoclonal antibodies are also used as a  
 PT vaccine against HCV.  
 XX  
 PS Disclosure; Page 16; 85pp; English.  
 CC The present sequence is the FLAG epitope which may be fused to antibodies  
 CC as a label for their identification and isolation. The label may be added  
 CC to monoclonal antibodies which bind to conformational epitopes of the  
 CC envelope glycoprotein E2 from multiple HCV genotypes. These antibodies  
 CC may be useful in the prevention and treatment of the majority of HCV  
 CC infections. For example, a subset of antibodies (CBH-2, CBH-5, CBH-7, CBH  
 CC -8C, CBH-8E and CBH-11) have the ability to prevent the binding of HCV E2  
 CC proteins of multiple genotypes to human CD81, a possible coreceptor for  
 CC HCV infection. Thus the antibodies are useful in passive immunotherapy  
 CC strategies for reducing viral load of infected individuals and  
 CC interfering with infection of target cells  
 CC  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 47; DB 3; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
| | | | |  
Db 1 DYKDDDDK 8

## RESULT 90

AAB10961

ID AAB10961 standard; protein; 8 AA.

AC AAB10961;

DT 07-FEB-2001 (first entry)

DE FLAG epitope tag peptide.

XX APP; amyloid precursor protein; human; alpha-secretase; ADAM 10;  
XX disintegrin-metalloprotease; protease; neurotrophic; neuroprotective;  
KW gene therapy; Alzheimer's disease.

OS Synthetic.

DE19910108-A1.

PD 21-SEP-2000.

PE 08-MAR-1999; 99DE-01010108.

PR 08-MAR-1999; 99DE-01010108.

PA (FAHR/) FAHRENHOLZ F.

PI Fahrenholz F, Postina R;

DR WPI; 2000-588391/56.

PT Recombinant cells, for identifying alpha-secretase active agents and  
PT identifying risk factors associated with Alzheimer's disease, comprise  
PT amyloid precursor protein and alpha-secretase.

PS Example 4; Page 8; 24bp; German.

XX This invention describes a novel recombinant cell comprising recombinant  
CC nucleic acids encoding a region of human amyloid precursor protein  
CC containing an alpha-secretase cleavage site and a protease or a  
CC heterologous RNA coding for a substrate protein and a protease. The  
CC invention also describes a recombinant cell, characterized in that it  
CC contains recombinant nucleic acids comprising either: (a) a gene for a  
CC substrate protein (SP), which comprises a sequence region of 18 amino  
CC acids of the human amyloid precursor protein (APP) or a homologous  
CC protein, where the sequence region contains the alpha-secretase cleavage  
CC site at a reference of 6 residues at the N-terminal and 12 residues at  
CC the C-terminal; and (b) a gene for a protease protein (PP), that either  
CC comprises a proteolytically active necessary sequence region or a  
CC sequence region of the disintegrin metalloprotease ADAM 10 from a cow  
CC (Bos taurus), from a human or other mammal or a mutant of this, which  
CC shows the same enzymatic properties, where the genes are under the  
CC control of heterologous promoters; or a heterologous RNA coding for a SP  
CC and a PP. The products of the invention have neurotrophic and  
CC neuroprotective activity and can be used for gene therapy. The protease  
CC proteins of the invention are useful for proteolytic cleavage of  
CC substrate proteins, especially human amyloid precursor protein. Dominant  
CC negative forms of bovine, human or other mammalian disintegrin-  
CC metalloprotease ADAM 10 proteins and their coding sequences are useful  
CC for suppressing the alpha-secretase activity of a cell. Nucleic acid  
CC sequences encoding the proteases are useful for constructing vectors for  
CC gene therapy. The proteins and recombinant cells are useful for  
CC identifying secretases and pharmaceutical agents and to identify risk  
CC factors associated with Alzheimer's disease

SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.1e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DYKDDDDK 8  
| | | | |  
Db 1 DYKDDDDK 8

## RESULT 91

AAV87937

ID AAV87937 standard; peptide; 8 AA.

AC AAV87937;

DT 11-SEP-2000 (first entry)

DE Intracellular C-terminal HDL-receptor domain FLAG epitope #1.

XX Intracellular C-terminal HDL receptor domain; cholesterol; bile acid;  
KW high density lipoprotein; lipid metabolism; peroxisome; gene therapy;  
KW treatment; hyperlipidemia.

OS Synthetic.

WO200023475-A1.

PD 27-APR-2000.

PE 22-OCT-1999; 99WO-SE001902.

PR 22-OCT-1998; 98SE-00003609.

PA (CARL/) CARLSSON B.

PA (CARL/) CARLSSON L.

PA (JOHN/) JOHNSON M.

PI Carlsson B, Carlsson L, Johnson M;

DR WPI; 2000-339657/29.

PT New peptide homologous to the intracellular C-terminal domain of a  
PT mammalian HDL-receptor useful in identifying drug targets and the  
PT treatment of hyperlipidemia.

PS Example 1; Page 8; 23bp; English.

XX This invention describes a novel peptide (P), homologous to the  
CC intracellular C-terminal domain of a mammalian HDL-receptor. The products  
CC of the invention can modulate cholesterol, bile acid and lipid  
CC metabolism. The peptides may alter the activity of the enzymes in the  
CC peroxisome to inhibit cholesterol synthesis and promote cholesterol  
CC elimination. The cDNA encoding the peptide is used in gene therapy and is  
CC also used for the production of the peptide. The peptide can be used in  
CC the treatment of hyperlipidemia and for the modulation of cholesterol,  
CC bile acid and/or lipid metabolism of a patient. The peptide can also be  
CC used for the identification of drug targets for treatment of  
CC hyperlipidemia. The drug targets thus identified are targets for  
CC modulation of the metabolism of cholesterol, bile acid and/or lipids. In  
CC addition the peptide may also be used for the production of a medicinal  
CC product for treatment of hyperlipidemia. This sequence represents a FLAG  
CC epitope used in the method of the invention

SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
| | | | |  
Db 1 DYKDDDDK 8

## RESULT 92

AA10094  
ID AAB10094 standard; peptide; 8 AA.  
XX  
AC AAB10094;  
XX  
DT 10-NOV-2000 (first entry)  
XX  
DE Combinatorial chemical library peptide 1.  
XX  
KM Combinatorial library; diagnosis; disease detection; cancer; infection;  
KM autoimmune disease; drug development; diagnostic marker.  
XX  
OS Synthetic.  
XX  
PN WO200035940-A2.  
XX  
PD 22-JUN-2000.  
XX  
PF 14-DEC-1999; 99WO-DE003982.  
XX  
PR 14-DEC-1998; 98DE-01057529.  
PR 30-JUL-1999; 99DE-01035553.  
XX  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
PA (EUWO-) EURO LAB MOLEKULARBIOLOGIE.  
PI Poustka A, Breitling F, Gross K, Duebel S, Saffrich R;  
PI MPI; 2000-442358/38.  
XX  
PT Applying materials to a support, useful for combinatorial synthesis of  
PT peptides, e.g. for diagnosis, by incorporating materials in meltable  
PT particles and delivery through a printer.  
XX  
PS Disclosure; Page 36; 77pp; German.  
XX  
CC This invention describes a novel method for applying substances (I),  
CC especially monomers for combinatorial synthesis of molecule libraries, to  
CC a carrier by embedding (I) in a matrix, an applying the matrix to the  
CC carrier either as a solid or a gel. (I) is first embedded in a matrix  
CC comprising at least 1 first solvent (S1) that is solid at below 90  
CC (preferably 50) plusoc so as to form transport units (TU) that can be  
CC moved individually. TU are applied to the carrier as solid, at below 90  
CC plusoc or are applied dissolved in second solvent (S2), which at the same  
CC temperature is a liquid, so that, after evaporating at least some S2, a  
CC solid or gel is formed on the carrier. (I) is then rendered mobile by  
CC altering the physical conditions, brought into contact with the carrier  
CC surface by a physical process and coupled covalently to molecules (II) on  
CC the surface (or it undergoes, or catalyzes, a reaction with (II). Coupled  
CC (I) may be (or may generate) many different substances and application of  
CC (I) can be repeated sequentially, with intermediate rinsing off of any  
CC uncoupled (I). The method is used to produce combinatorial chemical  
CC libraries (e.g. of peptides or oligonucleotides) for use in scientific or  
CC medical investigations, e.g. diagnostically for detecting markers of a  
CC wide range of diseases (cancer, autoimmune disease or infections, also  
CC diseases of unknown or uncertain etiology) in blood samples or for  
CC identifying lead compounds (specific binding agents) for drug  
CC development. Encapsulation of (I) significantly reduces its diffusion  
CC away from its target site on the carrier, resulting in simpler and more  
CC compact assembly of a library relatively free of artefacts. The library  
CC may have a very high density, increasing the chances of detecting  
CC diagnostic markers or potential therapeutic agents and allows  
CC simultaneous screening for many different diseases. This sequence  
CC represents a peptide used to illustrate the method of the invention  
XX  
SQ Sequence 8 AA;  
Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
|||||||

Db 1 DYKDDDDK 8  
RESULT 93  
AAV51938  
ID AAV51938 standard; protein; 8 AA.  
XX  
AC AAV51938;  
XX  
DT 23-JUN-2000 (first entry)  
XX  
DE FLAP epitope.  
XX  
KM PRO201; human; NSP; SH2-containing protein; cytosolic; modulator;  
KM Src Homology-2 containing protein; Nsp1; PRO308; Nsp2; PRO309; Nsp3;  
KM cellular response; tumorigenesis; integrin stimulation; signalling.  
XX  
XX Homo sapiens.  
OS  
PN US6051403-A.  
PN  
PD 18-APR-2000.  
XX  
PF 04-AUG-1999; 99US-00369028.  
XX  
PR 23-APR-1998; 98US-00065275.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Lu Y, Stewart TA;  
XX  
DR MPI; 2000-328246/78.  
XX  
PT New isolated nucleic acid molecules encoding novel Src Homology-2  
PT containing proteins capable of modulating the activity of cellular  
PT response to external signaling.  
XX  
PS Example 3; Col 71-72; 63pp; English.  
XX  
CC This invention describes the novel isolated Src Homology-2 (SH2)  
CC containing proteins (Nsp) (I) PRO201 (Nsp1), PRO308 (Nsp2) or PRO309  
CC (Nsp3), respectively which have cytosolic activity. (I) plays an  
CC important role in modulating the cellular response to external stimuli.  
CC (I) binds and affects e.g. block or modulate an activity such as  
CC regulation of tumorigenesis, response to stimulation by integrin  
CC receptors, epidermal growth factor, insulin growth factor and through  
CC other tyrosine receptor ligands, of cellular response to external  
CC signalling. (I) is useful for producing antibodies, agonists and  
CC antagonists to modulate the activity of cellular response to external  
CC signalling. The encoding NSP nucleotides are useful as hybridization  
CC probes in chromosome and gene mapping. In cDNA library and in the  
CC generation of anti-sense RNA and DNA. They are also useful for preparing  
CC the NSP proteins, for producing transgenic animals and for gene therapy.  
CC NI are also useful for treating and diagnosing cells associated with cell  
CC proliferative disorders. This sequence represents the FLAP epitope which  
CC is used in the method of the invention  
XX  
SQ Sequence 8 AA;  
Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
|||||||

Db 1 DYKDDDDK 8

RESULT 94  
AAB22877  
ID AAB22877 standard; peptide; 8 AA.  
XX  
AC AAB22877;  
XX

XX 10-JAN-2001 (first entry)  
 DT FLAG epitope, SEQ ID NO:36.  
 XX  
 XX Bioreactor protein; fusion protein; recognition site;  
 KW cellular targeting sequence; cellular localisation; fluorescent protein;  
 KW protease activity detection; toxin detection; cellular stress detection;  
 KW drug discovery; cell based screening; epitope.  
 XX  
 OS Synthetic.  
 XX  
 XX WO200050872-A2.  
 XX  
 XX 31-AUG-2000.  
 XX  
 XX 25-FEB-2000; 2000WO-US004794.  
 XX  
 XX 26-FEB-1999; 99US-0122152P.  
 PR 08-MAR-1999; 99US-0123399P.  
 PR 12-JUL-1999; 99US-0035217L.  
 XX  
 XX (CELL-) CELLCOMICS INC.  
 PA  
 XX Giuliano KA, Kapur R;  
 PI  
 XX WPI, 2000-594086/56.  
 DR N-PSDB; AAA93368.  
 XX  
 XX Automated cell-based characterization of toxin by contacting cells  
 PT containing luminescent reporter molecules with test substance and  
 PT analyzing optically.  
 XX  
 XX Example 11; Fig 29A; 336pp; English.  
 PS  
 XX  
 XX The invention relates to systems, methods and reagents for cell-based  
 CC screening or detection of compounds which affect particular biological  
 CC functions. The methods of the invention utilise fluorescent bioreactor  
 CC molecules which, when acted on by a compound of interest, cause an  
 CC alteration in the cellular distribution of at least the fluorescent  
 CC moiety. In one embodiment, the biosensors comprise heat shock proteins  
 CC (HSPs) fused to a fluorescent protein (e.g., jellyfish green fluorescent  
 CC protein (GFP), or derivatives thereof). Such biosensors are located in  
 CC the cytoplasm, but on stress activation translocate to the nucleus. In  
 CC another embodiment bioreactor proteins can be used to detect protease  
 CC activity. Such protease bioreactor fusion proteins comprise one or more  
 CC fluorescent proteins; a recognition signal which is cleaved by the  
 CC protease; and at least one cellular localisation signal. The latter two  
 CC components may be components of a single protein which is acted upon by  
 CC the protease, or may be from heterologous sources. Due to the  
 CC localisation signal, the bioreactor protein is localised to a particular  
 CC region of the cell. Once acted on by the protease of interest, the  
 CC fluorescent protein is cleaved from the localisation sequence, and is  
 CC free to migrate to other locations within the cell. The presence of a  
 CC second localisation signal attached to the fluorescent protein enables  
 CC the fluorescent protein to be directed to a different cellular  
 CC compartment after cleavage of the protease recognition sequence. The  
 CC change in distribution of the fluorescent protein can be detected using  
 CC imaging methods with a high degree of spatial resolution. The methods and  
 CC biosensors of the invention can be used to investigate a wide range of  
 CC cellular activities and to screen compounds which modulate these  
 CC activities. Biosensors containing a recognition site for caspase, for  
 CC example, may be used for the screening of compounds which modulate  
 CC apoptosis, while biosensors containing other protease recognition sites  
 CC may be used for the detection of proteolytic toxins (such as anthrax  
 CC lethal factor). The method provides improved target validation and  
 CC candidate compound optimisation by combining many cell screening formats  
 CC with fluorescence-based molecular reagents and computer-based feature  
 CC extraction, data analysis and automation, resulting in increased quantity  
 CC and speed of data collection and faster evaluation of drug candidates.  
 CC Sequences AAB2877-B2280 represent epitope sequences that can be used in  
 CC biosensor fusion proteins of the invention  
 XX

SQL Sequence 8 AA;  
 Query Match 100.0%; Score 47; DB 3; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0;  
 QY 1 DYKDDDDK 8  
 Db 1 DYKDDDDK 8  
 RESULT 95  
 AAB26126  
 ID AAB26126 standard; protein; 8 AA.  
 XX  
 XX AAB26126;  
 XX  
 XX 30-JAN-2001 (first entry)  
 XX  
 XX Human TGF-beta superfamily protein PCIGF recognition site.  
 DE  
 XX Human; TGF-beta superfamily; prostate cancer-induced growth factor;  
 KW PCIGF; prostate disease; prostate cancer; benign prostatic hyperplasia;  
 KW prostatitis; prostatic intraepithelial neoplasia; affinity purification.  
 XX  
 OS Synthetic.  
 XX  
 XX WO200056352-A2.  
 XX  
 XX 28-SEP-2000.  
 XX  
 XX 24-MAR-2000; 2000WO-US007945.  
 XX  
 XX 25-MAR-1999; 99US-00276600.  
 XX  
 XX (ABBO ) ABBOTT LAB.  
 PA  
 XX Billing-Medel PA, Cohen M, Colpitts TL, Gordon J, Granados EN;  
 PI Russell JC, Stroupe SD;  
 DR WPI; 2000-628218/60.  
 XX  
 XX Novel prostate cancer induced growth factor derived polynucleotide useful  
 PT for detecting, diagnosing, prognosing, preventing or treating conditions  
 PT of the prostate, especially prostate cancer.  
 XX  
 XX Example 11a; Page 78; 117pp; English.  
 PS  
 XX The present sequence comprises the translated sequence of an affinity  
 CC purification recognition system site. It was inserted into a vector for  
 CC the human prostate cancer-induced growth factor (PCIGF). The protein is a  
 CC member of the TGF-beta superfamily. The 3' part of its gene has been  
 CC shown to be upregulated in prostate cancer, and thus can be used in the  
 CC diagnosis of the disease. It is also useful for the identification of  
 CC antagonists to the PCIGF protein which can be used to treat cancer. In  
 CC addition, benign prostatic hyperplasia, prostatitis and prostatic  
 CC intraepithelial neoplasia can be detected using the gene and protein  
 XX  
 XX Sequence 8 AA;  
 SQL  
 Query Match 100.0%; Score 47; DB 3; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0;  
 QY 1 DYKDDDDK 8  
 Db 1 DYKDDDDK 8  
 RESULT 96  
 AAB28432  
 ID AAB28432 standard; peptide; 8 AA.  
 XX

AC AAB2432;  
 XX  
 DT 29-JAN-2001 (first entry)  
 XX  
 DE FLAG epitope.  
 XX  
 KW FLAG epitope; gene therapy; gene-trapping retrovirus; transgenic animal.  
 XX  
 OS Unidentified.  
 XX  
 PN W0200056874-A1.  
 XX  
 PD 28-SEP-2000.  
 XX  
 PF 24-MAR-2000; 2000WO-US007841.  
 XX  
 PR 25-MAR-1999; 99US-0126123P.  
 XX  
 PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
 XX  
 PI Hopkins N, Chen W, Burgess S, Amsterdam A;  
 XX  
 DR WPI; 2000-628260/60.  
 XX  
 PT Recombinant retrovirus for gene trapping, gene mutation and for  
 PT transgenic animal production, comprises a branch point sequence,  
 PT polyuridine tract, splice acceptor, splice donor and long-terminal  
 PT repeats.  
 XX  
 PS Disclosure; Page 13; 38pp; English.  
 XX  
 CC The present sequence is the FLAG epitope, which may be incorporated into  
 CC an artificial mini-exon used in a novel gene-trapping retrovirus. The  
 CC retrovirus comprises a branch point sequence, a polyuridine tract, a  
 CC splice acceptor, a splice donor and long-terminal repeats (LTRs). It is  
 CC useful for introducing a mutation into a gene in a cell, for determining  
 CC the expression pattern of a gene in a non-human animal, and for gene  
 CC therapy. It is also useful for producing transgenic animals such as mice,  
 CC zebrafish, pufferfish, medaka, frogs, flies, goats, sheep, cows, pigs and  
 CC chickens. High-titre virus producer cell lines have been developed which  
 CC permit efficient production of retroviral vectors for the construction of  
 CC transgenic animals and for human gene therapy  
 CC  
 SQ Sequence 8 AA;  
 \* Query Match 100.0%; Score 47; DB 3; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYKDDDDK 8  
 |||||  
 DB 1 DYKDDDDK 8  
 |||||  
 RESULT 97  
 AAY95914  
 ID AAY95914 standard; peptide; 8 AA.  
 XX  
 AC AAY95914;  
 XX  
 DT 20-NOV-2000 (first entry)  
 XX  
 DE FLAG peptide.  
 XX  
 KW FLAG; Goodpasture antigen binding protein; GBP, autoimmune disease;  
 KW apoptosis; cancer; tumour; diagnosis; therapy.  
 XX  
 OS Synthetic.  
 XX  
 PN W0200050607-A2.  
 XX  
 PD 31-AUG-2000.  
 XX

PF 24-FEB-2000; 2000WO-IB000324.  
 XX  
 PR 24-FEB-1999; 99US-0121483P.  
 XX  
 PA (SAUS/). SAUS J.  
 XX  
 PI Saus J;  
 XX  
 DR WPI; 2000-572094/53.  
 XX  
 PT Novel Goodpasture antigen binding proteins useful for diagnosing and  
 PT treating autoimmune disorders, tumor, and preventing cell apoptosis.  
 PT  
 XX  
 PS Example 1; Page 22; 158pp; English.  
 XX  
 CC The present sequence is that of FLAG peptide. FLAG was expressed at the N  
 CC -terminus of recombinant human Goodpasture antigen binding protein (GBP)  
 CC constructs (see AAY95907-11) of the invention to facilitate purification  
 CC from host cells. GBP (see AAY95900) is a novel serine/threonine kinase  
 CC that specifically binds to and phosphorylates the N-terminus of  
 CC Goodpasture antigen. The invention provides nucleic acids (see AAY50341-  
 CC 53) encoding GBP, recombinant vectors, host cells, encoded polypeptides  
 CC (see AAY95900-11) and antibodies. It also provides methods for detecting  
 CC the presence of an autoimmune condition or apoptosis by detecting an  
 CC increase in GBP expression, and methods for treating an autoimmune  
 CC disorder, apoptosis or a tumour by modifying GBP expression or activity  
 CC  
 SQ Sequence 8 AA;  
 \* Query Match 100.0%; Score 47; DB 3; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYKDDDDK 8  
 |||||  
 DB 1 DYKDDDDK 8  
 |||||  
 RESULT 98  
 AAY53260  
 ID AAY53260 standard; peptide; 8 AA.  
 XX  
 AC AAY53260;  
 XX  
 DT 17-JUL-2000 (first entry)  
 XX  
 DE Mouse neurotactin FLAG epitope tag SEQ ID NO:14.  
 XX  
 KW Neurotactin; identification; characterisation; chemokine; inflammation;  
 KW anti-inflammatory; anti-arteriosclerotic; chemotaxis inhibitor; brain;  
 KW viral encephalitis; multiple sclerosis; meningitis; head trauma; stroke;  
 KW neuro-degenerative disease; HIV encephalopathy; primary brain tumour;  
 KW lupus associated cerebritis; inflammatory disease; atherosclerosis;  
 KW respiratory infection; diagnosis; gene therapy.  
 XX  
 OS Mus musculus.  
 XX  
 PN US6043086-A.  
 XX  
 PD 28-MAR-2000.  
 XX  
 PF 28-AUG-1998; 98US-00143470.  
 XX  
 PR 07-MAY-1996; 96US-00643798.  
 PR 05-MAY-1997; 97US-00851160.  
 PR 16-DEC-1997; 97US-00991426.  
 XX  
 PA (MILL-) MILLENIUM BIOTHERAPEUTICS INC.  
 XX  
 PI Pan Y;  
 XX  
 DR WPI; 2000-270344/23.  
 XX

PT stimulating lymphocyte development and proliferation.

CC Parkinson's diseases, amyotrophic lateral sclerosis, ischaemia etc.) and



CC malignant cell growth. MLK3 which is also known as PTK1 was cloned by  
 CC using degenerate primers derived from the highly conserved V1b and IX  
 CC subdomains of PTK polypeptides. To obtain MLK3 the cDNA was cloned into a  
 CC baculoviral expression vector pFB-FLAG. pFB-FLAG is derived from pFB and  
 CC has the coding sequence for the FLAG epitope with a start codon added to  
 CC the polylinker in the BamHI site

XX Sequence 8 AA;

Query Match 100.0%; Score 47; DB 3; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.1e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8

Db 1 DYKDDDDK 8

Search completed: June 29, 2006, 11:35:36  
 Job time : 215 secs

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OM protein - protein search, using sw model

Run on: June 29, 2006, 11:35:56 ; Search time 39 Seconds  
(without alignments)  
19.737 Million cell updates/sec

Title: US-10-671-054-2

Perfect score: 47

Sequence: 1 DYKDDDK 8

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 500 summaries

Database :

PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	47	T10471	potassium channel-
2	41	87.2	423	S59425	SP28 protein - ye
3	38	80.9	306	S32834	methyloxygen-red
4	38	80.9	565	AC0184	malate dehydrogena
5	38	80.9	1085	S55352	IFM1 protein - yea
6	38	80.9	1277	S54451	hypothetical prote
7	38	80.9	2067	A42854	probable spindle p
8	37	78.7	351	T10503	fruit bromelain (E
9	37	78.7	513	B96524	hypothetical prote
10	37	78.7	721	B96974	superfamily I DNA
11	37	78.7	791	T20815	hypothetical prote
12	37	78.7	838	T05410	hypothetical prote
13	36	76.6	195	B70192	hypothetical prote
14	36	76.6	215	T31963	hypothetical prote
15	36	76.6	289	S39814	DNA polymerase hom
16	36	76.6	312	S39823	DNA polymerase hom
17	36	76.6	485	T49237	hypothetical prote
18	36	76.6	748	H84913	probable ATP-depen
19	36	76.6	796	S56231	hypothetical prote
20	36	76.6	917	S07183	hypothetical prote
21	36	76.6	987	A88746	protein C18f3.2 (I
22	36	76.6	1076	S50536	hypothetical prote
23	36	76.6	1287	T30988	hypothetical prote
24	36	76.6	2295	B71621	probable membrane
25	36	76.6	2457	T18492	hypothetical prote
26	35	74.5	78	AF2345	hypothetical prote
27	35	74.5	151	A40592	heat shock protein
28	35	74.5	151	G97355	molecular chaperon
29	35	74.5	287	T32029	hypothetical prote

30	35	74.5	288	A86384	unknown protein (i
31	35	74.5	306	D96708	unknown protein, 9
32	35	74.5	338	PC4365	calcium-binding pr
33	35	74.5	374	T09106	gibberellin 20-oxi
34	35	74.5	410	T25165	hypothetical prote
35	35	74.5	430	S67161	hypothetical prote
36	35	74.5	451	S58653	hypothetical prote
37	35	74.5	472	S41720	intermediate filam
38	35	74.5	635	D84920	hypothetical prote
39	35	74.5	679	G71615	phospholipase A2-1
40	35	74.5	1010	T34314	hypothetical prote
41	35	74.5	1345	S46817	hypothetical prote
42	35	74.5	2452	RNAQ2L	DNA-directed RNA p
43	35	74.5	2573	D71614	hypothetical prote
44	34	72.3	140	T32477	hypothetical prote
45	34	72.3	165	A36237	melanin-concentrat
46	34	72.3	177	R8BYG1	regulatory protein
47	34	72.3	197	T15725	hypothetical prote
48	34	72.3	259	S46286	RNA-binding protei
49	34	72.3	300	T52379	zinc finger protei
50	34	72.3	337	T24387	probable cysteine
51	34	72.3	362	T48564	probable serine ri
52	34	72.3	381	S45766	hypothetical prote
53	34	72.3	386	T05781	hypothetical prote
54	34	72.3	396	T26987	hypothetical prote
55	34	72.3	430	T23899	hypothetical prote
56	34	72.3	467	A85363	probable calmoduli
57	34	72.3	484	S66713	hypothetical prote
58	34	72.3	502	S36494	E2 protein - human
59	34	72.3	609	T40660	hypothetical C2H2-
60	34	72.3	614	T10862	phaseolin G-box bi
61	34	72.3	734	T13674	hypothetical prote
62	34	72.3	743	T13673	hypothetical prote
63	34	72.3	860	A84833	hypothetical prote
64	34	72.3	936	E96508	hypothetical prote
65	34	72.3	984	A41996	NF-kappa-B p50 sub
66	34	72.3	1099	T18257	phospholipase C -
67	34	72.3	1157	C96761	hypothetical prote
68	34	72.3	1350	AF2005	RNA polymerase bet
69	34	72.3	1953	S63244	BNI protein - yea
70	34	72.3	4550	T18440	hypothetical prote
71	33	70.2	125	S76216	hypothetical prote
72	33	70.2	145	JX0313	E4 protei - human
73	33	70.2	147	B46315	hypothetical prote
74	33	70.2	151	E69077	hypothetical prote
75	33	70.2	175	S59766	translational elonga
76	33	70.2	188	A61442	conserved hypotet
77	33	70.2	190	T43013	FUN34 protein - ye
78	33	70.2	205	S36720	translation elonga
79	33	70.2	225	S25432	translational prote
80	33	70.2	225	S62593	hypothetical prote
81	33	70.2	235	G90525	hypothetical prote
82	33	70.2	258	H84905	homeodomain trans
83	33	70.2	262	A33470	fibroin light chai
84	33	70.2	267	S47137	homeotic protein A
85	33	70.2	270	B86466	protein P289.7 (I
86	33	70.2	280	T00737	myb-related protei
87	33	70.2	280	T51667	myb-related trans
88	33	70.2	299	S49469	glucose-1-phosphat
89	33	70.2	322	G95244	hypothetical prote
90	33	70.2	333	T20033	hypothetical prote
91	33	70.2	393	S16321	light-induced prot
92	33	70.2	436	AH1387	cell wall binding
93	33	70.2	450	T40337	probable saccharop
94	33	70.2	504	DB1224	catalase (EC 1.11.
95	33	70.2	517	S26606	myb-related protei
96	33	70.2	524	A48341	nucleocapsid prote
97	33	70.2	524	VANZT1	arganyl-tRNA synth
98	33	70.2	553	A89830	hypothetical prote
99	33	70.2	563	C71529	hypothetical prote
100	33	70.2	650	T06648	DNA topoisomerase
101	33	70.2	651	G64068	hypothetical prote
102	33	70.2	799	S65192	hypothetical prote

103	33	70.2	810	2	S67696	probable membrane
104	33	70.2	829	2	T32744	hypothetical prote
105	33	70.2	830	2	T18860	hypothetical prote
106	33	70.2	836	1	S34399	dynamn 3 - fruit
107	33	70.2	836	2	S17974	dynamn-like prote
108	33	70.2	836	2	S15413	dynamn-like prote
109	33	70.2	848	2	S15498	testicular dynam
110	33	70.2	849	2	A35791	pre-mRNA processin
111	33	70.2	851	2	B40671	dynamn, internal
112	33	70.2	851	2	S11508	d100 protein - rat
113	33	70.2	854	2	S33558	unc-33 protein - C
114	33	70.2	864	2	A40671	dynamn, internal
115	33	70.2	863	2	S16130	dynamn 4 - fruit
116	33	70.2	883	2	S17975	dynamn-like prote
117	33	70.2	902	2	S33918	dynamn-like prote
118	33	70.2	997	2	T43523	cut17 protein - fi
119	33	70.2	1063	2	S18211	hypothetical prote
120	33	70.2	1111	2	T01239	hypothetical prote
121	33	70.2	1193	2	G71605	hypothetical prote
122	33	70.2	1230	2	T42735	TBP-interacting pr
123	33	70.2	1325	2	T25753	hypothetical prote
124	33	70.2	1329	2	T33136	hypothetical prote
125	33	70.2	1802	2	G71616	hypothetical prote
126	33	70.2	1880	2	T18531	tractin - mediana
127	33	70.2	2206	2	JC5280	voltage-dependent
128	33	70.2	2437	2	T18482	hypothetical prote
129	33	70.2	2829	2	A42771	reticulocyte-bindi
130	32	68.1	49	2	B26815	peptide pyr.-amide
131	32	68.1	153	2	T09405	conserved hypochet
132	32	68.1	200	2	F85020	hypothetical prote
133	32	68.1	213	2	D71669	adenylate kinase (
134	32	68.1	220	2	T02014	hypothetical prote
135	32	68.1	221	2	A84638	hypothetical prote
136	32	68.1	224	2	T45992	hypothetical prote
137	32	68.1	222	2	T22698	hypothetical prote
138	32	68.1	240	2	S11293	5A85-1.2 protein -
139	32	68.1	250	2	T16728	hypothetical prote
140	32	68.1	289	2	C96778	hypothetical prote
141	32	68.1	298	2	T37251	homeobox protein c
142	32	68.1	303	2	A69542	conserved hypochet
143	32	68.1	306	2	T26126	hypothetical prote
144	32	68.1	321	2	A86857	ribose-phosphate d
145	32	68.1	324	2	T10518	fruit bromelain (B
146	32	68.1	332	2	A81675	conserved hypochet
147	32	68.1	335	2	E71140	hypothetical prote
148	32	68.1	340	2	T10516	fruit bromelain (B
149	32	68.1	344	2	T48827	hypothetical prote
150	32	68.1	345	2	T07839	ananain (EC 3.4.22
151	32	68.1	349	2	T29256	hypothetical prote
152	32	68.1	352	2	T10501	fruit bromelain (B
153	32	68.1	352	2	AD0927	major capsid prote
154	32	68.1	356	2	T07840	ananain (EC 3.4.22
155	32	68.1	356	2	T10514	probable stem brom
156	32	68.1	357	2	T07851	ananain (EC 3.4.22
157	32	68.1	363	2	F87752	protein C43B11.1 l
158	32	68.1	381	2	D89922	conserved hypochet
159	32	68.1	391	1	VFXRIB	major inner capsid
160	32	68.1	398	2	S06324	dnab protein homol
161	32	68.1	401	2	A34856	49K photoreceptor
162	32	68.1	401	2	S11566	arrestin homolog -
163	32	68.1	401	2	B55081	arrestin 2 - blueb
164	32	68.1	401	2	T48495	hypothetical prote
165	32	68.1	421	2	B82023	probable periplasm
166	32	68.1	421	2	F81244	conserved hypochet
167	32	68.1	429	2	T23152	hypothetical prote
168	32	68.1	432	2	T00949	hypothetical prote
169	32	68.1	440	2	T51278	hypothetical prote
170	32	68.1	451	2	A37386	dnab protein homol
171	32	68.1	451	2	S01921	dnab protein homol
172	32	68.1	458	2	S53936	hypothetical prote
173	32	68.1	461	2	T01825	hypothetical prote
174	32	68.1	469	2	C82495	glycerol-3-phospha
175	32	68.1	474	2	A81732	glycogen synthase
176	32	68.1	176	2	T51121	probable DNA photo
177	32	68.1	177	2	H86148	hypothetical prote
178	32	68.1	178	2	JC5678	minor core protein
179	32	68.1	179	2	VHMZSV	nucleocapsid prote
180	32	68.1	180	2	T41631	hypothetical prote
181	32	68.1	181	2	S19476	hypothetical prote
182	32	68.1	182	2	T00979	hypothetical prote
183	32	68.1	183	2	T06467	phosphoinositide-s
184	32	68.1	184	2	S74239	secretogranin II p
185	32	68.1	185	2	T37719	chymotrypsin synth
186	32	68.1	186	2	T32454	hypothetical prote
187	32	68.1	187	2	E96612	probable membrane
188	32	68.1	188	2	S61693	probable transcrip
189	32	68.1	189	2	S46308	initiator-binding
190	32	68.1	190	2	S46309	initiator-binding
191	32	68.1	191	2	T18426	hypothetical prote
192	32	68.1	192	2	S40904	FUN2 protein - yea
193	32	68.1	193	2	S55119	hypothetical prote
194	32	68.1	194	2	T19065	probable protein k
195	32	68.1	195	2	T27276	hypothetical prote
196	32	68.1	196	2	T02702	hypothetical prote
197	32	68.1	197	2	D87965	protein Y63D3A.6b
198	32	68.1	198	2	A56244	DNA repair/recombi
199	32	68.1	199	2	S75209	dnak protein - Syn
200	32	68.1	200	2	G86273	hypothetical prote
201	32	68.1	201	2	T05576	hypothetical prote
202	32	68.1	202	2	C84546	probable transport
203	32	68.1	203	2	ZPECPB	penicillin-binding
204	32	68.1	204	2	A85499	peptidoglycan synt
205	32	68.1	205	2	A93648	peptidoglycan synt
206	32	68.1	206	2	H70470	hypothetical prote
207	32	68.1	207	2	F75289	alanyl-L-cRNA synthe
208	32	68.1	208	2	B43817	transforming prote
209	32	68.1	209	2	F71426	hypothetical prote
210	32	68.1	210	2	S03313	hypothetical prote
211	32	68.1	211	2	A43817	transforming prote
212	32	68.1	212	2	E85276	hypothetical prote
213	32	68.1	213	2	AH1906	hypothetical prote
214	32	68.1	214	2	T51904	hypothetical prote
215	32	68.1	215	2	S56039	RIC1 protein - Yea
216	32	68.1	216	2	S37932	hypothetical prote
217	32	68.1	217	2	S49956	probable membrane
218	32	68.1	218	2	A39577	protein-tyrosine k
219	32	68.1	219	2	T23467	hypothetical prote
220	32	68.1	220	2	T44236	hypothetical prote
221	32	68.1	221	2	T44051	hypothetical prote
222	32	68.1	222	2	T22490	hypothetical prote
223	32	68.1	223	2	T14022	reverse transcript
224	32	68.1	224	2	T30211	autolysin B - Stap
225	32	68.1	225	2	T18416	hypothetical prote
226	32	68.1	226	2	T52359	hypothetical prote
227	32	68.1	227	2	A57570	Bloom's syndrome x
228	32	68.1	228	2	T28048	hypothetical prote
229	32	68.1	229	2	T33100	hypothetical prote
230	32	68.1	230	2	T13823	frizzled gene prot
231	32	68.1	231	2	RGBYC5	cell division cont
232	32	68.1	232	2	S15047	SNF2 protein - Yea
233	32	68.1	233	2	A56011	transcription fact
234	32	68.1	234	2	T29999	hypothetical prote
235	32	68.1	235	2	VFIHBI	FI protein - avian
236	32	68.1	236	2	F82885	hypothetical prote
237	31	66.0	237	37	S21665	S-layer protein -
238	31	66.0	238	131	T1BPUL	minor tail protein
239	31	66.0	239	131	G90833	minor tail protein
240	31	66.0	240	2	A85691	probable tail comp
241	31	66.0	241	2	A81060	conserved hypochet
242	31	66.0	242	2	S34360	hypothetical prote
243	31	66.0	243	2	T03087	conserved hypochet
244	31	66.0	244	2	T28547	hypothetical prote
245	31	66.0	245	2	C72164	A6R protein - vari
246	31	66.0	246	2	F36848	ASR protein - vari
247	31	66.0	247	2	D64141	hypothetical prote
248	31	66.0	248	2	PH0261	hypothetical 17.8K

249	31	66.0	177	2	T32856	hypothetical prote
250	31	66.0	178	2	S26481	calcium-binding pr
251	31	66.0	183	1	RSBY32	ribosomal protein
252	31	66.0	185	1	WVZ5W	Swf8a protein - sw
253	31	66.0	201	2	A34146	hypothetical prote
254	31	66.0	205	2	UC4964	beta-B2-crystallin
255	31	66.0	205	2	S05015	beta-B2-crystallin
256	31	66.0	205	2	A10967	conserved hypotet
257	31	66.0	207	2	A39757	beta-crystallin B2
258	31	66.0	210	2	T40719	hypothetical prote
259	31	66.0	210	2	T28771	hypothetical prote
260	31	66.0	211	2	T25911	hypothetical prote
261	31	66.0	218	2	T30415	host range factor
262	31	66.0	219	2	T19897	hypothetical prote
263	31	66.0	224	2	JH0456	tumor rejection an
264	31	66.0	227	2	E97719	ribonuclease III (
265	31	66.0	237	2	D89990	hypothetical prote
266	31	66.0	243	2	H70227	antigen, P35 homol
267	31	66.0	253	2	B29653	aspartic acid-rich
268	31	66.0	253	2	A75252	conserved hypotet
269	31	66.0	264	2	T10155	hypothetical prote
270	31	66.0	269	2	B84849	hypothetical prote
271	31	66.0	283	2	B11068	hypothetical prote
272	31	66.0	283	2	C85912	hypothetical prote
273	31	66.0	294	1	A37818	osteopontin precu
274	31	66.0	300	2	E96585	osteopontin precu
275	31	66.0	301	1	S12361	heat shock transcr
276	31	66.0	301	2	JC5811	osteopontin - rat
277	31	66.0	309	2	D57126	tRNA delta(2) - Isop
278	31	66.0	317	1	A25917	osteopontin precu
279	31	66.0	319	2	AF0406	transcription regu
280	31	66.0	319	2	A47499	thiamine diphospho
281	31	66.0	334	2	A29561	prostatic spermine
282	31	66.0	336	2	T38175	hypothetical prote
283	31	66.0	345	2	T38894	hypothetical colle
284	31	66.0	350	2	A40459	nuclear phosphopro
285	31	66.0	366	2	B84265	hypothetical prote
286	31	66.0	374	2	D81937	probable ribosomal
287	31	66.0	374	2	A81168	ribosomal large ch
288	31	66.0	374	2	A37282	52K active chromac
289	31	66.0	379	2	C84577	probable nucleosom
290	31	66.0	387	2	C86133	hypothetical prote
291	31	66.0	387	2	A98292	hypothetical prote
292	31	66.0	389	2	T03691	calreticulin - com
293	31	66.0	390	2	T51197	hypothetical prote
294	31	66.0	395	2	T25651	hypothetical prote
295	31	66.0	400	2	T45919	hypothetical prote
296	31	66.0	401	2	D87368	imidazolonepropion
297	31	66.0	406	2	S59296	probable finger pr
298	31	66.0	407	2	T26127	hypothetical prote
299	31	66.0	409	2	S70119	hypothetical prote
300	31	66.0	412	2	T40155	mannose-6-phosphat
301	31	66.0	416	1	S06763	calreticulin precu
302	31	66.0	416	2	T16968	calreticulin call
303	31	66.0	421	2	E96522	DnaJ-like protein
304	31	66.0	423	2	T09338	histidine-tRNA lig
305	31	66.0	424	2	A10821	biphenyl dioxygena
306	31	66.0	426	2	T31278	3-phosphoshikimate
307	31	66.0	432	2	H89924	probable tyrosine
308	31	66.0	434	2	S55155	hypothetical prote
309	31	66.0	440	2	S60423	hypothetical prote
310	31	66.0	449	2	C96992	metaxin homolog -
311	31	66.0	450	2	T40446	RNA helicase RH5
312	31	66.0	451	2	T51143	hypothetical prote
313	31	66.0	455	2	T38517	hypothetical prote
314	31	66.0	460	2	B82549	hypothetical prote
315	31	66.0	466	2	T46054	26S proteasome reg
316	31	66.0	467	2	S34354	serine/threonine p
317	31	66.0	467	2	H84441	lipoprotein (impor
318	31	66.0	467	2	S35782	RNA helicase-like
319	31	66.0	493	2	D90587	ribosome releasing
320	31	66.0	496	2	T46157	
321	31	66.0	498	2	D71616	

395	31	66.0	2391	2	T18410	carbamoyl-phosphat
396	31	66.0	5170	2	T15348	hypothetical prote
397	30.5	64.9	48	2	D64514	hypothetical prote
398	30.5	64.9	48	2	E71501	hypothetical prote
399	30.5	64.9	258	1	SNBY3	proteasome endope
400	30.5	64.9	367	2	T22663	hypothetical prote
401	30.5	64.9	786	2	T26811	hypothetical prote
402	30.5	64.9	1092	2	T18305	replication factor
403	30.5	64.9	1092	2	T18306	replication factor
404	30	63.8	67	2	E95089	hypothetical prote
405	30	63.8	73	2	H97956	hypothetical prote
406	30	63.8	73	2	AC2049	hypothetical prote
407	30	63.8	78	2	QJ1781	Salfer 8.8K protei
408	30	63.8	79	2	AF1065	hypothetical prote
409	30	63.8	81	2	AF2998	hypothetical prote
410	30	63.8	95	2	T46086	hypothetical prote
411	30	63.8	101	2	T09662	multicatalytic end
412	30	63.8	111	2	A69932	hypothetical prote
413	30	63.8	112	2	T05198	hypothetical prote
414	30	63.8	112	2	C91216	hypothetical prote
415	30	63.8	112	2	D86062	hypothetical prote
416	30	63.8	112	2	G65179	hypothetical prote
417	30	63.8	112	2	AE0475	conserved hypochet
418	30	63.8	121	1	A40157	androgen-regulated
419	30	63.8	122	2	A43644	sarccocystatin A pr
420	30	63.8	128	2	H97101	uncharacterized pr
421	30	63.8	128	2	H97354	hypothetical prote
422	30	63.8	130	4	S58337	hypothetical prote
423	30	63.8	132	2	T13098	probable minor tal
424	30	63.8	132	2	T17907	hypothetical prote
425	30	63.8	133	2	T15449	hypothetical prote
426	30	63.8	135	2	T06681	hypothetical prote
427	30	63.8	137	2	B82998	hypothetical prote
428	30	63.8	144	2	T23275	hypothetical prote
429	30	63.8	145	2	D84458	probable translati
430	30	63.8	145	2	T49102	hypothetical prote
431	30	63.8	147	2	A33675	beta-crystallin BC
432	30	63.8	149	1	MMVZK7	K7 protein 28R - v
433	30	63.8	152	2	T31054	hypothetical prote
434	30	63.8	155	2	T15930	hypothetical prote
435	30	63.8	157	2	F69368	transcription regu
436	30	63.8	164	2	G84068	hypothetical prote
437	30	63.8	166	2	F64693	hypothetical prote
438	30	63.8	170	2	AH3318	hypothetical cytos
439	30	63.8	173	2	T41773	lbf-6 ortf28 - Bomb
440	30	63.8	181	1	B64167	cytochrome c bioge
441	30	63.8	187	2	H71819	hypothetical prote
442	30	63.8	193	2	E59095	hypothetical prote
443	30	63.8	194	2	H84771	probable AP2 domai
444	30	63.8	194	2	D87357	hypothetical prote
445	30	63.8	194	2	G83696	hypothetical prote
446	30	63.8	199	2	D64482	hypothetical prote
447	30	63.8	200	2	T25406	hypothetical prote
448	30	63.8	202	2	D84013	hypothetical prote
449	30	63.8	205	2	JC2009	beta-crystallin B2
450	30	63.8	205	2	JC4528	beta-crystallin B2
451	30	63.8	206	2	S63180	hypothetical prote
452	30	63.8	214	2	T10681	hypothetical prote
453	30	63.8	217	2	T46225	alpha NAC-like pro
454	30	63.8	217	2	T28343	hypothetical prote
455	30	63.8	223	2	T05755	hypothetical prote
456	30	63.8	226	2	S33024	hypothetical prote
457	30	63.8	233	2	A84745	hypothetical prote
458	30	63.8	235	2	A82667	conserved hypochet
459	30	63.8	237	2	B83728	phosphoribosylamin
460	30	63.8	239	2	E64699	hypothetical prote
461	30	63.8	240	2	T37432	probable 27.6K pro
462	30	63.8	240	2	JQ1784	Salfer protein - v
463	30	63.8	240	2	E72170	A56R protein - var
464	30	63.8	240	2	T28591	21R protein - vari
465	30	63.8	240	2	H36853	A52R protein - vari
466	30	63.8	240	2	E84390	24-stetrol C-methyl
467	30	63.8	250	2	T09160	proteasome subunit

468	30	63.8	250	2	T51969	20S proteasome sub
469	30	63.8	253	2	F89836	ABC transporter AT
470	30	63.8	255	2	JG0179	superoxide dismuta
471	30	63.8	261	2	B82462	hypothetical prote
472	30	63.8	263	1	A26147	egg-laying hormone
473	30	63.8	263	2	B85076	hypothetical prote
474	30	63.8	265	1	MNVV4	nonstructural prot
475	30	63.8	269	2	S11400	phosphotransferase
476	30	63.8	271	1	JX0316	phosphatidylinosit
477	30	63.8	271	2	S64615	hypothetical prote
478	30	63.8	286	2	T02641	probable C2H2-type
479	30	63.8	288	2	D64694	hypothetical prote
480	30	63.8	288	2	B40722	homeotic protein 1
481	30	63.8	290	2	G71623	Irfin PFB0065w - m
482	30	63.8	292	2	T41772	IAP1 ortf27 - Bomby
483	30	63.8	293	2	H64158	hypothetical prote
484	30	63.8	295	2	B86371	hypothetical prote
485	30	63.8	295	2	A41241	ubiquitin-conjugat
486	30	63.8	297	2	A89582	protein C18A11.3 l
487	30	63.8	298	2	T52117	zinc finger protei
488	30	63.8	300	2	T32133	hypothetical prote
489	30	63.8	301	2	JC7882	esterase (EC 3.1.1
490	30	63.8	308	2	D30315	methyl viologen-re
491	30	63.8	308	2	C30315	coenzyme-M-7-merca
492	30	63.8	315	2	T45099	methenyltetrahydro
493	30	63.8	315	2	T00528	hypothetical prote
494	30	63.8	317	2	H70566	hypothetical prote
495	30	63.8	320	2	S50716	hypothetical prote
496	30	63.8	320	2	E84681	probable bHLH tran
497	30	63.8	321	2	F98318	hypothetical prote
498	30	63.8	321	2	AG2964	fibrinogen binding
499	30	63.8	324	2	A84295	probable DNA helic
500	30	63.8	328	2	T07610	MS176 protein - ri

## ALIGNMENTS

## RESULT 1

T10471 potassium channel-blocking toxin K-alpha - Pandinus imperator (fragment)

C/Species: Pandinus imperator

C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004

C/Accession: T10471

R:Rogowski, R.S.; Collins, J.H.; O'Neill, T.J.; Gustafson, T.A.; Werkmann, T.R.; Rogawsk

Mol.Pharmacol. 50, 1167-1177, 1996

A&gt;Title: Three new coxins from the scorpion Pandinus imperator selectively block certai

A/Reference number: Z17036; PMID:97070422; PMID:8913348

A/Accession: T10471

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-47 &lt;ROG&gt;

A/Cross-references: UNIPROT:P55927; UNIPARC:UPI0000135658; EMBL:U79579; NID:g1945405; P

C/Genetics:

A/Gene: PTX-1

C/Superfamily: kaliotoxin

C/Keywords: neurotoxin; potassium channel inhibitor; venom

Query Match	100.0%;	Score 47;	DB 2;	Length 47;
Best Local Similarity	100.0%;	Pred. No. 0.14;		
Matches	8;	Conservative	0;	Mismatches
			0;	Gaps
				0;
Qy	1	DYKDDDK	8	
Db	5	DYKDDDK	12	

## RESULT 2

S59425 SPR28 protein - yeast (Saccharomyces cerevisiae)

N/Alternate names: protein YD934.03c; protein YDR218c

C/Species: Saccharomyces cerevisiae

C/Date: 30-Nov-1995 #sequence\_revision 16-Feb-1996 #text\_change 09-Jul-2004

C/Accession: S59425  
 R/Murphy, L.; Harris, D.  
 Submitted to the EMBL Data Library, March 1995  
 A/Reference number: S59423  
 A/Accession: S59425  
 A/Molecule type: DNA  
 A/Residues: 1-423 <MOR>  
 A/Cross-references: UNIPROT:Q04921; UNIPARC:UPI000006C4F5; EMBL:Z48612; NID:G728671; PID  
 A/Experimental source: strain AB972  
 C/Genetics:  
 A/Gene: SGD:SPR28  
 A/Cross-references: SGD:S0002626; MIPS:YDR218c  
 A/Map position: 4R  
 C/Superfamily: Saccharomyces cerevisiae cell division control protein CDC10

Query Match 87.2%; Score 41; DB 2; Length 423;  
 Best Local Similarity 87.5%; Pred. No. 14;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
 Db 62 DYDDDDK 69

RESULT 3  
 S32834  
 methylviologen-reducing hydrogenase chain vhcG [similarity] - Methanococcus voltae  
 C/Species: Methanococcus voltae  
 C/Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 09-Jul-2004  
 C/Accession: S32834; S16726  
 R/Klein, A.  
 Submitted to the EMBL Data Library, August 1991  
 A/Reference number: S32833  
 A/Accession: S32834  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-306 <KDE>  
 A/Cross-references: UNIPROT:Q00406; UNIPARC:UPI00000625CA; EMBL:X61203; NID:G296614; PID  
 R/Halboch, S.; Klein, A.  
 Submitted to the EMBL Data Library, August 1991  
 A/Description: Methanococcus voltae harbors two gene groups each of homologous (NiFe) - a  
 A/Reference number: S16721  
 A/Accession: S16726  
 A/Molecule type: DNA  
 A/Residues: 1-99, 'TA', '102-107', 'P', '126', '129-306' <HAL>  
 A/Cross-references: UNIPARC:UPI0000174FE0; EMBL:X61203  
 A/Note: the sequence is revised in GenBank entry X61203, release 117, (PIDN:CAA43505.1)  
 R/Halboch, S.; Klein, A.  
 Mol. Gen. Genet. 233, 217-224, 1992  
 A/Title: Methanococcus voltae harbors four gene clusters potentially encoding two [NiFe]  
 A/Reference number: A59304; MUID:92293118; PMID:1603063  
 A/Contents: annotation  
 C/Genetics:  
 A/Gene: vhcG  
 C/Superfamily: methyl viologen-reducing hydrogenase gamma chain

Query Match 80.9%; Score 38; DB 2; Length 306;  
 Best Local Similarity 87.5%; Pred. No. 33;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
 Db 260 DYKVDK 267

RESULT 4  
 AC0184  
 malate dehydrogenase (oxaloacetate-decarboxylating) (EC 1.1.1.38) [imported] - Yersinia  
 C/Species: Yersinia pestis  
 C/Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 05-Oct-2004  
 C/Accession: AC0184  
 R/Parhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.;  
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall  
 Nature 413, 523-527, 2001  
 A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
 A/Reference number: AB0001; MUID:21470413; PMID:11586360  
 A/Accession: AC0184  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-565 <KUR>  
 A/Cross-references: UNIPROT:Q8ZG09; UNIPARC:UPI00000DC2B; GB:AL590842; PIDN:CMC90334.1  
 C/Genetics:  
 A/Gene: sica  
 C/Superfamily: malic enzyme  
 C/Keywords: oxidoreductase

Query Match 80.9%; Score 38; DB 2; Length 565;  
 Best Local Similarity 75.0%; Pred. No. 62;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
 Db 66 DFKDDDK 73

RESULT 5  
 S53352  
 IFH1 protein - yeast (Saccharomyces cerevisiae)  
 N/Alternate names: protein L8083.9; protein YLR223c; RRP3 protein  
 C/Species: Saccharomyces cerevisiae  
 C/Date: 10-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004  
 C/Accession: S53352; S51446; S47477  
 R/Cherel, I.; Thuriaux, P.  
 Yeast 11, 261-270, 1995  
 A/Title: The IFH1 gene product interacts with a fork head protein in Saccharomyces cere  
 A/Reference number: S53352; MUID:95304839; PMID:7785326  
 A/Accession: S53352  
 A/Status: nucleic acid sequence not shown  
 A/Molecule type: DNA  
 A/Residues: 1-1085 <CHE>  
 A/Cross-references: UNIPROT:P39520; UNIPARC:UPI000012D3D6; EMBL:Z29488; NID:G531491; PI  
 R/Hallsworth, K.  
 Submitted to the EMBL Data Library, December 1994  
 A/Description: The sequence of S. cerevisiae cosmid 8083.  
 A/Reference number: S51443  
 A/Accession: S51446  
 A/Molecule type: DNA  
 A/Residues: 1-1085 <HAL>  
 A/Cross-references: UNIPARC:UPI000012D3D6; EMBL:U19027; NID:G609363; PID:G609372; MIPS:  
 C/Genetics:  
 A/Gene: SGD:IFH1; RRP3  
 A/Cross-references: SGD:S0004213; MIPS:YLR223c  
 A/Map position: 12R

Query Match 80.9%; Score 38; DB 2; Length 1085;  
 Best Local Similarity 85.7%; Pred. No. 1,2e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 7  
 Db 612 DYEDDD 618

RESULT 6  
 S54451  
 hypothetical protein YMR07c - yeast (Saccharomyces cerevisiae)  
 N/Alternate names: hypothetical protein YMR582.01c; hypothetical protein YMR916.15c  
 C/Species: Saccharomyces cerevisiae  
 C/Date: 08-Jul-1995 #sequence\_revision 09-Mar-1996 #text\_change 09-Jul-2004  
 C/Accession: S54451; S52836  
 R/Gentles, S.; Bowman, S.  
 Submitted to the EMBL Data Library, May 1995  
 A/Reference number: S54451  
 A/Accession: S54451  
 A/Molecule type: DNA

A/Residues: 1-682 <GEN>  
A/Cross-references: UNIPROT:Q04264; UNIPARC:UPI0000168AB1; EMBL:Z49259; NID:g807956; PID  
A/Experimental source: strain AB972  
R/Pearson, D.; Bowman, S.  
Submitted to the EMBL Data Library, April 1995  
A/Reference number: S52814  
A/Accession: S52836  
A/Molecule type: DNA  
A/Residues: 659-1277 <PEA>  
A/Cross-references: UNIPARC:UPI0000168AC7; EMBL:Z48952; NID:g763008; PIDN:CAA88801.1; PI  
A/Experimental source: strain AB972  
C/Genetics:  
A/Gene: SGD:PDS5  
A/Cross-references: SGD:S0004681; MIPS:YMR076c  
A/Map position: 13R

Query Match 80.9%; Score 38; DB 2; Length 1277;  
Best Local Similarity 85.7%; Pred. No. 1.5e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
DB 1265 DYKDDDD 1271

RESULT 7  
A42854  
probable spindle pole body component bimB - *Emicella nidulans*  
N/Alternate names: cell division-associated protein bimB  
C/Species: *Emicella nidulans*, *Aspergillus nidulans*  
C/Date: 10-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C/Accession: A42854; S27411  
R/May, G.S.; McGoldrick, C.A.; Holt, C.L.; Denison, S.H.  
J./Biol. Chem. 267, 15737-15743, 1992  
A/Title: The bim3 mutation of *Aspergillus nidulans* uncouples DNA replication from the C  
A/Reference number: A42854; M0ID:92348436; PMID:1639810  
A/Accession: A42854  
A/Molecule type: mRNA  
A/Residues: 1-2067 <MA>  
A/Cross-references: UNIPROT:P33144; UNIPARC:UPI000012693F  
A/Note: Sequence extracted from NCBI backbone (NCBIN:112444, NCBIP:112445)  
R/May, G.S.; McGoldrick, C.A.; Denison, S.H.; Holt, C.L.  
Submitted to the EMBL Data Library, February 1992  
A/Description: The bim3 mutation of *Aspergillus nidulans* uncouples DNA replication from  
A/Reference number: S27411  
A/Accession: S27411  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-2010, 'PLSIG', 2016 <MA2>  
A/Cross-references: UNIPARC:UPI00001688E9; EMBL:M83232; NID:g168020; PID:g168021  
A/Note: this sequence differs by a frameshift after residue 2010  
C/Keyword: nucleus

Query Match 80.9%; Score 38; DB 2; Length 2067;  
Best Local Similarity 85.7%; Pred. No. 2.4e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
DB 899 DYKDDDD 905

RESULT 8  
T10503  
fruit bromelain (EC 3.4.22.33) FB18 precursor - pineapple  
C/Species: *Ananas comosus* (pineapple)  
C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C/Accession: T10503  
R/Muta, E.; Aramaki, H.; Takara, Y.; Kono, A.; Okamoto, Y.; Ota, S.  
Submitted to the EMBL Data Library, January 1993  
A/Description: Cloning and sequencing of fruit bromelain.  
A/Reference number: Z17060  
A/Accession: T10503

A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-351 <MT>  
A/Cross-references: UNIPROT:Q23791; UNIPARC:UPI0000044EB5; EMBL:D14059  
A/Experimental source: cv. N67-10; nearly mature fruit  
C/Function:  
A/Description: hydrolyses proteins; cysteine proteinase  
C/Superfamily: papain  
C/Keywords: cysteine proteinase; hydrolase  
F/-24/Domain: signal sequence #status predicted <SIG>  
F/-25-121/Domain: amino-terminal propeptide #status predicted <PRO>  
F/-122-339/Product: fruit bromelain #status predicted <MAT>  
F/-340-351/Domain: carboxyl-terminal propeptide #status predicted <CTP>  
F/-147,279,300/Active site: Cys, His, Asn #status predicted

Query Match 78.7%; Score 37; DB 2; Length 351;  
Best Local Similarity 85.7%; Pred. No. 56;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDDK 8  
DB 48 YKDDDDK 54

RESULT 9  
B96524  
hypothetical protein F11A17.5 [imported] - *Arabidopsis thaliana*  
C/Species: *Arabidopsis thaliana* (mouse-ear cress)  
C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C/Accession: B96524  
R/Theologas, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.  
ansen, N.P.; Hughes, B.; Hutzar, L.  
Nature 408, 816-820, 2000  
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maiz, R.; Marziani  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A/Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.  
A/Reference number: A86141; M0ID:21016719; PMID:11130712  
A/Accession: B96524  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-513 <STO>  
A/Cross-references: UNIPROT:Q9SX72; UNIPARC:UPI0000043573; GB:AE005173; NID:g5733869; P  
C/Genetics:  
A/Gene: F11A17.5  
A/Map position: 1  
C/Superfamily: *Arabidopsis thaliana* hypothetical protein F11A17.5.30

Query Match 78.7%; Score 37; DB 2; Length 513;  
Best Local Similarity 85.7%; Pred. No. 83;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
DB 282 DYKDDDD 288

RESULT 10  
B96974  
superfamily I DNA and RNA helicase [imported] - *Clostridium acetobutylicum*  
C/Species: *Clostridium acetobutylicum*  
C/Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
C/Accession: B96974  
R/Molling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee  
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1  
A/Reference number: A96900; M0ID:21359325; PMID:21359325  
A/Accession: B96974  
A/Status: preliminary



A:Molecule type: DNA  
 A:Residues: 1-721 <KUR>  
 A:Cross-references: UNIPROT:Q97LF8; UNIPARC:UPI00000C9F00; GB:AE001437; PIDD:AAK78581.1;  
 A:Experimental source: Clostridium acetobutylicum ATCC824  
 C:Genetics:  
 A:Gene: CAC0603  
 C:Superfamily: Bacillus subtilis hypothetical protein yvgs

Query Match 78.7%; Score 37; DB 2; Length 721;  
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
 |||:  
 Db 67 DYADDEK 74

## RESULT 11

hypothetical protein F26D2.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C:Accession: T20815; T21409

R:McMurray, A.

submitted to the EMBL Data Library, March 1997

A:Reference number: Z19327

A:Accession: T20815

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-791 <WIL>

A:Cross-references: UNIPROT:Q8WUP4; UNIPARC:UPI0000060F93; EMBL:Z93377; PIDD:CA807581.1;

A:Experimental source: clone F13A7

R:McMurray, A.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19418

A:Accession: T21409

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-791 <WIL>

A:Cross-references: UNIPARC:UPI0000060F93; EMBL:Z81513; PIDD:CA804186.1; GSEDB:GN00023;

A:Experimental source: clone F26D2

C:Genetics:

A:Gene: CESP:F26D2.2

A:Map position: 5

A:Introns: 28/3; 194/2; 195/3; 299/2; 404/1; 462/3; 500/1; 670/3; 698/3

## Query Match

Best Local Similarity 78.7%; Score 37; DB 2; Length 791;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
 |||:  
 Db 274 DYNDDD 280

## RESULT 12

hypothetical protein F10M6.180 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 23-Jul-1999

C:Accession: T05410

R:Bevan, M.; Weichselgartner, M.; Farmann, B.; Grandenath, K.; Dauner, D.; Herzl, A.; N

submitted to the Protein Sequence Database, February 1998

A:Reference number: Z15414

A:Accession: T05410

A:Molecule type: DNA

A:Residues: 1-838 <BEV>

A:Cross-references: UNIPARC:UPI000016DADA; EMBL:AL021811

A:Experimental source: cultivar Columbia; BAC clone F10M6

C:Genetics:

A:Map position: 4

A:Introns: 86/1; 158/1; 175/3; 214/3; 254/3; 286/2; 317/3; 361/3; 399/2; 463/3; 533/2; 5

Query Match 78.7%; Score 37; DB 2; Length 838;  
 Best Local Similarity 75.0%; Pred. No. 1.4e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
 |||:  
 Db 99 DYSNDDK 106

## RESULT 13

hypothetical protein BB0739 - Lyme disease spirochete

C:Species: Borrelia burgdorferi (Lyme disease spirochete)

C>Date: 13-Feb-1998 #sequence\_revision 13-Feb-1998 #text\_change 09-Jul-2004

C:Accession: B70192

R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Whi

son, D.; Peterson, J.; Kraljic, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vug

li; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Nature 390, 580-586, 1997

A:Authors: Smith, H.O.; Venter, J.C.

A>Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.

A:Reference number: A70100; MUID:98065943; PMID:9403685

A:Accession: B70192

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-195 <KLE>

A:Cross-references: UNIPROT:O51681; UNIPARC:UPI00000575C8; GB:AE001174; GB:AE000783; N

A:Experimental source: strain B31

C:Superfamily: Borrelia burgdorferi hypothetical protein BB0739

Query Match 76.6%; Score 36; DB 2; Length 195;

Best Local Similarity 100.0%; Pred. No. 44;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDD 7  
 |||:  
 Db 129 YKDDDD 134

## RESULT 14

T31963

hypothetical protein C33C12.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 31-Dec-2004

C:Accession: T31963

R:Gatung, S.; Schneet, P.

submitted to the EMBL Data Library, July 1997

A:Description: The sequence of C. elegans cosmid C33C12.

A:Reference number: Z21105

A:Accession: T31963

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-215 <GAT>

A:Cross-references: UNIPROT:O16579; UNIPARC:UPI0000078124; EMBL:AF016662; PIDD:AA866055

A:Experimental source: strain Bristol N2; clone C33C12

C:Genetics:

A:Gene: CESP:C33C12.7

A:Map position: 2

A:Introns: 63/3; 94/3; 124/2; 168/2

## Query Match

Best Local Similarity 76.6%; Score 36; DB 2; Length 215;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
 |||:  
 Db 182 DYKDDDK 189

## RESULT 15

S39814

DNA polymerase homolog pol-r - rye mitochondrion (strain Halo)

C/Species: mitochondrion Secale cereale (rye)  
A/Variety: strain Halo  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C/Accession: S39814  
R/Dohmen, G.; Tudzynski, P.  
Curr. Genet. 25, 59-65, 1994  
A/Title: A DNA-polymerase-related reading frame (pol-r) in the mtDNA of Secale cereale.  
A/Reference number: S39814; MUID:94363738; PMID:8082167  
A/Accession: S39814  
A/Molecule type: DNA  
A/Residues: 1-289 <DOH>  
A/Cross-references: UNIPROT:Q36545; UNIPARC:UPI000008F158; EMBL:X74132; NID:g439279; PII  
A/Experimental source: strain Halo; etiolated shoots  
C/Genetics:  
A/Gene: pol-r  
A/Genome: mitochondrion  
C/Keywords: mitochondrion

Query Match 76.6%; Score 36; DB 2; Length 289;  
Best Local Similarity 75.0%; Pred. No. 67;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 8  
|:|||||  
Db 252 DHKSDDDK 259

RESULT 16  
S39823  
DNA polymerase homolog pol-r - rye mitochondrion (strain B-P2)  
C/Species: mitochondrion Secale cereale (rye)  
A/Variety: strain B-P2  
C/Date: 10-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C/Accession: S39823  
R/Dohmen, G.; Tudzynski, P.  
Curr. Genet. 25, 59-65, 1994  
A/Title: A DNA-polymerase-related reading frame (pol-r) in the mtDNA of Secale cereale.  
A/Reference number: S39814; MUID:94363738; PMID:8082167  
A/Accession: S39823  
A/Status: nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-312 <DOH>  
A/Cross-references: UNIPROT:Q36546; UNIPARC:UPI0000096B6D; EMBL:X74133; NID:g439281; PII  
A/Experimental source: strain B-P2; etiolated shoots  
C/Genetics:  
A/Gene: pol-r  
A/Genome: mitochondrion  
C/Keywords: mitochondrion

Query Match 76.6%; Score 36; DB 2; Length 312;  
Best Local Similarity 75.0%; Pred. No. 72;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 8  
|:|||||  
Db 252 DHKSDDDK 259

RESULT 17  
T49237  
hypothetical protein F7K15.80 - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 09-Jul-2004  
C/Accession: T49237  
R/Obermaier, B.; Ottenwaelder, B.; Duchemin, D.; Zeitler, K.; Mewes, H.W.; Rudd, S.; Lem  
submitted to the Protein Sequence Database, April 2000  
A/Reference number: Z25019  
A/Accession: T49237  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-485 <OBE>  
A/Cross-references: UNIPROT:Q9LXL1; UNIPARC:UPI00000A1EFC; EMBL:AL353871; GSPDB:GN00061;

A/Experimental source: cultivar Columbia; BAC clone F7K15  
C/Genetics:  
A/Gene: ATSP:F7K15.80  
A/Map position: 3  
A/Intons: 292/3; 359/3; 425/1

Query Match 76.6%; Score 36; DB 2; Length 485;  
Best Local Similarity 85.7%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
|:|||||  
Db 22 DYDDDD 28

RESULT 18  
H84913  
probable ATP-dependent RNA helicase [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C/Accession: H84913  
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.T.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.  
eusa, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,  
Nature 402, 761-768, 1999  
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A/Reference number: A84420; MUID:20083487; PMID:10617197  
A/Accession: H84913  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-748 <STO>  
A/Cross-references: UNIPROT:Q22907; UNIPARC:UPI000017A71E; GB:AE02093; NID:g2275211; P  
C/Genetics:  
A/Gene: At2g47330  
A/Map position: 2

Query Match 76.6%; Score 36; DB 2; Length 748;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDD 7  
|:|||||  
Db 107 YKDDDD 112

RESULT 19  
S56231  
hypothetical protein YFL023w - yeast (Saccharomyces cerevisiae)  
C/Species: Saccharomyces cerevisiae  
C/Date: 02-Sep-1995 #sequence\_revision 19-Oct-1995 #text\_change 09-Jul-2004  
C/Accession: S56231  
R/Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasamura, S.I.; Sasan  
submitted to the EMBL Data Library, May 1995  
A/Description: Analysis of the nucleotide sequence of chromosome VI from Saccharomyces c  
A/Reference number: S56186  
A/Accession: S56231  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-796 <MOR>  
A/Cross-references: UNIPROT:P43573; UNIPARC:UPI000013ADF2; EMBL:D50617; NID:g836685; PII  
A/Genetics:  
A/Gene: SGD:FYV11  
A/Cross-references: SGD:S0001871  
A/Map position: 6L

Query Match 76.6%; Score 36; DB 2; Length 796;  
Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
|:|||||  
Db 583 DYDDDD 589

## RESULT 20

hypothetical protein 3 - maize mitochondrion plasmid S-1  
C:Species: mitochondrion Zea mays (maize)  
C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 31-Dec-2004  
C/Accession: S07183  
R:Paillard, M.; Sederoff, R.R.; Levings II, C.S.  
EMBO J. 4, 1125-1128, 1985  
A:Title: Nucleotide sequence of the S-1 mitochondrial DNA from the S cytoplasm of maize.  
A:Reference number: S07183  
A/Accession: S07183  
A/Status: translation not shown  
A/Molecule type: DNA  
A/Residues: 1-917 <PAI>  
A/Cross-references: UNIPROT:Q9MJC4; UNIPARC:UPI0000178E5; EMBL:X02451  
C/Genetics:  
A/Genome: mitochondrion  
C/Superfamily: DNA polymerase, mitochondrial plasmid type  
C/Keywords: mitochondrion

Query Match 76.6%; Score 36; DB 2; Length 917;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DYKDDDD 7  
Db 443 YKDDDD 448

## RESULT 21

protein Cl8F3.2 [imported] - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C/Accession: A88746  
R:anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog  
A:Reference number: A75000; MUID:99069613; PMID:9851916  
A/Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C.ele  
A/Accession: A88746  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-987 <STO>  
A/Cross-references: UNIPROT:Q18100; UNIPARC:UPI000017A61F; GB:chr\_IV; PIDN:AAA93439.1; F  
C/Genetics:  
A/Gene: Cl8F3.2  
A/Map position: 4

Query Match 76.6%; Score 36; DB 2; Length 987;  
Best Local Similarity 75.0%; Pred. No. 2.4e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DYKDDDD 8  
Db 922 DYKDDDD 929

## RESULT 22

hypothetical protein YER033c - yeast (Saccharomyces cerevisiae)  
C:Species: Saccharomyces cerevisiae  
C>Date: 28-May-1993 #sequence\_revision 24-Feb-1995 #text\_change 09-Jul-2004  
C/Accession: S50536  
R:Dietrich, F.S.  
submitted to the EMBL Data Library, December 1994  
A:Description: The sequence of S. cerevisiae cosmid 9379, 9501, and lambda clone 4678.  
A:Reference number: S50432  
A/Accession: S50536  
A/Molecule type: DNA  
A/Residues: 1-1076 <DIE>

A/Cross-references: UNIPROT:P40021; UNIPARC:UPI000013AC6F; EMBL:U18796; NID:G603265; P  
C/Genetics:  
A/Gene: SGD:ZRG8; MIPS:YER033c  
A/Cross-references: SGD:S0000835  
A/Map position: 5R

Query Match 76.6%; Score 36; DB 2; Length 1076;  
Best Local Similarity 85.7%; Pred. No. 2.7e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DYKDDDD 7  
Db 436 DYKDDDD 442

## RESULT 23

hypothetical protein Cl8F3.2 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T30988  
R:Du, Z.; Gattung, S.  
submitted to the EMBL Data Library, August 1999  
A:Description: The sequence of C. elegans cosmid Cl8F3.  
A:Reference number: Z20953  
A/Accession: T30988  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-1287 <DUZ>  
A/Cross-references: UNIPROT:Q18100; UNIPARC:UPI0000081960; EMBL:U50067; PIDN:AAA93439.2  
A/Experimental source: strain Bristol N2  
C/Genetics:  
A/Map position: IV  
A/Insertions: 34/3; 72/1; 131/2; 157/1; 254/3; 303/1; 400/1; 495/1; 592/1; 681/3; 950/1; 1  
A/Note: Cl8F3.2  
C/Superfamily: neural cell adhesion molecule L1; fibronectin type III repeat homology;

Query Match 76.6%; Score 36; DB 2; Length 1287;  
Best Local Similarity 75.0%; Pred. No. 3.2e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DYKDDDD 8  
Db 1222 DYKDDDD 1229

## RESULT 24

probable membrane associated protein PFB0190C - malaria parasite (Plasmodium falciparum)  
C:Species: Plasmodium falciparum  
C>Date: 13-Nov-1998 #sequence\_revision 13-Nov-1998 #text\_change 09-Jul-2004  
C/Accession: B71621  
R:Gardner, M.J.; Tetteh, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V  
; Pereira, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.C  
Science 282, 1126-1132, 1998  
A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.  
A:Reference number: A71600; MUID:99021743; PMID:9804551  
A/Accession: B71621  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-2295 <GAR>  
A/Cross-references: UNIPROT:Q9TY98; UNIPARC:UPI000007C03B; GB:AE001379; GB:AE001362; NI  
A/Experimental source: clone 3D7  
C/Genetics:  
A/Gene: PFB0190C

Query Match 76.6%; Score 36; DB 2; Length 2295;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDD 6  
Db 1504 DYKDD 1509

RESULT 25  
T18492  
hypothetical protein C0805w - malaria parasite (Plasmodium falciparum)  
C/Species: Plasmodium falciparum  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T18492  
R/Lawson, D.; Bowman, S.; Barrell, B.  
submitted to the EMBL Data Library, August 1997  
A/Reference number: Z18935  
A/Accession: T18492  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-2457 <LAW>  
A/Cross-references: UNIPROT:O77375; UNIPARC:UPI00000829FD; EMBL:Z98551; PIDD:CA81131.1  
C/Genetics:  
A/Map position: 3  
A/Note: C0805w  
C/Superfamily: Plasmodium DNA-directed RNA polymerase II large chain

Query Match                      76.6%; Score 36; DB 2; Length 2457;  
Best Local Similarity    85.7%; Pred. NO. 6.4e+02;  
Matches    6; Conservative    0; Mismatches    1; Indels    0; Gaps    0;

QY    1 DYKDDDD 7  
      |||  
Db    1264 DYDDDD 1270

RESULT 26  
AF2345  
hypothetical protein asl4317 [imported] - Nostoc sp. (strain PCC 7120)  
C/Species: Nostoc sp. PCC 7120  
A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C/Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C/Accession: AF2345  
R/Kanehiko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi, Nakazaki, N.; Shimpou, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S  
DNA Res. 8, 205-213, 2001  
A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena  
A/Reference number: AB1807; MUID:21595285; PMID:11759840  
A/Accession: AF2345  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-78 <KUR>  
A/Cross-references: UNIPROT:Q8YPR2; UNIPARC:UPI000000CEAB9; GB:BA000019; PIDD:BA876016.1;  
C/Genetics:  
A/Gene: asl4317

Query Match                      74.5%; Score 35; DB 2; Length 78;  
Best Local Similarity    85.7%; Pred. NO. 25;  
Matches    6; Conservative    0; Mismatches    1; Indels    0; Gaps    0;

QY    1 DYKDDDD 7  
      |||  
Db    64 DYDDDD 70

RESULT 27  
A40592  
heat shock protein hsp18 - Clostridium acetobutylicum  
C/Species: Clostridium acetobutylicum  
C/Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 09-Jul-2004  
C/Accession: A40592; S25534  
R/Sauer, U.; Duetre, P.  
J. Bacteriol. 175, 3394-3400, 1993  
A/Title: Sequence and molecular characterization of a DNA region encoding a small heat shock  
A/Reference number: A40592; MUID:33273706; PMID:8501044  
A/Accession: A40592  
A/Status: preliminary  
A/Molecule type: DNA

A/Residues: 1-151 <SAU>  
A/Cross-references: UNIPROT:Q03928; UNIPARC:UPI000012CC00; EMBL:X65276; NID:g40362; PIDD:CA81131.1  
C/Superfamily: alpha-crystallin-related small heat shock protein

Query Match                      74.5%; Score 35; DB 2; Length 151;  
Best Local Similarity    75.0%; Pred. NO. 50;  
Matches    6; Conservative    1; Mismatches    1; Indels    0; Gaps    0;

QY    1 DYKDDDD 8  
      |||  
Db    48 DYEKDDK 55

RESULT 28  
G97355  
molecular chaperone (small heat shock protein), Hsp18 [imported] - Clostridium acetobutylicum  
C/Species: Clostridium acetobutylicum  
C/Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
C/Accession: G97355  
R/Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum  
A/Reference number: A96900; MUID:21359325; PMID:21359325  
A/Accession: G97355  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-151 <KUR>  
A/Cross-references: UNIPROT:Q03928; UNIPARC:UPI000012CC00; GB:AE001437; PIDD:AA81634.1  
A/Experimental source: Clostridium acetobutylicum ATCC824  
C/Genetics:  
A/Gene: CAC3714  
C/Superfamily: alpha-crystallin-related small heat shock protein

Query Match                      74.5%; Score 35; DB 2; Length 151;  
Best Local Similarity    75.0%; Pred. NO. 50;  
Matches    6; Conservative    1; Mismatches    1; Indels    0; Gaps    0;

QY    1 DYKDDDD 8  
      |||  
Db    48 DYEKDDK 55

RESULT 29  
T32029  
hypothetical protein C03H5.3 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T32029  
R/Rohlfing, T.; Wohldmann, P.  
submitted to the EMBL Data Library, July 1997  
A/Description: The sequence of C. elegans cosmid C03H5.  
A/Reference number: Z21114  
A/Accession: T32029  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-287 <ROH>  
A/Cross-references: UNIPROT:O16657; UNIPARC:UPI0000077A6F; EMBL:AF016674; PIDD:AAB66130  
A/Experimental source: strain Bristol NZ; clone C03H5  
C/Genetics:  
A/Gene: CESP:C03H5.3  
A/Map position: 2  
A/Introns: 2/1; 15/3; 234/2

Query Match                      74.5%; Score 35; DB 2; Length 287;  
Best Local Similarity    62.5%; Pred. NO. 98;  
Matches    5; Conservative    3; Mismatches    0; Indels    0; Gaps    0;

QY    1 DYKDDDD 8  
      |||  
Db    106 DFEKDDDE 113

RESULT 30  
A86384  
unknown protein [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C/Accession: A86384  
R/Thellogis: A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chih, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, U.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A/Reference number: A86141; MUID:21016719; PMID:11130712  
A/Accession: A86384  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-288 <STO>  
A/Cross-references: UNIPROT:Q9C6L0; UNIPARC:UPI000005EAA4; GB:AE005172; NID:g10092327; F C/Genetics:  
A/Map position: 1

Query Match 74.5%; Score 35; DB 2; Length 288;  
Best Local Similarity 85.7%; Pred. No. 98;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YKDDDD 8  
DB 128 YHDDDDK 134

RESULT 31  
D96708  
unknown protein, 9003-8083 [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C/Accession: D96708  
R/Thellogis: A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chih, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, U.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A/Reference number: A86141; MUID:21016719; PMID:11130712  
A/Accession: D96708  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-306 <STO>  
A/Cross-references: UNIPROT:Q9M9C9; UNIPARC:UPI00000A11A6; GB:AE005173; NID:g6714347; PT C/Genetics:  
A/Map position: 1

Query Match 74.5%; Score 35; DB 2; Length 306;  
Best Local Similarity 85.7%; Pred. No. 1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
DB 137 DYDDDD 143

RESULT 32  
PC4365  
calcium-binding protein - tapeworm (Echinococcus granulosus) (fragment)  
C/Species: Echinococcus granulosus

C/Date: 15-Oct-1997 #sequence\_revision 07-Nov-1997 #text\_change 09-Jul-2004  
C/Accession: PC4365  
R/Rodrigues, J.J.S.; Ferreira, H.B.; Farias, S.E.; Zaha, A.  
Biochem. Biophys. Res. Commun. 237, 451-456, 1997  
A/Title: A protein with a novel calcium-binding domain associated with calcareous corals  
A/Reference number: PC4365; MUID:97415820; PMID:9268732  
A/Accession: PC4365  
A/Status: nucleic acid sequence not shown  
A/Molecule type: mRNA  
A/Residues: 1-338 <ROD>  
A/Cross-references: UNIPROT:Q24795; UNIPARC:UPI0000755B8; GB:I33817; NID:g499140; PID F.1-7-8-20,21-33,34-45,46-89,90-103,104-116,117-129,130-141,142-155,156-169,170-182,18

Query Match 74.5%; Score 35; DB 2; Length 338;  
Best Local Similarity 85.7%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
DB 3 DYDDDD 9

RESULT 33  
T09106  
gibberellin 20-oxidase (EC 1.14.11.-) - spinach  
C/Species: Spinacia oleracea (spinach)  
C/Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C/Accession: T09106  
R/Mu, K.; Li, L.; Gage, D.A.; Zeevaert, J.A.D.  
Plant Physiol. 110, 547-554, 1996  
A/Title: Cloning and photoperiod-regulated expression of the gibberellin 20-oxidase from ci  
A/Reference number: 216564; MUID:96351185; PMID:8742334  
A/Accession: T09106  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-374 <MW>  
A/Cross-references: UNIPROT:Q41366; UNIPARC:UPI0000A09D6; EMBL:U33330; NID:g1144389; F C/Suprafamily: 1-aminocyclopropane-1-carboxylate oxidase  
C/Keywords: oxidoreductase

Query Match 74.5%; Score 35; DB 2; Length 374;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YKDDDD 8  
DB 150 YDDDDDK 156

RESULT 34  
T25165  
hypothetical protein T23D8.3 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T25165  
R/Wild, A.  
submitted to the EMBL Data Library, October 1996  
A/Reference number: 219989  
A/Accession: T25165  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-410 <WIL>  
A/Cross-references: UNIPROT:Q02327; UNIPARC:UPI000078796; EMBL:Z81128; PIDN:CAB03401.1  
C/Genetics:  
A/Map position: 1  
A/Introns: 61/3; 208/3; 247/3; 396/3

Query Match 74.5%; Score 35; DB 2; Length 410;  
Best Local Similarity 75.0%; Pred. No. 1.4e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 DYKDDDDK 8  
Db 338 DMEDDDDK 345

## RESULT 35

S67161

hypothetical protein YOR264w - yeast (*Saccharomyces cerevisiae*)

N/Alternate names: hypothetical protein O5375

C/Species: *Saccharomyces cerevisiae*

C/Date: 12-Jul-1996 #sequence\_revision 12-Jul-1996 #text\_change 09-Jul-2004

C/Accession: S67161

R/Jauniaux, J.C.; Poirey, R.

submitted to the Protein Sequence Database, July 1996

A/Reference number: S67143

A/Accession: S67161

A/Molecule type: DNA

A/Residues: 1-430 &lt;JUN&gt;

A/Cross-references: UNIPROT:Q08729; UNIPARC:UPI00006A307; EMBL:Z75171; NID:g1420592; PI

C/Experimental source: strain S288C

C/Genetics:

A/Gene: MIPS:YOR264w

A/Cross-references: SGD:S0005790

A/Map position: 15R

Query Match 74.5%; Score 35; DB 2; Length 430;

Best Local Similarity 62.5%; Pred. No. 1.5e+02;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 38 DFEDDDDK 45

## RESULT 36

S58653

hypothetical protein YFR024c-a - Yeast (*Saccharomyces cerevisiae*)C/Species: *Saccharomyces cerevisiae*

C/Date: 27-Oct-1995 #sequence\_revision 10-Nov-1995 #text\_change 15-Mar-2004

C/Accession: S58653

R/Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasannuma, S.I.; Sasanu

submitted to the EMBL Data Library, May 1995

A/Description: Analysis of the nucleotide sequence of chromosome VI from *Saccharomyces ce*

A/Reference number: S56186

A/Accession: S58653

A/Molecule type: DNA

A/Residues: 1-451 &lt;MUR&gt;

A/Cross-references: UNIPARC:UPI000053060; EMBL:D50617; GSPDB:GN00006; MIPS:YFR024c-a

C/Genetics:

A/Gene: MIPS:YFR024c-a

A/Map position: 6R

A/Intons: 16/2

F/399-448/Domain: SH3 homology &lt;SH3&gt;

Query Match 74.5%; Score 35; DB 2; Length 451;

Best Local Similarity 85.7%; Pred. No. 1.6e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
Db 226 DYYDDDD 232

## RESULT 37

S41720

intermediate filament - goldfish

C/Species: *Carassius auratus* (goldfish)

C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004

C/Accession: S41720

R/Glasgow, E.; Dräger, R.K.; Fuchs, C.; Lane, W.S.; Schechter, N.

EMBO J. 13, 297-305, 1994

A/Title: Molecular cloning of gefitin (ON11): serial expression of two new neurofilam  
A/Reference number: S41720; MUID:94147974; PMID:8313874  
A/Accession: S41720  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-472 <GLA>  
A/Cross-references: UNIPROT:Q07962; UNIPARC:UPI00000FB57F; EMBL:L19595; NID:g304478; PI  
C/Superfamily: cytoskeletal keratin

Query Match 74.5%; Score 35; DB 2; Length 472;

Best Local Similarity 75.0%; Pred. No. 1.6e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 430 EVKDDDDK 437

## RESULT 38

D84920

hypothetical protein At2g47860 [imported] - *Arabidopsis thaliana*C/Species: *Arabidopsis thaliana* (mouse-ear cress)

C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004

C/Accession: D84920

R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Niernann, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,

Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A/Reference number: A84420; MUID:20083487; PMID:10617197

A/Accession: D84920

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-635 &lt;STO&gt;

A/Cross-references: UNIPROT:Q82253; UNIPARC:UPI00000A0189; GB:AE002093; NID:g3738298; P

C/Genetics:

A/Gene: At2g47860

A/Map position: 2

C/Superfamily: Arabidopsis hypothetical protein F19F18.80

Query Match 74.5%; Score 35; DB 2; Length 635;

Best Local Similarity 71.4%; Pred. No. 2.3e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
Db 358 EYRDDDD 364

## RESULT 39

G71615

phospholipase A2-like a/b fold hydrolase PFB0410C - malaria parasite (*Plasmodium falcip*C/Species: *Plasmodium falciparum*

C/Date: 13-Nov-1998 #sequence\_revision 13-Nov-1998 #text\_change 09-Jul-2004

C/Accession: G71615

R/Gardner, M.J.; Tetteelin, H.; Carucci, D.J.; Cummings, L.M.; Atavind, L.; Koonin, E.V.

science 282, 1126-1132, 1998

A/Title: Chromosome 2 sequence of the human malaria parasite *Plasmodium falciparum*.

A/Reference number: A71600; MUID:99021743; PMID:9804531

A/Accession: G71615

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-679 &lt;GAR&gt;

A/Cross-references: UNIPROT:O96176; UNIPARC:UPI0000077A97; GB:AE001393; GB:AE001362; NIT

A/Experimental source: clone 3D7

C/Genetics:

A/Gene: PFB0410C

Query Match 74.5%; Score 35; DB 2; Length 679;

Best Local Similarity 85.7%; Pred. No. 2.4e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YKDDDDK 8  
 |||||  
 DB 251 YDDDDK 257

## RESULT 40

T34314  
 hypothetical protein F59G1.3 - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
 C/Accession: T34314  
 R/Latzeille, P.  
 submitted to the EMBL Data Library, April 1996  
 A/Description: The sequence of C. elegans cosmid F59G1.  
 A/Reference number: 221504  
 A/Accession: T34314  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-1010 <LAT>  
 A/Cross-references: UNIPARC:UPI000017BA5D; EMBL:U53332; PIDN:AAC71155.1; GSPDB:GN00020;  
 A/Experimental source: strain Bristol N2; clone F59G1  
 C/Genetics:  
 A/Gene: CESP:F59G1.3  
 A/Map position: 2  
 A/Intons: 13/3; 65/1; 113/1; 149/3; 188/2; 224/3; 255/1; 297/2; 593/2; 714/3; 793/3; 94

Query Match 74.5% Score 35; DB 2; Length 1010;  
 Best Local Similarity 75.0%; Pred. No. 3.7e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DYKDDDDK 8  
 |||||  
 DB 751 DMKDEDDK 758

## RESULT 41

S46817  
 hypothetical protein YHR080C - Yeast (Saccharomyces cerevisiae)  
 C/Species: Saccharomyces cerevisiae  
 C/Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 05-Oct-2004  
 C/Accession: S46817  
 R/Favell, T.  
 submitted to the EMBL Data Library, June 1994  
 A/Description: The sequence of S. cerevisiae cosmid 9205.  
 A/Reference number: S46795  
 A/Accession: S46817  
 A/Molecule type: DNA  
 A/Residues: 1-1345 <FAV>  
 A/Cross-references: UNIPROT:P38800; UNIPARC:UPI000013B2B1; EMBL:U10556; NID:g500825; PIR  
 C/Genetics:  
 A/Cross-references: SGD:S0001122  
 A/Map position: 8R  
 C/Superfamily: uncharacterized conserved protein  
 C/Keywords: transmembrane protein

Query Match 74.5% Score 35; DB 2; Length 1345;  
 Best Local Similarity 85.7%; Pred. No. 5e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DYKDDDD 7  
 |||||  
 DB 691 DYGDddd 697

## RESULT 42

RN202L  
 DNA-directed RNA polymerase (EC 2.7.7.6) II large chain - malaria parasite (Plasmodium f  
 C/Species: Plasmodium falciparum  
 C/Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
 C/Accession: S07485  
 R/Li, W.B.; Bzik, D.J.; Gu, H.; Tanaka, M.; Fox, B.A.; Inselburg, J.  
 Nucleic Acids Res. 17, 9621-9636, 1989  
 A/Title: An enlarged largest subunit of Plasmodium falciparum RNA polymerase II defines

A/Reference number: S07485; MUID:90098832; PMID:2690004  
 A/Accession: S07485  
 A/Molecule type: DNA  
 A/Residues: 1-2452 <LTM>  
 A/Cross-references: UNIPROT:P14248; UNIPARC:UPI00001345CB; EMBL:X16561; NID:g9942; PID  
 C/Genetics:  
 A/Map position: 3  
 C/Superfamily: Plasmodium DNA-directed RNA polymerase II large chain  
 C/Keywords: DNA binding; nucleotidyltransferase; phosphoprotein; tandem repeat; transc  
 F/68-84/Region: zinc finger CCH motif  
 F/2247-2384/Region: 7-residue repeats  
 F/376/Binding site: ATP/GTP (Lys) #status predicted

Query Match 74.5% Score 35; DB 1; Length 2452;  
 Best Local Similarity 85.7%; Pred. No. 9.3e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DYKDDDD 7  
 |||||  
 DB 1264 DYVDDDD 1270

## RESULT 43

D71614  
 hypothetical protein PFB0460C - malaria parasite (Plasmodium falciparum)  
 C/Species: Plasmodium falciparum  
 C/Date: 13-Nov-1998 #sequence\_revision 13-Nov-1998 #text\_change 09-Jul-2004  
 C/Accession: D71614  
 R/Gardner, M.J.; Tetteh, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V  
 ; Pettes, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.C  
 Science 282, 1126-1132, 1998  
 A/Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.  
 A/Reference number: A71600; MUID:95021743; PMID:9804551  
 A/Accession: D71614  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-2573 <GAR>  
 A/Cross-references: UNIPROT:O96185; UNIPARC:UPI0000079076; GB:AE001396; GB:AE001362; N  
 A/Experimental source: clone 3D7  
 C/Genetics:  
 A/Gene: PFB0460C

Query Match 74.5% Score 35; DB 2; Length 2573;  
 Best Local Similarity 85.7%; Pred. No. 9.8e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
 |||||  
 DB 1331 DYVDDDD 1337

## RESULT 44

T32477  
 hypothetical protein F52H2.3 - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
 C/Accession: T32477  
 R/Chisoe, S.; Hawkins, J.  
 submitted to the EMBL Data Library, September 1997  
 A/Description: The sequence of C. elegans cosmid F52H2.  
 A/Reference number: 221175  
 A/Accession: T32477  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-140 <CHI>  
 A/Cross-references: UNIPROT:Q17393; UNIPARC:UPI0000074F66; EMBL:AF026214; PIDN:AAB71313  
 A/Experimental source: strain Bristol N2; clone F52H2  
 C/Genetics:  
 A/Gene: CESP:F52H2.3  
 A/Map position: X  
 A/Intons: 45/3; 88/2

Query Match 72.3% Score 34; DB 2; Length 140;

Best Local Similarity 100.0%; Pred. No. 68;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KDDDDK 8  
|:|||||  
Db 124 KDDDDK 129

## RESULT 45

A:Residues: 1-165 <THO>  
A:Cross-references: UNIPROT:P14200; UNIPARC:UPI000012P1D6; GB:M62641; NID:G205329; PIDN:  
R:Mahon, J.L.; Presse, F.; Bittencourt, J.C.; Sawchenko, P.E.; Vale, W.  
Endocrinology 125, 2056-2065, 1989  
A:Title: The rat melanin-concentrating hormone messenger ribonucleic acid encodes multiple  
A:Reference number: A37407; MUID:90005146; PMID:2477226  
A:Accession: A37407  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-165 <NMH>  
A:Cross-references: UNIPARC:UPI000012P1D6; GB:M29712; NID:G205327; PIDN:AAA41580.1; PID:  
R:Vaughan, J.M.; Fischer, W.H.; Hoeger, C.; Rivier, J.; Vale, W.  
Endocrinology 125, 1660-1665, 1989  
A:Title: Characterization of melanin-concentrating hormone from rat hypothalamus.  
A:Reference number: A37406; MUID:9338286; PMID:2759038  
A:Accession: A37406  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 147-165 <VAN>  
A:Cross-references: UNIPARC:UPI0000037310  
C:Superfamily: melanin-concentrating hormone

Query Match 72.3%; Score 34; DB 2; Length 165;  
Best Local Similarity 100.0%; Pred. No. 80;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KDDDDK 8  
|:|||||  
Db 75 KDDDDK 80

## RESULT 46

A:Residues: 1-177 <DOB>  
A:Cross-references: UNIPROT:P07249; UNIPARC:UPI0000125DF0; EMBL:X05327; NID:G3373; PIDN:  
R:Odell, C.; Bowman, S.  
submitted to the EMBL Data Library, February 1995  
A:Reference number: S52885  
A:Accession: S52891  
A:Molecule type: DNA

A:Residues: 1-177 <DOB>  
A:Cross-references: UNIPROT:P07249; UNIPARC:UPI0000125DF0; EMBL:X05327; NID:G3373; PIDN:  
R:Odell, C.; Bowman, S.  
submitted to the EMBL Data Library, February 1995  
A:Reference number: S52885  
A:Accession: S52891  
A:Molecule type: DNA

A:Residues: 1-177 <DOB>  
A:Cross-references: UNIPROT:P07249; UNIPARC:UPI0000125DF0; EMBL:X05327; NID:G3373; PIDN:  
R:Odell, C.; Bowman, S.  
submitted to the EMBL Data Library, February 1995  
A:Reference number: S52885  
A:Accession: S52891  
A:Molecule type: DNA

A:Residues: 1-177 <ODE>  
A:Cross-references: UNIPARC:UPI0000125DF0; EMBL:Z48502; NID:G695715; PIDN:CAA8408.1; P  
C:Genetics:  
A:Gene: SGD:ARG80; ARG1; MIPS:YMR042W  
A:Cross-references: SGD:S0004645; MIPS:YMR042W  
A:Map position: 13R  
C:Function:  
A:Description: required for arginine-dependent activation of CAR1  
C:Superfamily: regulatory protein ARG1; serum response factor DNA-binding domain homol  
C:Keywords: DNA binding; nucleus; transcription regulation  
F:79-134/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 72.3%; Score 34; DB 1; Length 177;  
Best Local Similarity 75.0%; Pred. No. 86;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
|:|||||  
Db 47 DEEDDDK 54

## RESULT 47

T15725  
hypothetical protein C31H1.2 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 31-Dec-2004  
C:Accession: T15725  
R:le, T.  
submitted to the EMBL Data Library, December 1995  
A:Description: The sequence of C. elegans cosmid C31H1.  
A:Reference number: Z18395  
A:Accession: T15725  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1197 <LEF>  
A:Cross-references: UNIPROT:Q18337; UNIPARC:UPI0000077BCA; EMBL:U42848; NID:G1125817; P  
A:Gene: CESP:C31H1.2  
A:Introns: 21/1; 98/3; 130/3; 143/1; 178/3

Query Match 72.3%; Score 34; DB 2; Length 197;  
Best Local Similarity 71.4%; Pred. No. 97;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
|:|||||  
Db 185 EYQDDDD 191

## RESULT 48

S46286  
RNA-binding protein - wood tobacco

C:Species: Nicotiana sylvestris (wood tobacco)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: S46286  
R:Hirose, T.; Sugita, M.; Sugitara, M.  
Mol. Gen. Genet. 244, 360-366, 1994  
A:Title: Characterization of a cDNA encoding a novel type of RNA-binding protein in tob  
A:Reference number: S46286; MUID:94359458; PMID:8078461  
A:Accession: S46286  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-259 <HR>  
A:Cross-references: UNIPROT:Q40436; UNIPARC:UPI00000A96B4; GB:D26182; NID:G575607; PIDN  
C:Superfamily: wood tobacco RNA-binding protein; ribonucleoprotein repeat homology  
F:41-108/Domain: ribonucleoprotein repeat homology <RNM1>

Query Match 72.3%; Score 34; DB 1; Length 259;  
Best Local Similarity 71.4%; Pred. No. 1.3e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDK 8  
|:|||||



Db 244 YRDDDE 250

## RESULT 49

T52379

Zinc finger protein ZPT3-3 [imported] - garden petunia

C/Species: Petunia x hybrida (garden petunia)

C/Date: 24-Oct-2000 #sequence\_revision 24-Oct-2000 #text\_change 09-Jul-2004

C/Accession: T52379

R/Kibo, K.; Sakamoto, A.; Kobayashi, A.; Rybka, Z.; Kanno, Y.; Nakagawa, H.; Nishino, T.

Nucleic Acids Res. 26, 608-615, 1998

A/Title: Cys2/His2 zinc-finger protein family of petunia: evolution and general mechanism

A/Reference number: 226061

A/Accession: T52379

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-300 &lt;KDB&gt;

A/Cross-references: UNIPROT:O22090; UNIPARC:UPI00000ACAC2C; EMBL:AB06605; PIDN:BAA21927.

A/Experimental source: strain Mitchell diploid

C/Superfamily: Arabidopsis thaliana hypothetical protein F12E4.290

Query Match 72.3%; Score 34; DB 2; Length 300;

Best Local Similarity 62.5%; Pred. No. 1.5e+02;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8

Db 141 DYSDDE 148

## RESULT 50

T24387

Probable cysteine proteinase (EC 3.4.22.-) T03E6.7 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C/Accession: T24387

R/Lloyd, C.

Submitted to the EMBL Data Library, March 1997

A/Reference number: Z19885

A/Accession: T24387

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-337 &lt;MTL&gt;

A/Cross-references: UNIPROT:O45734; UNIPARC:UPI000007623; EMBL:Z52812; PIDN:CAB07275.1;

A/Experimental source: clone T03E6

C/Genetics:

A/Gene: CESP.T03E6.7

A/Map position: 5

A/Introns: 86/3; 119/3; 269/1

C/Superfamily: papain

C/Keywords: cysteine proteinase; hydrolase

F;144,283,304/Active site: Cys, His, Asn #status predicted

Query Match 72.3%; Score 34; DB 2; Length 337;

Best Local Similarity 75.0%; Pred. No. 1.7e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8

Db 34 DYKEDPK 41

## RESULT 51

T48564

Probable serine rich protein - Arabidopsis thaliana

N/Alternate names: protein F14F18.220

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004

C/Accession: T48564

R/Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft,

submitted to the Protein Sequence Database, April 2000

A/Reference number: Z24490

A/Accession: T48564

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-362 &lt;BEV&gt;

A/Cross-references: UNIPROT:Q9LTH0; UNIPARC:UPI000009E7C1; EMBL:AL163812

A/Experimental source: cultivar Columbia; BAC clone F14F18

A/Map position: 5

A/Note: F14F18.220

Query Match 72.3%; Score 34; DB 2; Length 362;

Best Local Similarity 71.4%; Pred. No. 1.8e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 7

Db 310 DYEDDE 316

## RESULT 52

S45766

Hypothetical protein YBL032w - yeast (Saccharomyces cerevisiae)

N/Alternate names: hypothetical protein YBL0418

C/Species: Saccharomyces cerevisiae

C/Date: 26-Aug-1994 #sequence\_revision 09-Sep-1994 #text\_change 09-Jul-2004

C/Accession: S45766; S50299

R/Goffeau, A.; Jonniaux, J.L.; Purnelle, B.; Skala, J.; de Wergifosse, P.; van Dyck, L

submitted to the Protein Sequence Database, August 1994

A/Reference number: S45745

A/Accession: S45766

A/Molecule type: DNA

A/Residues: 1-381 &lt;GOF&gt;

A/Cross-references: UNIPROT:P38199; UNIPARC:UPI000005318E; EMBL:Z35793; NID:g536038; PI

A/Experimental source: strain S288C

R/van Dyck, L.; Jonniaux, J.L.; de Melo Barreiros, T.; Kleine, K.; Goffeau, A.

Yeast 10, 1663-1673, 1994

A/Title: Analysis of a 17.4 kb DNA segment of yeast chromosome II encompassing the ribc

human proliferation-associated p120 antigen.

A/Reference number: S50299; MUID:95242843; PMID:7725803

A/Accession: S50299

A/Molecule type: DNA

A/Residues: 1-381 &lt;VAN&gt;

A/Cross-references: UNIPARC:UPI000005318E; EMBL:X77291; NID:g602888; PIDN:CAA54496.1; F

A/Experimental source: strain S288C

C/Genetics:

A/Cross-references: SGD:S0000128

A/Map position: ZL

Query Match 72.3%; Score 34; DB 2; Length 381;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KDDDDK 8

Db 297 KDDDDK 302

## RESULT 53

T05781

Hypothetical protein M4E13.160 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004

C/Accession: T05781

R/Bevan, M.; Purnelle, B.; Boutry, M.; Goffeau, A.; Hohnsels, J.; Mewes, H.W.; Mayer, K

submitted to the Protein Sequence Database, April 1998

A/Reference number: Z15451

A/Accession: T05781

A/Molecule type: DNA

A/Residues: 1-386 &lt;BEV&gt;

A/Cross-references: UNIPROT:O49617; UNIPARC:UPI00000AC134; EMBL:AL022023

A/Experimental source: cultivar Columbia; BAC clone M4E13

A/Map position: 4

A/Introns: 42/1; 140/3

A>Note: M4E13.160

Query Match 72.3%; Score 34; DB 2; Length 386;  
Best Local Similarity 62.5%; Pred. No. 2e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8

DB 185 DFSDDDDE 192

RESULT 54

T26987

hypothetical protein Y48A6B.13 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C/Accession: T26987

R/Gardner, A.

submitted to the EMBL Data Library, June 1998

A/Reference number: Z20295

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-396 <WIL>

A/Cross-references: UNIPROT:Q9XXC7; UNIPARC:UPI000007A333; EMBL:AL023844; PIDN:CAA19534.

C/Genetics:

A/Gene: CRSP:Y48A6B.13

A/Map position: 3

A/Introns: 11/2; 48/3; 224/3; 298/1; 387/1

Query Match

Best Local Similarity 71.4%; Pred. No. 2e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7

DB 71 NYRDDDD 77

RESULT 55

T23899

hypothetical protein R04D3.3 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C/Accession: T23899

R/Swinburne, J. submitted to the EMBL Data Library, March 1996

A/Reference number: Z19815

A/Accession: T23899

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1430 <WIL>

A/Cross-references: UNIPROT:Q21713; UNIPARC:UPI000007D6C1; EMBL:Z70212; PIDN:CAA94163.1;

C/Genetics:

A/Gene: CRSP:R04D3.3

A/Map position: X

A/Introns: 108/3; 296/3; 352/3

Query Match

Best Local Similarity 71.4%; Pred. No. 2.2e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7

DB 339 DYEDDD 345

RESULT 56

A85363

probable calmodulin-binding protein [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 31-Dec-2004

C/Accession: A85363

R/Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Harbor Laboratory, 1999

A/Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A/Reference number: A85001; MIMD:20083488; PMID:10617198

A/Accession: A85363

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-467 <SNO>

A/Cross-references: UNIPROT:O65550; UNIPARC:UPI00000AB646; GB:NC\_001268; NID:G7270002;

C/Genetics:

A/Gene: AT4G31000

A/Map position: 4

C/Superfamily: Calmodulin-binding protein

Query Match 72.3%; Score 34; DB 2; Length 467;

Best Local Similarity 62.5%; Pred. No. 2.4e+02;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8

DB 55 DFNDEDDK 62

RESULT 57

S66713

hypothetical protein YOL030W - yeast (Saccharomyces cerevisiae)

N/Alternate names: hypothetical protein O2145

C/Species: Saccharomyces cerevisiae

C/Date: 12-Jul-1996 #sequence\_revision 12-Jul-1996 #text\_change 09-Jul-2004

C/Accession: S66713

R/Habib, B.; Hattenhorst, U.; Hollenberg, C.P.; Ramezani Rad, M.

submitted to the Protein Sequence Database, July 1996

A/Reference number: S66703

A/Accession: S66713

A/Molecule type: DNA

A/Residues: 1-484 <HAB>

A/Cross-references: UNIPROT:Q08193; UNIPARC:UPI000013BC67; EMBL:Z74772; NID:G1419818; P

C/Genetics:

A/Gene: MIPS:YOL030W

A/Cross-references: SGD:S0005390

A/Map position: 15L

C/Superfamily: glycopospholipid-anchored surface glycoprotein GAS1

Query Match 72.3%; Score 34; DB 2; Length 484;

Best Local Similarity 75.0%; Pred. No. 2.5e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8

DB 392 DAKDDDE 399

RESULT 58

S36494

E2 protein - human papillomavirus type 25

C/Species: human papillomavirus type 25

C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004

C/Accession: S36494

R/Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A/Description: Primer-directed sequencing of human papillomavirus types.

A/Reference number: S36469

A/Accession: S36494

A/Molecule type: DNA

A/Residues: 1-502 <DEB>

A/Cross-references: UNIPROT:P36787; UNIPARC:UPI0000138340; EMBL:X74471; NID:G396948; PI

C/Superfamily: papillomavirus E2 protein

C/Keywords: DNA binding; early protein; transcription regulation

Query Match 72.3%; Score 34; DB 2; Length 502;

Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 YKDDDDK 8  
DB 139 YVDDDDK 145

## RESULT 59

T10660

hypothetical C2H2-type zinc-finger protein - fission yeast (Schizosaccharomyces pombe)

C/Species: Schizosaccharomyces pombe  
C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C/Accession: T10660

R/Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, W.  
submitted to the EMBL Data Library, November 1998

A/Reference number: Z21889  
A/Accession: T10660

A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA

A/Residues: 1-609 <L/N>  
A/Cross-references: UNIPROT:O94326; UNIPARC:UPI000006C388; EMBL:AL034352; PIDD:CAA22180.

A/Experimental source: strain 972h-; cosmid c725  
C/Genetics:

A/Gene: SPDB:SPBC725.08  
A/Map position: 2

A/Intons: 22/1; 58/1; 68/2  
C/Superfamily: Schizosaccharomyces hypothetical C2H2-type zinc-finger protein

Query Match 72.3%; Score 34; DB 2; Length 609;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KDDDDK 8  
DB 359 KDDDDK 364

## RESULT 60

T10862

phaeosolin G-box binding protein pg2 - kidney bean (fragment)

C/Species: Phaseolus vulgaris (kidney bean)  
C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 31-Dec-2004

C/Accession: T10862

R/Kawagoe, Y.; Murai, N.  
Plant Physiol. 117, 720, 1998

A/Title: FBP2, a second bHLH protein binding to the E-box motif of the bean seed-storage

A/Reference number: Z17191  
A/Accession: T10862  
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA  
A/Residues: 1-614 <KAW>  
A/Cross-references: UNIPROT:Q41102; UNIPARC:UPI00000A8095; EMBL:U18349; NID:G1142620; PI

A/Experimental source: strain Contender  
C/Genetics:

A/Gene: PG2  
A/Function: transcription factor  
C/Superfamily: BHLH containing MYC-related DNA binding protein

Query Match 72.3%; Score 34; DB 2; Length 614;  
Best Local Similarity 85.7%; Pred. No. 3.2e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YKDDDDK 8  
DB 43 YKDDDDK 49

## RESULT 61

T13674

hypothetical protein EG0002.1 - fruit fly (Drosophila melanogaster)  
C/Species: Drosophila melanogaster

C/Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004  
C/Accession: T13674

R/Bolshakov, V.; Borkova, D.; Minna, B.; Kafatos, F.  
submitted to the EMBL Data Library, September 1998

A/Description: Sequencing the distal X chromosome of Drosophila melanogaster.  
A/Reference number: Z17698

A/Accession: T13674  
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA  
A/Residues: 1-734 <BOL>

A/Cross-references: UNIPROT:O77282; UNIPARC:UPI0000075017; EMBL:AL031130; PIDD:CAA20015  
C/Genetics:

A/Cross-references: FlyBase:FBgn0025376  
A/Intons: 18/3; 46/1; 122/2

A/Note: EG:EG0002.1  
C/Superfamily: peptide transport protein PEPT1

Query Match 72.3%; Score 34; DB 2; Length 734;  
Best Local Similarity 71.4%; Pred. No. 3.9e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
DB 681 DFEDDDD 687

## RESULT 62

T13673

hypothetical protein EG0002.1 - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster  
C/Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004

C/Accession: T13673  
R/Bolshakov, V.; Borkova, D.; Minna, B.; Kafatos, F.

submitted to the EMBL Data Library, September 1998  
A/Description: Sequencing the distal X chromosome of Drosophila melanogaster.  
A/Reference number: Z17698

A/Accession: T13673  
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA  
A/Residues: 1-743 <BOL>

A/Cross-references: UNIPROT:Q9W4P7; UNIPARC:UPI000016BB3A; EMBL:AL031130; PIDD:CAA20014  
C/Genetics:

A/Cross-references: FlyBase:FBgn0025376  
A/Intons: 27/3; 55/1; 131/2

A/Note: EG:EG0002.1  
C/Superfamily: peptide transport protein PEPT1

C/Keywords: alternative splicing  
Query Match 72.3%; Score 34; DB 2; Length 743;  
Best Local Similarity 71.4%; Pred. No. 3.9e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
DB 690 DFEDDDD 696

## RESULT 63

A84833

hypothetical protein At2g40720 [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004

C/Accession: A84833  
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanKien, S.E.; Umeyam, L.; Tallon, L.  
eues, D.; Nierman, W.C.; White, O.; Eissen, J.A.; Salberg, S.L.; Fraser, C.M.; Venter,  
Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A/Reference number: A84420; MUID:20083487; PMID:10617197

A/Accession: A84833  
A/Status: preliminary

A/Molecule type: DNA  
A/Residues: 1-860 <STO>

A:/Cross-references: UNIPROT:Q7XJN6; UNIPARC:UPI00001623FA; GB:AE002093; NID:g4895221; P  
C:/Species: Arabidopsis thaliana (mouse-ear cross)  
A:/Gene: At2g40720  
A:/Map position: 2

Query Match 72.3%; Score 34; DB 2; Length 860;  
Best Local Similarity 85.7%; Pred. No. 4.6e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
Db 464 DKMDDDD 470

RESULT 64  
E96508  
hypothetical protein T12C22.19 [imported] - Arabidopsis thaliana  
C:/Species: Arabidopsis thaliana (mouse-ear cross)  
C:/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:/Accession: E96508

R:/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Hutzar, L.  
Nature 408, 816-820, 2000

A:/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:/Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:/Reference number: A86141; MUID:21016719; PMID:11130712

A:/Accession: E96508  
A:/Status: preliminary  
A:/Molecule type: DNA  
A:/Residues: 1-936 <STO>  
A:/Cross-references: UNIPROT:Q9LPP9; UNIPARC:UPI00000AA9E4; GB:AE005173; NID:98656002; P  
C:/Species: Arabidopsis thaliana (mouse-ear cross)  
A:/Gene: T12C22.19  
A:/Map position: 1  
C:/Superfamily: replication licensing factor MCM2; MCM homology

Query Match 72.3%; Score 34; DB 2; Length 936;  
Best Local Similarity 71.4%; Pred. No. 5e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
Db 183 DYDDEDD 189

RESULT 65  
A41996  
NF-kappa-B p50 subunit precursor p105 - chicken  
C:/Species: Gallus gallus (chicken)  
C:/Date: 06-Nov-1992 #sequence\_revision 06-Nov-1992 #text\_change 09-Jul-2004  
C:/Accession: A41996

R:/Capiolano, A.J.; Chang, D.; Mosialos, G.; Gilmore, T.D.  
J. Virol. 66, 3758-3767, 1992  
A:/Title: p105, the NF-kappa-B p50 precursor protein, is one of the cellular proteins com  
A:/Reference number: A41996; MUID:92260650; PMID:11533881

A:/Accession: A41996  
A:/Status: preliminary  
A:/Molecule type: mRNA  
A:/Residues: 1-984 <CMP>

A:/Cross-references: UNIPROT:Q04861; UNIPARC:UPI000012DC52; GB:M66930; NID:g212525; P1DN;  
C:/Superfamily: human transcription factor NF-kappa-B2; ankryrin repeat homology; rel hom  
C:/Keywords: DNA binding; nucleus; phosphoprotein; transcription regulation  
F:/47-371/Domain: rel homology <REL>

F:/366-370/Region: nuclear location signal  
F:/342/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predic  
Query Match 72.3%; Score 34; DB 2; Length 984;  
Best Local Similarity 85.7%; Pred. No. 5.3e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 DYKDDDD 7  
Db 757 DYKDDDD 763

RESULT 66  
T18257  
phospholipase C - yeast (Candida albicans)

C:/Species: Candida albicans  
C:/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:/Accession: T18257

R:/Bennett, D.E.; McCreary, C.E.; Coleman, D.C.  
Microbiology 144, 55-72, 1998  
A:/Title: Genetic characterization of a phospholipase C gene from Candida albicans: pres  
A:/Reference number: Z18844; MUID:98129081; PMID:9467900

A:/Accession: T18257  
A:/Status: preliminary; translated from GB/EMBL/DBJ  
A:/Molecule type: DNA  
A:/Residues: 1-1099 <BER>

A:/Cross-references: UNIPROT:O13433; UNIPARC:UPI000011BCA; EMBL:Y13975; NID:g2462981; P  
C:/Species: Candida albicans  
A:/Gene: PLC1  
F:/566-726/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X h

Query Match 72.3%; Score 34; DB 2; Length 1099;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KDDDDK 8  
Db 628 KDDDDK 633

RESULT 67

C96761  
hypothetical protein T9L24.35 [imported] - Arabidopsis thaliana  
C:/Species: Arabidopsis thaliana (mouse-ear cross)  
C:/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C:/Accession: C96761  
R:/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.  
ansen, N.F.; Hughes, B.; Hutzar, L.  
Nature 408, 816-820, 2000

A:/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:/Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:/Reference number: A86141; MUID:21016719; PMID:11130712

A:/Accession: C96761  
A:/Status: preliminary  
A:/Molecule type: DNA  
A:/Residues: 1-1157 <STO>

A:/Cross-references: UNIPROT:Q9FX39; UNIPARC:UPI000009E7EF; GB:AE005173; NID:g11120792;  
C:/Species: Arabidopsis thaliana (mouse-ear cross)  
A:/Gene: T9L24.35  
A:/Map position: 1

Query Match 72.3%; Score 34; DB 2; Length 1157;  
Best Local Similarity 71.4%; Pred. No. 6.2e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
Db 421 EYEDDD 427

RESULT 68

AF2005  
RNA polymerase beta prime chain [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C:Accession: AF2005  
R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shimoto, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
DNA Res. 8, 205-215, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120  
A:Accession: AF2005  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1350 <KOR>  
A:Cross-references: UNIPROT:P22705; UNIPARC:UPI00001655C2; GB:BA000019; PIDN:BAW77962.1;  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: rpoC2  
C:Superfamily: chloroplast DNA-directed RNA polymerase beta'-2 chain

Query Match 72.3%; Score 34; DB 2; Length 1350;  
Best Local Similarity 71.4%; Pred. No. 7.3e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDD 7  
Db 1337 DYEDDDE 1343

RESULT 69  
S63244  
BNI1 protein - yeast (Saccharomyces cerevisiae)  
A:Alternate names: protein N0646; protein YNL271C  
C:Species: Saccharomyces cerevisiae  
C:Date: 27-Apr-1996 #sequence\_revision 03-May-1996 #text\_change 09-Jul-2004  
C:Accession: S63244; S63245; S48523; S60909; S65111  
R:Sen-Gupta, M.; Lyck, R.; Niedenthal, R.K.; Fleig, U.N.; Hegemann, J.H.  
submitted to the Protein Sequence Database, April 1996  
A:Reference number: S63235  
A:Accession: S63244  
A:Molecule type: DNA  
A:Residues: 1-1553 <SEN>  
A:Cross-references: UNIPROT:P41832; UNIPARC:UPI0000168B2A; EMBL:Z71547; MIPS:YNL271C  
A:Experimental source: strain S288C  
R:Messenguy, F.; Dubois, E.; Viereckels, F.; Scherens, B.; Pierard, A.; Glandsdorff, N.  
submitted to the Protein Sequence Database, April 1996  
A:Reference number: S63245  
A:Accession: S63245  
A:Molecule type: DNA  
A:Residues: 987-1953 <MES>  
A:Cross-references: UNIPARC:UPI000017B262; EMBL:Z71547; MIPS:YNL271C  
A:Experimental source: strain S288C  
R:Pares, H.P.; Pringle, J.R.  
submitted to the EMBL Data Library, April 1994  
A:Description: Synthetic lethals of CDC12.  
A:Reference number: S48524  
A:Accession: S48523  
A:Molecule type: DNA  
A:Residues: 1-937, 'A', 939-1429, 'C', 1431-1953 <PAR>  
A:Cross-references: UNIPARC:UPI0000168B2A; EMBL:X92494; NID:g1045236; PIDN:AAA4455.1; PI  
R:Sen-Gupta, M.; Lyck, R.; Fleig, U.; Niedenthal, R.N.; Hegemann, J.M.  
submitted to the EMBL Data Library, October 1995  
A:Description: The sequence of a 24152 bp segment from the left arm of chromosome XIV fr  
A:Reference number: S60909  
A:Accession: S60909  
A:Molecule type: DNA  
A:Residues: 1-1553 <SE2>  
A:Cross-references: UNIPARC:UPI0000168B2A; EMBL:X92494; NID:g1045236; PIDN:CAA63225.1; B  
R:Sen-Gupta, M.; Lyck, R.; Fleig, U.; Niedenthal, R.K.; Hegemann, J.H.  
Yeast 12, 505-514, 1996  
A:Title: The sequence of a 24 152 bp segment from the left arm of chromosome XIV from Sa  
A:Reference number: S65111; MUID:96310631; PMID:8740425  
A:Accession: S65111  
A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA  
A:Residues: 1-1553 <SEW>  
A:Cross-references: UNIPARC:UPI0000168B2A; EMBL:X92494; NID:g1045236; PIDN:CAA63225.1;  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995  
C:Genetics:  
A:Gene: SGD:BN1; SHE5; SYL39  
A:Cross-references: SGD:S0005215; MIPS:YNL271C  
A:Map position: 14L

Query Match 72.3%; Score 34; DB 2; Length 1953;  
Best Local Similarity 75.0%; Pred. No. 1.1e+03;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8  
Db 849 DYKDDSKK 856

RESULT 70  
T18440  
hypothetical protein C0425W - malaria parasite (Plasmodium falciparum)  
C:Species: Plasmodium falciparum  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T18440  
R:Lawson, D.; Bowman, S.; Barrell, B.  
submitted to the EMBL Data Library, August 1997  
A:Reference number: Z18935  
A:Accession: T18440  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-4550 <LAW>  
A:Cross-references: UNIPROT:O77336; UNIPARC:UPI0000110116; EMBL:Z98547; NID:e1325376; I  
C:Genetics:  
A:Map position: 3  
A:Note: C0425W

Query Match 72.3%; Score 34; DB 2; Length 4550;  
Best Local Similarity 75.0%; Pred. No. 2.6e+03;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8  
Db 3543 DYKDDNDK 3550

RESULT 71  
S76216  
hypothetical protein - Synechocystis sp. (strain PCC 6803)  
C:Species: Synechocystis sp.  
A:Variety: PCC 6803  
C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C:Accession: S76216  
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N  
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yaeu  
DNA Res. 3, 109-136, 1996  
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocyst  
A:Reference number: S74322; MUID:97061201; PMID:8905231  
A:Accession: S76216  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-125 <KAN>  
A:Cross-references: UNIPROT:P74379; UNIPARC:UPI00000C0D6F; EMBL:D90914; GB:AB001339; NI  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C:Genetics:  
A:Start codon: GTG

Query Match 70.2%; Score 33; DB 2; Length 125;  
Best Local Similarity 62.5%; Pred. No. 88;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8

Db 44 DYQDDHDR 51

# RESULT 72

JK0313

dnak-type molecular chaperone mag29 - house-dust mite (Dermatophagoides farinae)  
N/Alternate names: mite allergen mag 29 protein

C/Species: Dermatophagoides farinae

C/Date: 28-Aug-1985 #sequence\_revision 07-Oct-1994 #text\_change 31-Dec-2004

C/Accession: JK0313, PC2125

R/Aki, T.; Fujikawa, A.; Wada, T.; Uyo, T.; Shigeta, S.; Murooka, Y.; Oka, S.; Ono, K.

J. Biochem. 115, 435-440, 1994

A/Title: Cloning and expression of cDNA coding for a new allergen from the house dust mite.

A/Reference number: JK0313; MUID:94334283; PMID:8056755

A/Accession: JK0313

A/Molecule type: mRNA

A/Residues: 1-145 <AK11>

A/Cross-references: UNIPROT:P39674; UNIPARC:UPI0000128AEB; DDBJ:D17676; NID:9642918; PID

A/Note: the nucleotide sequence for this amino acid sequence is inconsistent with that of

A/Accession: PC2125

A/Molecule type: protein

A/Residues: 1-17 <AK2>

A/Cross-references: UNIPARC:UPI0000177D21

C/Genetics:

A/Gene: mag29

C/Function:

A/Description: involved in protein folding and assembling/disassembling of protein comp

C/Superfamily: bcr protein

C/Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 70.2%; Score 33; DB 2; Length 145;

Best Local Similarity 71.4%; Pred. No. 1e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDK 8

Db 14 YKEDDK 20

# RESULT 73

B46315

E4 protein - human papillomavirus type 4

C/Species: human papillomavirus type 4

C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 16-Jul-1999

C/Accession: B46315

R/Doordat, J.; Coneron, I.; Gallimore, P.H.

Virology 172, 51-62, 1989

A/Title: Sequence divergence yet conserved physical characteristics among the E4 protein

A/Reference number: A46315; MUID:89370332; PMID:2549722

A/Accession: B46315

A/Molecule type: DNA

A/Residues: 1-147 <DOO>

A/Cross-references: UNIPARC:UPI00000F4EFO; GB:M28744; NID:9333136; PIDN:AAA47015.1; PID:

C/Superfamily: papillomavirus type 4 E4 protein

C/Keywords: early protein

Query Match 70.2%; Score 33; DB 1; Length 147;

Best Local Similarity 62.5%; Pred. No. 1e+02;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8

Db 78 DYEDDK 85

# RESULT 74

E69077

hypothetical protein MTH1578 - Methanobacterium thermoautotrophicum (strain Delta H)

C/Species: Methanobacterium thermoautotrophicum

C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004

C/Accession: E69077

R/Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;

; Oiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N

Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

J. Bacteriol. 179, 7135-7155, 1997

A/Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func

A/Reference number: A69000; MUID:98037514; PMID:9371463

A/Accession: E69077

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-151 <MTH>

A/Cross-references: UNIPROT:Q27619; UNIPARC:UPI000062BDE; GB:AE000918; GB:AE000666; NI

A/Experimental source: strain Delta H

C/Genetics:

A/Gene: MTH1578

Query Match 70.2%; Score 33; DB 2; Length 151;

Best Local Similarity 83.3%; Pred. No. 1.1e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDD 6

Db 69 DYRDD 74

# RESULT 75

S59766

hypothetical protein YPR101w - yeast (Saccharomyces cerevisiae)

N/Alternate names: hypothetical protein P8283.11

C/Species: Saccharomyces cerevisiae

C/Date: 11-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004

C/Accession: S59766

R/Nelson, J.

submitted to the EMBL Data Library, July 1995

A/Description: The sequence of S. cerevisiae cosmid 8283.

A/Reference number: S59764

A/Accession: S59766

A/Molecule type: DNA

A/Residues: 1-175 <NEL>

A/Cross-references: UNIPROT:Q06091; UNIPARC:UPI00000531P2; EMBL:U32445; NID:9914969; PI

C/Genetics:

A/Gene: SGD:SWT109; MIPS:YPR101w

A/Cross-references: SGD:S0006305

A/Map position: 16R

C/Superfamily: Saccharomyces cerevisiae hypothetical protein YPR101w

Query Match 70.2%; Score 33; DB 2; Length 175;

Best Local Similarity 71.4%; Pred. No. 1.3e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7

Db 78 DFNDDD 84

# RESULT 76

A61442

translation elongation factor eEF-1 beta chain - pig (fragments)

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 09-Jul-2004

C/Accession: A61442

R/Amos, R.; Schipper, A.; van Damme, H.; Kriek, J.; Moeller, W.

J. Protein Chem. 11, 404, 1992

A/Title: The primary structure of elongation factor 1beta from pig liver.

A/Reference number: A61442

A/Accession: A61442

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-188 <AMO>

A/Cross-references: UNIPROT:Q7M397; UNIPARC:UPI00001782A2

C/Superfamily: translation elongation factor eEF-1 beta chain; translation elongation f

Query Match 70.2%; Score 33; DB 2; Length 188;

Best Local Similarity 85.7%; Pred. No. 1.4e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
| | | | |  
Db 88 DSKDDDD 94

## RESULT 77

T43013  
conserved hypothetical protein SPCC645.03c - fission yeast (Schizosaccharomyces pombe)  
C/Species: Schizosaccharomyces pombe  
C/Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004  
C/Accession: T43013; T41520  
R/Ioshioaka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.  
DNA Res. 4, 363-369, 1997  
A/Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.  
A/Reference number: Z17323; MUID:98162722; PMID:9501991  
A/Accession: T43013  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-190 <YOS>  
A/Cross-references: UNIPROT:P78859; UNIPARC:UPI000013A6A4; EMBL:D89209; NID:g1749625; PI  
R/Mood, V.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.  
submitted to the EMBL Data Library, March 1999  
A/Reference number: Z22000  
A/Accession: T41520  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-190 <MOO>  
A/Cross-references: UNIPARC:UPI000013A6A4; EMBL:AL049498; PIDN:CAB39899.1; GSPDB:GN00068  
C/Experimental source: strain 972h-; cosmid c645  
C/Genetics:  
A/Gene: SPCC645.03c  
A/Map position: 3  
A/Introns: 85/3

Query Match  
Best Local Similarity 83.3%; Score 33; DB 2; Length 190;  
Pred. No. 1.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 6  
| | | | |  
Db 159 DYRDDD 164

## RESULT 78

S36720  
FUN34 protein - yeast (Saccharomyces cerevisiae)  
N/Alternate names: protein YAL014c  
C/Species: Saccharomyces cerevisiae  
C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C/Accession: S36720  
R/Ouellette, F.; Clark, M.W.; Keng, T.; Storms, R.K.; Zhong, W.; Zeng, B.; Fortin, N.; D  
submitted to the EMBL Data Library, January 1993  
A/Description: Sequencing of Chromosome I from Saccharomyces cerevisiae: analysis of a 3  
A/Reference number: S36711  
A/Accession: S36720  
A/Molecule type: DNA  
A/Residues: 1-205 <OUE>  
A/Cross-references: UNIPROT:P31377; UNIPARC:UPI000013A006; EMBL:L05146; NID:g171851; PII  
C/Genetics:  
A/Gene: FUN34; MIPS:YAL014c  
A/Cross-references: SGD:S0000012  
A/Map position: 1L

Query Match  
Best Local Similarity 70.2%; Score 33; DB 2; Length 205;  
Pred. No. 1.5e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDDK 8  
| | | | |  
Db 113 YKDDDDQ 119

## RESULT 79

S25432  
translation elongation factor eEF-1 beta chain - human  
C/Species: Homo sapiens (man)  
C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C/Accession: S25432; J01038; B61013; S15689  
R/Sanders, J.; Maassen, J.A.; Amos, R.; Moeller, W.  
Nucleic Acids Res. 19, 4551, 1991  
A/Title: Nucleotide sequence of human elongation factor-1-beta cDNA.  
A/Reference number: S25432; MUID:91360360; PMID:1886777  
A/Accession: S25432  
A/Status: nucleic acid sequence not shown  
A/Molecule type: mRNA  
A/Residues: 1-225 <SAN>  
A/Cross-references: UNIPROT:P24534; UNIPARC:UPI0000000C68; EMBL:X60489; NID:g31099; PI  
R/Von der Kammer, H.; Klaudiny, J.; Zimmer, M.; Scheitl, K.H.  
Biochem. Biophys. Res. Commun. 177, 312-317, 1991  
A/Title: Human elongation factor 1beta: cDNA and derived amino acid sequence.  
A/Reference number: J01038; MUID:91254293; PMID:1710449  
A/Accession: J01038  
A/Molecule type: mRNA  
A/Residues: 1-225 <VON>  
A/Cross-references: UNIPARC:UPI0000000C68; GB:X60656; NID:g31134; PIDN:CAA43063.1; PID  
R/Bauw, G.; Raamussen, H.H.; Van Den Bulcke, M.; Van Damme, J.; Puype, M.; Geeser, B.;  
Electrophoresis 11, 528-536, 1990  
A/Title: Two-dimensional gel electrophoresis, protein electrophoretic and microsequen  
A/Reference number: A61002; MUID:91031404; PMID:1699755  
A/Accession: B61013  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 2-6, 'X', 'X', 56-60 <BAU>  
A/Cross-references: UNIPARC:UPI0000174808; UNIPARC:UPI0000174809  
C/Genetics:  
A/Gene: GDB:EBF1B2  
A/Cross-references: GDB:682589  
A/Map position: 2pter-2qter  
C/Superfamily: translation elongation factor eEF-1 beta chain; translation elongation f  
C/Keywords: phosphoprotein; protein biosynthesis  
F/2-225/Product: translation elongation factor eEF-1 beta chain #status predicted <MAT>

Query Match  
Best Local Similarity 70.2%; Score 33; DB 1; Length 225;  
Pred. No. 1.6e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
| | | | |  
Db 94 DSKDDDD 100

## RESULT 80

S62693  
translation elongation factor eEF-1 beta chain - rabbit  
C/Species: Oryctolagus cuniculus (domestic rabbit)  
C/Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C/Accession: S62693; S62688; S37087  
R/Chen, C.J.; Traugh, J.A.  
Biochim. Biophys. Acta 1264, 303-311, 1995  
A/Title: Expression of recombinant elongation factor 1 beta from rabbit in Escherichia  
A/Reference number: S62688; MUID:96138552; PMID:8547318  
A/Accession: S62693  
A/Molecule type: mRNA  
A/Residues: 1-225 <CHE>  
A/Cross-references: UNIPROT:P34826; UNIPARC:UPI00001782A6; EMBL:X74728  
A/Accession: S62688  
A/Molecule type: protein  
A/Residues: 80-91 <CHF>  
A/Cross-references: UNIPARC:UPI00001782A7  
R/Chen, C.J.  
submitted to the EMBL Data Library, August 1993  
A/Reference number: S37087  
A/Accession: S37087

A:Molecule type: mRNA  
A:Residues: 1-77, 'T', 79-225 <CHW>  
A:Cross-references: UNIPARC:UPI000016C566; EMBL:X174728; NID:g398394; P1DN:CAA52741.1; P1  
C:Genetics:  
A:Gene: EFLB  
C:Function:  
A:Pathway: protein biosynthesis  
C:Superfamily: translation elongation factor eEF-1 beta chain; translation elongation fa  
C:Keywords: GTP exchange; phosphoprotein  
F:2-225/Product: translation elongation factor eEF-1 beta chain #status predicted <MAT>  
F:97-105/Region: beta, beta and delta chain signature  
F:106/Binding site: phosphate (Ser) (covalent) (by unidentified kinase) #status predicted

Query Match 70.2%; Score 33; DB 2; Length 225;  
Best Local Similarity 85.7%; Pred. No. 1.6e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
|||  
Db 94 DSKDDDD 100

RESULT 81  
G90525  
hypothetical protein MYPU 1110 [imported] - Mycoplasma pulmonis (strain UAB CTIP)  
C:Species: Mycoplasma pulmonis  
C>Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
C:Accession: G90525  
R:Chamblaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;  
Nucleic Acids Res. 29, 2145-2153, 2001  
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm  
A:Reference number: A9512; MUID:21267165; PMID:11353084  
A:Accession: G90525  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-235 <KIR>  
A:Cross-references: UNIPROT:Q98R99; UNIPARC:UPI00000CTFF8; GB:AL445566; PID:g14089524; F  
A:Experimental source: strain UAB CTIP  
C:Genetics:  
A:Gene: MYPU\_1110  
A:Genetic code: SGC3

Query Match 70.2%; Score 33; DB 2; Length 235;  
Best Local Similarity 71.4%; Pred. No. 1.7e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
|||  
Db 39 DYKDDDD 45

RESULT 82  
H84905  
homodomain transcription factor (ATHB-7) [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 05-Oct-2004  
C:Accession: H84905  
R:Lin, X.; Kail, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffitt, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Unayam, L.; Tallon, L.;  
euser, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197  
A:Accession: H84905  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-258 <STO>  
A:Cross-references: UNIPROT:P46897; UNIPARC:UPI0000126233; GB:AB002093; NID:g3831442; P1  
C:Genetics:  
A:Gene: At2g46680  
A:Map position: 2  
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 70.2%; Score 33; DB 2; Length 258;  
Best Local Similarity 71.4%; Pred. No. 1.9e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
|||  
Db 189 DYKDDDD 195

RESULT 83  
A33470  
fibroin light chain precursor - silkworm  
C:Species: Bombyx mori (silkworm)  
C>Date: 27-Feb-1990 #sequence\_revision 27-Feb-1990 #text\_change 09-Jul-2004  
C:Accession: A33470; JH0580; S41445; S41446; S10622  
R:Yamaguchi, K.; Kikuchi, Y.; Takagi, T.; Kikuchi, A.; Oyama, F.; Shimura, K.; Mizuno,  
J. Mol. Biol. 210, 127-139, 1989  
A:Title: Primary structure of the silk fibroin light chain determined by cDNA sequencin  
A:Reference number: A33470; MUID:90064541; PMID:2585514  
A:Accession: A33470  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-262 <YAM>  
A:Cross-references: UNIPROT:P21828; UNIPARC:UPI000012A56D; GB:X17291; NID:g5920; P1DN:C  
R:Kikuchi, Y.; Mori, K.; Suzuki, S.; Yamaguchi, K.; Mizuno, S.  
Gene 110, 151-158, 1992  
A:Title: Structure of the Bombyx mori fibroin light-chain-encoding gene: upstream sequen  
A:Reference number: JH0580; MUID:92165053; PMID:1147033  
A:Accession: JH0580  
A:Molecule type: DNA  
A:Residues: 1-45, 'R', 47-262 <RIK>  
A:Cross-references: UNIPARC:UPI000016B892; GB:M76430; NID:g289362; P1DN:AAA27840.1; PID  
A:Experimental source: strain J-139  
A:Note: the authors translated the codon CGA for residue 46 as Ala  
R:Mori, K.; Kikuchi, Y.; Homma-Waga, M.; Waga, S.; Mizuno, S.  
submitted to the EMBL Data Library, October 1993  
A:Description: Production of a chimeric fibroin light-chain polypeptide as a consequenc  
A:Reference number: S41445  
A:Accession: S41445  
A:Molecule type: mRNA  
A:Residues: 1-105, 'SMGSVISTSLTPANVYKIQDINDIGHTRK', 'FTLVNLIARAYKNTAHVPSITKDPYRK', 'TA  
YKRMCE' <MOR1>  
A:Cross-references: UNIPARC:UPI0000077132; EMBL:Z26884; NID:g452377; P1DN:CAA81529.1; P  
A:Experimental source: Nd-s mutant  
A:Accession: S41446  
A:Molecule type: mRNA  
A:Residues: 1-105, 'SMGSVISTSLTPANVYKIQDINDIGHTRK', 'FTLVNLIARAYKNTAHVPSITKDPYRK', 'TA  
YKRMCE' <MOR2>  
A:Cross-references: UNIPARC:UPI000007794F; EMBL:Z26885; NID:g452391; P1DN:CAA81530.1; P  
A:Experimental source: Nd-sd mutant  
R:Hui, C.; Suzuki, Y.; Kikuchi, Y.; Mizuno, S.  
J. Mol. Biol. 213, 395-398, 1990  
A:Title: Homeodomain binding sites in the 5' flanking region of the Bombyx mori silk fi  
A:Reference number: S10622; MUID:90278949; PMID:1972197  
A:Accession: S10622  
A:Molecule type: DNA  
A:Residues: 1-12 <HUI>  
A:Cross-references: UNIPARC:UPI0000178C89; GB:X53319; NID:g10893  
A:Note: the complete translation is not shown  
C:Comment: Silk fibroin is secreted from the posterior silk gland.  
C:Genetics:  
A:Insertions: 12/3; 40/2; 105/3; 153/3; 183/2; 231/3  
C:Superfamily: fibroin light chain  
C:Keywords: extracellular protein  
F:1-16/Domain: signal sequence #status predicted <SIG>  
F:17-26/Product: fibroin light chain #status predicted <MAT>

Query Match 70.2%; Score 33; DB 2; Length 262;  
Best Local Similarity 75.0%; Pred. No. 1.9e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DYKDDDD 8  
|||



Db 48 DYVDDTK 55

# RESULT 84

S47137  
homeotic protein Atchb-7 - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Oct-2004  
C/Accession: S47137; S52653  
R/Soderman, E.; Mattsson, J.; Svensson, M.; Borkird, C.; Engstrom, P.  
submitted to the EMBL Data Library, June 1992  
A/Reference number: S47135  
A/Accession: S47137  
A/Molecule type: mRNA  
A/Residues: 1-267 <SOB>  
A/Cross-references: UNIPARC:UPI000016DA98; EMBL:K67032; NID:G493163; PIDN:CAA47425.1; PI  
R/Soderman, E.; Mattsson, J.; Svensson, M.; Borkird, C.; Engstrom, P.  
Plant Mol. Biol. 26, 145-154, 1994  
A/Title: Expression patterns of novel genes encoding homeodomain leucine-zipper proteins  
A/Reference number: S52651; MUID:95035986; PMID:7948864  
A/Accession: S52653  
A/Status: nucleic acid sequence not shown  
A/Molecule type: mRNA  
A/Residues: 37-45, 'N', 47-133 <SOB>  
A/Cross-references: UNIPARC:UPI000017A2CA; EMBL:X67032  
C/Keywords: DNA binding; homeobox; leucine zipper; nucleus; transcription regulation  
F/39-95/Domain: homeobox homology <HOX>

Query Match 70.2%; Score 33; DB 2; Length 267;  
Best Local Similarity 71.4%; Pred. No. 2e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
Db 198 DYEDDDN 204

# RESULT 85

B86486  
protein F28J9.7 [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C/Accession: B86486  
R/Theologis, A.; Becker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A/Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A/Reference number: A86141; MUID:21016719; PMID:11130712  
A/Accession: B86486  
A/Status: Preliminary  
A/Molecule type: DNA  
A/Residues: 1-270 <STO>  
A/Cross-references: UNIPROT:Q9S9S2; UNIPARC:UPI00000A508D; GB:AE005172; NID:96272376; PI  
C/Genetics:  
A/Gene: F28J9.7  
A/Map position: 1

Query Match 70.2%; Score 33; DB 2; Length 270;  
Best Local Similarity 71.4%; Pred. No. 2e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDDK 8  
Db 257 FKDDDE 263

# RESULT 86

T00737

myb-related protein F22013.32 - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 12-Feb-1995 #sequence\_revision 12-Feb-1999 #text\_change 31-Dec-2004  
C/Accession: T00737  
R/Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; C  
eologis, A.; Becker, J.R.  
submitted to the EMBL Data Library, April 1998  
A/Description: Genomic sequence for Arabidopsis thaliana BAC F22013.  
A/Reference number: Z14200  
A/Accession: T00737  
A/Status: translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-280 <SHI>  
A/Cross-references: UNIPROT:O8GYP5; UNIPARC:UPI000000C547; EMBL:AC003981; NID:G3063438  
A/Experimental source: cultivar Columbia  
C/Genetics:  
A/Gene: ATSP:F22013.32  
A/Map position: 1  
A/Introns: 45/1; 88/2  
C/Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology  
F/9-61/Domain: myb DNA-binding repeat homology <MYB1>  
F/62-112/Domain: myb DNA-binding repeat homology <MYB>

Query Match 70.2%; Score 33; DB 2; Length 280;  
Best Local Similarity 71.4%; Pred. No. 2.1e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
Db 236 DHEDDDD 242

# RESULT 87

T51667  
myb-related transcription factor MYB60 [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 31-Dec-2004  
C/Accession: T51667  
R/Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.; Greco, R.;  
; Paz-Ares, J.; Weisshaar, B.  
Plant J. 16, 263-276, 1998  
A/Title: Towards functional characterisation of the members of the R2R3-MYB gene from  
A/Reference number: Z14349; MUID:9839469; PMID:9839469  
A/Accession: T51667  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-280 <KTA>  
A/Cross-references: UNIPROT:Q9S8G0; UNIPARC:UPI000009EF40; EMBL:AF062895; PIDN:AC8361;  
A/Experimental source: cultivar Columbia  
C/Genetics:  
A/Gene: MYB60  
A/Map position: 1  
C/Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology  
C/Keywords: transcription factor

Query Match 70.2%; Score 33; DB 2; Length 280;  
Best Local Similarity 71.4%; Pred. No. 2.1e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
Db 236 DHEDDDD 242

# RESULT 88

S49469  
glucose-1-phosphate cytidylyltransferase (EC 2.7.7.33) strQ - Streptomyces glaucescens  
C/Species: Streptomyces glaucescens  
C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C/Accession: S49469  
R/Beyer, S.; Mayer, G.M.; Piepersberg, W.  
submitted to the EMBL Data Library, October 1994

A:Reference number: S49469  
A:Accession: S49469  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-299 <BBY>  
A:Cross-references: UNIPROT:Q54266; UNIPARC:UPI000008A7DC; EMBL:X82177; NID:G902359; PTD  
C:Superfamily: glucose-1-phosphate cytidylyltransferase  
C:Keywords: nucleotidyltransferase

Query Match 70.2%; Score 33; DB 2; Length 299;  
Best Local Similarity 75.0%; Pred. No. 2.2e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
DB 206 DYKDDPK 213

RESULT 89  
G95244  
hypothetical protein SP2093 [imported] - Streptococcus pneumoniae (strain TIGR4)  
C:Species: Streptococcus pneumoniae  
C>Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004  
C:Accession: G95244  
R:Teitelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid  
nson, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtapple,  
nson, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
A.; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A:Reference number: A95000; MUID:21357209; PMID:11463916  
A:Accession: G95244  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-322 <KUR>  
A:Cross-references: UNIPROT:Q97NFO; UNIPARC:UPI0000051AFB; GB:AE005672; PIDN:AAK76152.1;  
A:Experimental source: strain TIGR4  
C:Genetics:  
A:Gene: SP2093

Query Match 70.2%; Score 33; DB 2; Length 322;  
Best Local Similarity 75.0%; Pred. No. 2.4e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
DB 127 DYKDDDK 134

RESULT 90  
T20033  
hypothetical protein CATG2.2 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T20033  
R:Palmer, S.  
submitted to the EMBL Data Library, April 1995  
A:Reference number: Z19213  
A:Accession: T20033  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-333 <WIL>  
A:Cross-references: UNIPROT:Q18694; UNIPARC:UPI0000080191; EMBL:Z49125; PIDN:CAA88935.1;  
A:Experimental source: clone CATG2  
C:Genetics:  
A:Gene: CESP:C47G2.2  
A:Map position: 2  
A:Introns: 113/2; 222/2

Query Match 70.2%; Score 33; DB 2; Length 333;  
Best Local Similarity 85.7%; Pred. No. 2.5e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
DB 101 DAKDDDD 107

RESULT 91  
S16321  
light-induced protein CPR-2 - parsley  
C:Species: Petroselinum crispum (parsley)  
C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 31-Dec-2004  
C:Accession: S16321  
R:Weishaar, B.; Armstrong, G.A.; Block, A.; da Costa e Silva, O.; Hanlbrock, K.  
EMBO J. 10, 1777-1786, 1991  
A:Title: Light-inducible and constitutively expressed DNA-binding proteins recognizing  
A:Reference number: S16320; MUID:91266906; PMID:2050115  
A:Accession: S16321  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-393 <WEI>  
A:Cross-references: UNIPROT:Q99090; UNIPARC:UPI00001794P2; EMBL:X58577  
C:Superfamily: BZIP protein; fos/jun DNA-binding domain homology  
C:Keywords: DNA binding; nucleus; transcription regulation  
F;185-225/Domain: fos/jun DNA-binding domain homology <FUD>

Query Match 70.2%; Score 33; DB 2; Length 393;  
Best Local Similarity 62.5%; Pred. No. 3e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
DB 168 DHSDDDE 175

RESULT 92  
AH1387  
cell wall binding proteins homolog lmo2504 [imported] - Listeria monocytogenes (strain  
C:Species: Listeria monocytogenes  
C>Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
C:Accession: AH1387  
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke  
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fath, H  
D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Krefelt, J.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maitournam, A.; M  
ok, C.; Schlutener, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland  
A:Title: Comparative genomics of Listeria species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AH1387  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-436 <GLA>  
A:Cross-references: UNIPROT:Q8Y4E2; UNIPARC:UPI0000055221; GB:NC\_003210; PIDN:CAD00582.  
A:Experimental source: strain EGD-e  
C:Genetics:  
A:Gene: lmo2504

Query Match 70.2%; Score 33; DB 2; Length 436;  
Best Local Similarity 75.0%; Pred. No. 3.3e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
DB 168 DQKDDDDK 175

RESULT 93  
T40337  
probable saccharopine dehydrogenase (NADP, L-glutamate-forming) (EC 1.5.1.10) [similari.  
C:Species: Schizosaccharomyces pombe  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: T40337  
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Beck, A.; Reinhardt, R.; Pohl, T.  
submitted to the EMBL Data Library, March 1998

A:Reference number: Z21921  
A:Accession: T40337  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-450 <LVN>  
A:Cross-references: UNIPROT:O59711; UNIPARC:UPI0000069880; EMBL:AL022244; PIDN:CAA18292.  
A:Experimental source: strain 972h; cosmid C3B8  
C:Genetics:  
A:Gene: SPDB:SPBC3B8.03  
A:Map position: 2  
C:Keywords: oxidoreductase

Query Match 70.2%; Score 33; DB 2; Length 450;  
Best Local Similarity 71.4%; Pred. No. 3.4e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YKDDDDK 8  
Db 308 FKEDDDK 314

RESULT 94  
D81224  
Catalase (EC 1.11.1.6) NMA0050 [similarity] - Neisseria meningitidis (strain MCS8 serogr  
C:Species: Neisseria meningitidis  
C>Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C:Accession: D81224; C81996  
R:Teitelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A  
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scharlato, V.; Maignan, V.; Pizze, M.  
Science 287, 1809-1815, 2000  
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve  
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.  
A:Reference number: A81000; MUID:2017555; PMID:10710307  
A:Accession: D81224  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-504 <TER>  
A:Cross-references: UNIPROT:Q9URF5; UNIPARC:UPI00000C4DD7; GB:AE002379; GB:AE002098; NID  
A:Experimental source: serogroup B, strain MCS8  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajadream,  
Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
A:Reference number: A81775; MUID:2022556; PMID:10761919  
A:Accession: C81996  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-504 <PAR>  
A:Cross-references: UNIPARC:UPI00000C4DD7; GB:AL162752; GB:AL157959; NID:G7378778; PIDN:  
A:Experimental source: serogroup A, strain Z2491  
C:Genetics:  
A:Gene: katA; NMB0216; NMA0050  
C:Superfamily: catalase  
C:Keywords: heme; iron; metalloprotein; oxidoreductase  
F:59,99,133/Active site: His, Thr, Asn #status predicted  
F:342/Binding site: heme iron (Tyr) (axial ligand) #status predicted

Query Match 70.2%; Score 33; DB 2; Length 504;  
Best Local Similarity 71.4%; Pred. No. 3.8e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DYKDDDD 7  
Db 416 DYKDDDD 422

R:Avila, J.; Nieto, C.; Canas, L.; Benito, M.; Paz-Ares, J.  
submitted to the EMBL Data Library, July 1992  
A:Description: Petunia hybrida genes related to the maize regulatory C1 gene and to an  
A:Reference number: S26604  
A:Accession: S26606  
A:Molecule type: DNA  
A:Residues: 1-517 <AVI>  
A:Cross-references: UNIPROT:Q02994; UNIPARC:UPI000009D660; EMBL:Z13998; NID:G20564; PIL  
A:Experimental source: strain v26, developing flowers  
C:Superfamily: petunia myb-related protein 3; myb DNA-binding repeat homology  
C:Keywords: DNA binding; duplication; nucleus; transcription regulation  
F:25-77/Domain: myb DNA-binding repeat homology <MYB1>  
F:78-128/Domain: myb DNA-binding repeat homology <MYB2>

Query Match 70.2%; Score 33; DB 1; Length 517;  
Best Local Similarity 71.4%; Pred. No. 3.9e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YKDDDDK 8  
Db 457 YEDEDK 463

RESULT 96  
A48341  
Nucleocapsid protein - parainfluenza virus type 1 (strains A1426, 86-315, 62M-753)  
N:Alternate names: nucleoprotein  
C:Species: parainfluenza virus type 1  
C>Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 09-Jul-2004  
C:Accession: A48341  
R:Myahara, K.; Kitada, S.; Yoshimoto, M.; Matsumura, H.; Kawano, M.; Komada, H.; Teur  
Arch. Virol. 124, 255-268, 1992  
A:Title: Molecular evolution of human paramyxoviruses. Nucleotide sequence analyses of  
human paramyxoviruses.  
A:Reference number: A48341; MUID:92296894; PMID:1605738  
A:Accession: A48341  
A:Molecule type: genomic RNA  
A:Residues: 1-524 <MTY>  
A:Cross-references: UNIPROT:P36354; UNIPARC:UPI000012PFD; GB:S38060; NID:G250340; PIDN  
A:Note: Sequence extracted from NCBI backbone (NCBIN:106078, NCBI:P:106079)  
C:Genetics:  
A:Gene: NP  
C:Superfamily: paramyxovirus nucleocapsid protein  
C:Keywords: nucleocapsid; nucleoprotein

Query Match 70.2%; Score 33; DB 1; Length 524;  
Best Local Similarity 71.4%; Pred. No. 4e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDD 7  
Db 508 DYKDDDD 514

RESULT 97  
VHNZT1  
nucleocapsid protein - parainfluenza virus type 1  
N:Alternate names: nucleoprotein  
C:Species: parainfluenza virus type 1  
C>Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C:Accession: A38401  
R:Lyn, D.; Gill, D.S.; Scroggs, R.A.; Portner, A.  
J. Gen. Virol. 72, 983-987, 1991  
A:Title: The nucleoproteins of human parainfluenza virus type 1 and Sendai virus share  
A:Reference number: A38401; MUID:91202138; PMID:1707951  
A:Accession: A38401  
A:Molecule type: mRNA  
A:Residues: 1-524 <LVN>  
A:Cross-references: UNIPROT:P26590; UNIPARC:UPI000012PFD; GB:D01070; NID:G222271; PIDN  
C:Superfamily: paramyxovirus nucleocapsid protein  
C:Keywords: nucleocapsid; nucleoprotein

Query Match 70.2%; Score 33; DB 1; Length 524;

Best Local Similarity 71.4%; Pred. No. 4e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
|:|||||  
Db 508 DYENDD 514

## RESULT 98

A89830

arginyl-tRNA synthetase [imported] - Staphylococcus aureus (strain N315)

C/Species: Staphylococcus aureus

C/Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004

C/Accession: A89830

R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc

ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsuku, K.

Lancet 357, 1225-1240, 2001

A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A/Reference number: A89758; MUID:21311952; PMID:11418146

A/Accession: A89830

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-553 &lt;KUR&gt;

A/Cross-references: UNIPROT:Q99W05; UNIPARC:UPI0000030ADB; GB:BA000018; PTD:913700499; F

A/Experimental source: strain N315

C/Genetics:

A/Gene: args

C/Superfamily: Bacillus arginine-tRNA ligase

Query Match 70.2%; Score 33; DB 2; Length 553;  
Best Local Similarity 62.5%; Pred. No. 4.2e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
|:|||||  
Db 296 DFRDCKDR 303

## RESULT 99

C71529

hypothetical protein CT326 - Chlamydia trachomatis (serotype D, strain UW3/Cx)

C/Species: Chlamydia trachomatis

C/Date: 13-Sep-1998 #sequence\_revision 13-Sep-1998 #text\_change 09-Jul-2004

C/Accession: C71529

R/Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,

Science 282, 754-759, 1998

A/Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac

A/Reference number: A71570; MUID:99000809; PMID:9784136

A/Accession: C71529

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-563 &lt;ARN&gt;

A/Cross-references: UNIPROT:O84328; UNIPARC:UPI00000C0B2F; GB:AE001305; GB:AE001273; NIT

A/Experimental source: serotype D, strain UW-3/Cx

C/Genetics:

A/Gene: CT326

Query Match 70.2%; Score 33; DB 2; Length 563;  
Best Local Similarity 71.4%; Pred. No. 4.3e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
|:|||||  
Db 30 DFRSDDD 36

## RESULT 100

T06648

hypothetical protein T6G15.10 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004

C/Accession: T06648

R/Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.  
submitted to the Protein Sequence Database, April 1999

A/Reference number: Z15791

A/Accession: T06648

A/Molecule type: DNA

A/Residues: 1-650 &lt;BEV&gt;

A/Cross-references: UNIPROT:Q9T0G7; UNIPARC:UPI00000A733C; EMBL:AL049656; GSPDB:GN00062

A/Experimental source: cultivar Columbia; BAC clone T6G15

C/Genetics:

A/Gene: ATSP:T6G15.10

A/Map position: 4

Query Match 70.2%; Score 33; DB 2; Length 650;  
Best Local Similarity 71.4%; Pred. No. 5e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDD 8  
|:|||||  
Db 259 YEDDDQ 265

Search completed: June 29, 2006, 11:41:16  
Job time : 54 secs

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 29, 2006, 11:32:11 ; Search time 295 Seconds  
(without alignments)  
25.085 Million cell updates/sec

Title: US-10-671-054-2

Perfect score: 47

Sequence: 1 DYKDDDK 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 500 summaries

Database :

1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	47	1	SCKA_PANIN
2	47	100.0	319	2	Q8NF6G_HUMAN
3	43	91.5	246	2	Q36Q46_MARBY
4	42	89.4	154	2	Q4XJ6_PLACH
5	42	89.4	284	2	Q7Y283_PLACH
6	42	89.4	586	2	Q6FN57_CANGA
7	42	89.4	603	2	Q2PEW5_TRIER
8	42	89.4	1385	2	Q6FK24_CANGA
9	41	87.2	399	2	Q91BJ4_NPVST
10	41	87.2	423	1	SPR28_YEAST
11	41	87.2	452	2	Q21W25_RHOA
12	40	85.1	1767	2	Q6VZM2_CNPV
13	39	83.0	322	2	Q8UKJ5_VIRIR
14	39	83.0	432	2	Q4N797_THRPA
15	39	83.0	506	2	Q7UOZ7_RHOA
16	39	83.0	561	1	CWC25_YARLI
17	39	83.0	648	1	Q54DA4_DICDI
18	39	83.0	706	2	Q8XMT9_CLOPE
19	39	83.0	1254	2	Q54UVO_DICDI
20	38	80.9	110	2	Q46VH5_RALEJ
21	38	80.9	125	2	Q5CQAS_CRYPV
22	38	80.9	154	2	Q9FM73_ARATH
23	38	80.9	171	2	Q8DAG1_VIBU
24	38	80.9	235	2	Q76542_DICDI
25	38	80.9	242	2	Q8L7V6_ARATH
26	38	80.9	265	2	Q4X8B5_PLACH
27	38	80.9	294	2	Q9LJVB_ARATH
28	38	80.9	301	2	Q54VA8_DICDI
29	38	80.9	305	2	WHCG_METNO
30	38	80.9	332	2	Q5AF51_CANAL
31	38	80.9	369	2	Q4XYM1_PLACH
32	38	80.9	416	2	Q5F360_CHICK
33	38	80.9	418	2	Q5ZKN5_CHICK
34	38	80.9	475	2	Q8OHJ7_CHICK
35	38	80.9	475	2	Q4XQ6_PLACH
36	38	80.9	565	1	MAOI_YERPE
37	38	80.9	565	1	MAOI_YERPE
38	38	80.9	587	1	DPH2_KLULA
39	38	80.9	588	2	Q55CB4_DICDI
40	38	80.9	590	2	Q6BYD0_DEBHA
41	38	80.9	629	2	Q2UGP9_ASFOR
42	38	80.9	782	2	Q2UF79_ASFOR
43	38	80.9	804	2	Q3QT20_RHOA
44	38	80.9	823	2	Q96505_DROME
45	38	80.9	823	2	Q9VK34_DROME
46	38	80.9	862	2	Q4Y0Z6_PLACH
47	38	80.9	926	2	Q6CG65_YARLI
48	38	80.9	1018	2	Q416U9_GIBZE
49	38	80.9	1085	1	IFH1_YEAST
50	38	80.9	1212	2	Q4P6M8_USTMA
51	38	80.9	1228	2	Q7MXW4_PORGI
52	38	80.9	1267	2	Q81LD1_PLAF7
53	38	80.9	1277	1	PD55_YEAST
54	38	80.9	1305	2	Q6FNZ8_CANGA
55	38	80.9	1523	2	Q813B1_PLAF7
56	38	80.9	1687	2	Q81BA8_PLAF7
57	38	80.9	1818	2	Q4XUN1_PLACH
58	38	80.9	1921	2	Q4URC4_THRAN
59	38	80.9	2051	2	Q5ASE7_EMENT
60	38	80.9	2067	1	B1MB_EMENT
61	38	80.9	2226	2	Q97225_PLAF7
62	38	80.9	2384	2	Q5KID7_CRYNE
63	38	80.9	2432	2	Q55U02_CRYNE
64	38	80.9	2577	2	Q81AM1_PLAF7
65	37	78.7	119	2	Q8ST86_PLAF7
66	37	78.7	132	2	Q6S869_PLAF7
67	37	78.7	136	2	Q7RB94_PLAF7
68	37	78.7	142	2	Q4Y0T6_PLACH
69	37	78.7	164	2	Q5TKF1_ORYSA
70	37	78.7	168	2	Q4Y3M3_PLACH
71	37	78.7	179	2	Q2ZA91_GGAMM
72	37	78.7	179	2	Q35Y65_GGAMM
73	37	78.7	179	2	Q366F4_GGAMM
74	37	78.7	179	2	Q8EFW6_SHEON
75	37	78.7	197	2	Q2M3Y9_PHYIN
76	37	78.7	225	2	Q4Z415_PLABE
77	37	78.7	259	2	Q5CPK3_CRYPV
78	37	78.7	268	2	Q74H22_IACDO
79	37	78.7	299	2	Q54U43_DICDI
80	37	78.7	335	2	Q38DT4_9TRYR
81	37	78.7	341	2	Q6C9S5_YARLI
82	37	78.7	351	1	BROM1_FANCO
83	37	78.7	364	1	BAMT_ANTWA
84	37	78.7	451	2	Q53LKL_ORYSA
85	37	78.7	452	1	TIG_RHOA
86	37	78.7	485	2	Q2R949_ORYSA
87	37	78.7	487	2	Q6BV75_DEBHA
88	37	78.7	487	2	Q56XW8_ARATH
89	37	78.7	497	1	VE2_HP20
90	37	78.7	513	2	Q9SX72_ARATH
91	37	78.7	524	2	Q59NM9_CANAL
92	37	78.7	554	2	Q8IEG8_PLAF7
93	37	78.7	567	2	Q5UI08_ORYSA
94	37	78.7	664	2	Q61OD3_CABER
95	37	78.7	690	2	Q5AAB5_CANAL
96	37	78.7	690	2	Q6VZ25_CNPV
97	37	78.7	691	2	Q5AA27_CNPV
98	37	78.7	697	2	Q54D84_DICDI
99	37	78.7	700	2	Q5A932_CANAL
100	37	78.7	702	2	Q4N9L1_THRPA
101	37	78.7	720	2	Q55WAB_CRYNE
102	37	78.7	721	2	Q97LFB_CLOAB
103	37	78.7	723	2	Q3YTB6_EHRCZ
104	37	78.7	724	2	Q5KJZ0_CRYNE
Q5F360	gallus galli				
Q5ZKN5	gallus galli				
Q8OHJ7	gallus galli				
Q4XQ6	plasmidium				
Q8ZG09	yersinia pe				
Q66C80	yersinia ps				
Q55CB4	dictyosteli				
Q6BYD0	deparomyce				
Q2UGP9	aspergillus				
Q2UF79	aspergillus				
Q3QT20	silicibacte				
Q96505	drosophila				
Q9VK34	drosophila				
Q4Y0Z6	plasmidium				
Q6CG65	yarowia li				
Q416U9	gibberella				
Q39520	saccharomyc				
Q4P6M8	ustilago ma				
Q7MXW4	porphyromon				
Q81LD1	plasmidium				
Q41264	saccharomyc				
Q6FNZ8	candida gla				
Q813B1	plasmidium				
Q81BA8	plasmidium				
Q4XUN1	plasmidium				
Q4URC4	theliera a				
Q5ASE7	aspergillus				
Q5KID7	emeticella				
P33144	emeticella				
Q5KID7	cryptococcu				
Q55U02	cryptococcu				
Q81AM1	plasmidium				
Q8ST86	plasmidium				
Q6S869	plasmidium				
Q7RB94	plasmidium				
Q4Y0T6	plasmidium				
Q5TKF1	oryza sativ				
Q4Y3M3	plasmidium				
Q2ZA91	shearwater				
Q35Y65	shearwater				
Q366F4	shearwater				
Q8EFW6	shearwater				
Q2M3Y9	phytophthor				
Q4Z415	plasmidium				
Q5CPK3	cryptospori				
Q74H22	lactobacilli				
Q54U43	dictyosteli				
Q38DT4	trypanosoma				
Q6C9S5	yarowia li				
Q21791	ananas como				
Q91Y29	anthrithum				
Q53LKL	oryza sativ				
Q66512	rhodospseudo				
Q2R949	oryza sativ				
Q6BV75	deparomyce				
Q56XW8	arabidopsis				
Q5UI08	human papil				
Q5AA27	candida alb				
Q54D84	dictyosteli				
Q5A932	candida alb				
Q4N9L1	theliera p				
Q55WAB	cryptococcu				
Q97LFB	clostridium				
Q3YTB6	erlichia c				
Q5KJZ0	cryptococcu				

105	37	78.7	74.1	1	PIOD3_MOUSE	Q9r0e1	mus	musculu	178	36	76.6	334	2	Q9L1V4_ORYSA	Q9L1V4	oryza	sativ
106	37	78.7	74.1	2	O542E0_ARATH	O542E0	m	2 days ne	179	36	76.6	357	2	O5BLI6_BRARE	O5BLI6	brachydanio	
107	37	78.7	783	2	O2V3C9_ARATH	O2V3C9	arabidopsis		180	36	76.6	366	2	O387Z3_ORYSA	O387Z3	trypanosoma	
108	37	78.7	824	2	O55BX2_DICDI	O55BX2	dicystosell		181	36	76.6	370	2	O79E00_PLAYO	O79E00	plasmodium	
109	37	78.7	827	2	Q7Q0Z9_ARATH	Q7Q0Z9	anopheles	g	182	36	76.6	378	2	O55E67_DICDI	O55E67	dicystosell	
110	37	78.7	859	2	O4DLM0_TRYCR	O4dLm0	trypanosoma		183	36	76.6	383	2	O6C5D9_YARLI	O6C5D9	yarrowia	11
111	37	78.7	869	2	O5Z8F2_ORYSA	O5z8F2	oryza	sativ	184	36	76.6	393	2	O9VDD0_DROME	O9VDD0	drosophila	
112	37	78.7	870	1	PANK2_ARATH	PANK2	arabidopsis		185	36	76.6	411	2	O6ZIK7_ORYSA	O6ZIK7	oryza	sativ
113	37	78.7	871	2	O6LPR8_ARATH	O6lPr8	arabidopsis		186	36	76.6	419	2	O2S776_PLAFA	O2S776	plasmodium	
114	37	78.7	885	2	O6CFP2_YARLI	O6cfE2	yarrowia	11	187	36	76.6	420	2	O2ZDS3_CALSA	O2ZDS3	caldicellul	
115	37	78.7	894	2	O8I5I1_PLAFA	O8I5I1	plasmodium		188	36	76.6	421	2	O38ZK1_9TRYP	O38ZK1	trypanosoma	
116	37	78.7	906	2	O97262_PLAFA	O97262	homarus	ame	189	36	76.6	422	2	O86AN7_DICDI	O86AN7	dicystosell	
117	37	78.7	936	2	O95VU2_HOMAM	O95vU2	homarus	ame	190	36	76.6	427	2	O54YR3_DICDI	O54YR3	dicystosell	
118	37	78.7	942	2	O9FMJ7_ARATH	O9fmJ7	arabidopsis		191	36	76.6	434	2	O4QAI2_LEIMA	O4QAI2	leishmania	
119	37	78.7	970	2	O2OV65_ORYSA	O2OV65	oryza	sativ	192	36	76.6	442	2	O53LE4_ORYSA	O53LE4	oryza	sativ
120	37	78.7	985	2	O8B9I7_NPVRO	O8b9I7	rachiplusia		193	36	76.6	446	2	O753Y9_ASHGO	O753Y9	ashbya	goss
121	37	78.7	1038	2	O54U73_DICDI	O54uV3	dicystosell		194	36	76.6	452	2	O7ZXV8_XENLA	O7ZXV8	xenopus	lae
122	37	78.7	1088	2	O4PIU4_USTMA	O4pIu4	ustiliago	ma	195	36	76.6	453	2	O6P368_XENTR	O6P368	xenopus	tro
123	37	78.7	1137	2	O4I9I7_GIBZE	O4I9I7	gibberella		196	36	76.6	458	2	O9W4D3_DROME	O9W4D3	drosophila	
124	37	78.7	1159	2	O5CS80_CRYPV	O5cS80	cryptospori		197	36	76.6	463	2	O5CST6_CRYPV	O5CST6	cryptospori	
125	37	78.7	1169	2	O5CJY3_CRYHO	O5cJY3	cryptospori		198	36	76.6	464	2	O2OXZ5_ORYSA	O2OXZ5	oryza	sativ
126	37	78.7	1210	2	O59VM4_CANAL	O59vM4	candida	alb	199	36	76.6	472	2	O6BID3_DEBHA	O6BID3	debaromyce	
127	37	78.7	1287	2	O7RMJ4_PLAYO	O7rmJ4	plasmodium		200	36	76.6	475	2	O55GJ8_DICDI	O55GJ8	dicystosell	
128	37	78.7	1299	2	O4P8T6_USTMA	O4p8T6	ustiliago	ma	201	36	76.6	479	2	O5STK6_CRYNE	O5STK6	cryptococcu	
129	37	78.7	1313	2	O8IBZ5_PLAFA	O8IBZ5	plasmodium		202	36	76.6	479	2	O5KIT9_CRYNE	O5KIT9	cryptococcu	
130	37	78.7	1377	2	O54WG7_DICDI	O54WG7	dicystosell		203	36	76.6	485	2	O9LXL1_ARATH	O9LXL1	arabidopsis	
131	37	78.7	1382	2	O4I064_GIBZE	O4I064	gibberella		204	36	76.6	486	2	O8LGB1_ARATH	O8LGB1	arabidopsis	
132	37	78.7	1468	2	O8GU85_ORYSA	O8gu85	oryza	sativ	205	36	76.6	493	2	O9PHI9_ARATH	O9PHI9	arabidopsis	
133	37	78.7	1482	2	O8I4X9_PLAFA	O8I4X9	plasmodium		206	36	76.6	495	2	O6K7I4_PICHO	O6K7I4	picophyllus	
134	37	78.7	1482	2	O8H7L0_ORYSA	O8H7L0	oryza	sativ	207	36	76.6	496	2	O4DFK6_TRYCR	O4DFK6	trypanosoma	
135	37	78.7	1618	2	O8I5I3_PLAFA	O8I5I3	plasmodium		208	36	76.6	519	2	O5ALV8_CANAL	O5ALV8	candida	alb
136	37	78.7	2200	2	O54MP8_DICDI	O54MP8	dicystosell		209	36	76.6	521	2	O4I3V7_GIBZE	O4I3V7	gibberella	
137	37	78.7	2221	2	O8I259_PLAFA	O8I259	plasmodium		210	36	76.6	521	2	O9CUB4_MOUSE	O9CUB4	mus	musculu
138	37	78.7	2491	2	O4YNO6_PLAFA	O4YnO6	plasmodium		211	36	76.6	523	2	O772J8_DROME	O772J8	drosophila	
139	37	78.7	2598	2	O7RNO6_PLAYO	O7rno6	plasmodium		212	36	76.6	533	2	O69S61_ORYSA	O69S61	oryza	sativ
140	37	78.7	2605	2	O8ID88_PLAFA	O8ID88	plasmodium		213	36	76.6	537	2	O5SG00_DICDI	O5SG00	dicystosell	
141	36	76.6	24	2	O6KXY7_PICHO	O6kY7	picophyllus		214	36	76.6	567	2	O3U7D5_MOUSE	O3U7D5	mus	musculu
142	36	76.6	77	2	O9ZTN5_PETHY	O9ztn5	petunia	hyb	215	36	76.6	572	2	O54AG9_CANAL	O54AG9	candida	alb
143	36	76.6	116	2	O16579_CABEL	O16579	caenorhabdit		216	36	76.6	573	2	O54T06_DICDI	O54T06	dicystosell	
144	36	76.6	122	2	O3BGE1_PLAFA	O3bge1	plasmodium		217	36	76.6	577	2	O54WX8_DICDI	O54WX8	dicystosell	
145	36	76.6	122	2	O3BGI9_PLAFA	O3bgi9	plasmodium		218	36	76.6	591	2	O7S883_NEURP	O7S883	neutrospora	
146	36	76.6	122	2	O3BIT2_PLAFA	O3biI2	plasmodium		219	36	76.6	596	2	O3J7B6_ORYSA	O3J7B6	oryza	sativ
147	36	76.6	122	2	O3BJR0_PLAFA	O3bjr0	plasmodium		220	36	76.6	616	2	O5APB5_CANAL	O5APB5	candida	alb
148	36	76.6	145	2	O922Q2_MOUSE	O922Q2	mus	musculu	221	36	76.6	633	2	O54LL9_DICDI	O54LL9	dicystosell	
149	36	76.6	156	2	O7XEAB_ORYSA	O7xeAB	oryza	sativ	222	36	76.6	634	2	O569P4_BRAAE	O569P4	brachydanio	
150	36	76.6	177	1	SIVA_RAT	P59692	rattus	norv	223	36	76.6	636	2	O2MOM9_DROS	O2MOM9	drosophila	
151	36	76.6	194	2	O6OF49_ORYSA	O6OF49	oryza	sativ	224	36	76.6	638	2	O2UFL4_ASPOB	O2UFL4	aspeggillus	
152	36	76.6	195	2	O5I6B1_BORBU	O5I6B1	borrelia	bu	225	36	76.6	644	2	O6LSV3_PHOBR	O6LSV3	photobacter	
153	36	76.6	197	2	O2RYO5_9SPHI	O2ryO5	salinibacte		226	36	76.6	653	2	O86KR4_DICDI	O86KR4	dicystosell	
154	36	76.6	202	2	O5NFD0_FRATY	O5nfd0	franciseila		227	36	76.6	660	2	O5AEE0_CANAL	O5AEE0	candida	alb
155	36	76.6	203	2	O54CW8_DICDI	O54CW8	dicystosell		228	36	76.6	670	2	O8MTJ1_DROME	O8MTJ1	drosophila	
156	36	76.6	206	2	O6DGA7_BRARE	O6dga7	brachydanio		229	36	76.6	675	2	O9VTX7_DROME	O9VTX7	drosophila	
157	36	76.6	210	2	O6FTC6_CANCA	O6ftc6	candida	gla	230	36	76.6	676	2	O5BHV4_DROME	O5BHV4	drosophila	
158	36	76.6	211	2	O5OMG9_ENTHI	O5OMG9	entamoeba	h	231	36	76.6	699	2	O2LYT2_DROS	O2LYT2	drosophila	
159	36	76.6	211	2	O5ONP8_ENTHI	O5ONP8	entamoeba	h	232	36	76.6	713	2	O8ID82_PLAFA	O8ID82	plasmodium	
160	36	76.6	214	2	O7PJZ7_ANOGA	O7PJZ7	anopheles	g	233	36	76.6	730	1	GP149_RAT	GP149	rattus	norv
161	36	76.6	222	2	O6MY92_ASPFU	O6MY92	aspeggillus		234	36	76.6	734	2	O6R9N8_MALZE	O6R9N8	zea	mays
162	36	76.6	227	2	O8ILS9_PLAFA	O8ILS9	plasmodium		235	36	76.6	738	1	PLOD3_HUMAN	PLOD3	homo	sapien
163	36	76.6	229	2	O4ESB6_LISMO	O4esb6	listeria	mo	236	36	76.6	738	2	PLOD3_PONPY	PLOD3	pongy	
164	36	76.6	232	2	O5ASB3_EMENT	O5asB3	aspergillus		237	36	76.6	741	1	O5R8K5_PONPY	O5R8K5	pongy	
165	36	76.6	236	2	O2XRE0_PLAFA	O2xre0	plasmodium		238	36	76.6	750	2	O9YOJ9_9ALPH	O9YOJ9	suid	harpes
166	36	76.6	278	2	O7SGQ0_NEURC	O7sgQ0	neutrospora		239	36	76.6	752	2	O6LKL3_PHOBR	O6LKL3	photobacter	
167	36	76.6	289	2	O36545_SECCR	O36545	seccale	cere	240	36	76.6	760	2	O22907_ARATH	O22907	arabidopsis	
168	36	76.6	290	2	O8T4S9_AEDAE	O8T4S9	aedes	aegypt	241	36	76.6	788	2	O7RAU2_PLAYO	O7RAU2	plasmodium	
169	36	76.6	290	2	O8T4T0_AEDAE	O8T4T0	aedes	aegypt	242	36	76.6	789	2	O6BXN0_DEBHA	O6BXN0	debaromyce	
170	36	76.6	290	2	O8T4T1_AEDAE	O8T4T1	aedes	aegypt	243	36	76.6	796	2	BUD27_YEAST	BUD27	saccharomyce	
171	36	76.6	290	2	O8T4T2_AEDAE	O8T4T2	aedes	aegypt	244	36	76.6	796	1	O8NC87_HUMAN	O8NC87	homo	sapien
172	36	76.6	290	2	O9SP61_AEDAE	O9SP61	aedes	aegypt	245	36	76.6	801	2	O59ZG4_CANAL	O59ZG4	candida	alb
173	36	76.6	300	2	O9BJW8_AEDAE	O9BJW8	aedes	aegypt	246	36	76.6	804	2	O59ZM8_CANAL	O59ZM8	candida	alb
174	36	76.6	300	2	O4E005_TRYCR	O4e005	trypanosoma		247	36	76.6	819	2	O54JY9_DICDI	O54JY9	dicystosell	
175	36	76.6	312	2	O36546_SECCR	O36546	seccale	cere	248	36	76.6	822	2	O7XCT3_ORYSA	O7XCT3	oryza	sativ
176	36	76.6	314	2	O4DCP4_TRYCR	O4dCP4	trypanosoma		249	36	76.6	822	2	O94HZ3_ORYSA	O94HZ3	oryza	sativ
177	36	76.6	318	2	O5ALF1_CANAL	O5aLI1	candida	alb	250	36	76.6	822	2				

251	36	76.6	825	2	Q6D1Y4_ERWCT	Q6d1y4_erwintia car	324	35	74.5	151	1	HSP18_CLOAB	003928_clostridium
252	36	76.6	844	2	Q6BT18_DEBHA	Q6bt18_debaryomyce	325	35	74.5	156	2	OSX233_BORGA	05x233_borrelia ga
253	36	76.6	853	2	Q59V55_CANAL	Q59v55_candida alb	326	35	74.5	163	2	Q8MZM8_TRESO	Q8mzm8_taeinia soli
254	36	76.6	865	2	Q54G58_DICDI	Q54g58_dictyosteli	327	35	74.5	175	2	Q4XAS8_PLACH	Q4xas8_plasmodium
255	36	76.6	894	2	Q54Y56_DICDI	Q54y56_dictyosteli	328	35	74.5	181	2	Q3E122_ACTSC	Q3e122_actinobacill
256	36	76.6	899	2	Q81BN8_PLAF7	Q81bn8_plasmodium	329	35	74.5	192	2	Q5XV07_ARATH	Q5xv07_arabidopsis
257	36	76.6	912	2	Q4CP12_TRYCR	Q4cp12_trypanosoma	330	35	74.5	193	2	Q9FK94_ARATH	Q9fk94_arabidopsis
258	36	76.6	917	2	Q5SB17_MAIZE	Q5sb17_zea mays (m	331	35	74.5	204	2	Q93K27_ARATH	Q93k27_arabidopsis
259	36	76.6	919	2	Q4DJL9_TRYCR	Q4djl9_trypanosoma	332	35	74.5	204	2	Q91J01_ORYSA	Q91j01_oryza sativ
260	36	76.6	923	2	Q4DDH2_TRYCR	Q4ddh2_trypanosoma	333	35	74.5	207	2	Q81J01_ORYSA	Q81j01_oryza sativ
261	36	76.6	929	1	DPOM_MAIZE	P10582_zea mays (m	334	35	74.5	236	2	Q6NLCS_ARATH	Q6n1cs_arabidopsis
262	36	76.6	929	1	Q9MJC4_MAIZE	Q9mjc4_zea mays (m	335	35	74.5	245	2	Q5BB45_EMENT	Q5bb45_aspergillus
263	36	76.6	997	2	Q7R191_PLAF7	Q7r191_plasmodium	336	35	74.5	247	2	Q4RV32_TETNG	Q4rv32_tetradodon n
264	36	76.6	1052	2	Q6BMH0_DEBHA	Q6bmh0_debaryomyce	337	35	74.5	269	1	IL1B_TRIVU	Q941h9_trichosurus
265	36	76.6	1055	2	Q59X70_CANAL	Q59x70_candida alb	338	35	74.5	277	2	Q51H20_ENTHI	Q51h20_nicotiana t
266	36	76.6	1055	2	Q59XHB_CANAL	Q59xhb_candida alb	339	35	74.5	279	2	Q51H20_ENTHI	Q51h20_nicotiana t
267	36	76.6	1076	1	YEM3_YEAST	P40021_saccharomyce	340	35	74.5	281	2	Q81L16_PLAF7	Q81l16_plasmodium
268	36	76.6	1100	2	Q5B316_EMENT	Q5b316_aspergillus	341	35	74.5	281	2	Q8FQC2_CORF	Q8fqc2_corynebacte
269	36	76.6	1144	2	Q18100_CAEEL	Q18100_caenorhabdi	342	35	74.5	287	2	Q6B2T8_YARLI	Q6b2t8_yarrowia li
270	36	76.6	1147	2	Q53U86_CAEEL	Q53u86_caenorhabdi	343	35	74.5	287	2	Q16657_CAEEL	Q16657_caenorhabdi
271	36	76.6	1177	2	Q2UKW0_ASPOR	Q2ukw0_aspergillus	344	35	74.5	288	2	Q9C610_ARATH	Q9c610_arabidopsis
272	36	76.6	1210	2	Q3E9P3_ARATH	Q3e9f3_arabidopsis	345	35	74.5	293	2	Q61M43_DICDI	Q61m43_dictyosteli
273	36	76.6	1239	2	Q81AN4_PLAF7	Q81ana_plasmodium	346	35	74.5	300	2	Q6L207_METMP	Q6l207_methanococc
274	36	76.6	1241	2	Q54DG6_DICDI	Q54dg6_dictyosteli	347	35	74.5	306	2	Q54CU2_DICDI	Q54cu2_dictyosteli
275	36	76.6	1250	2	Q624J4_CAEER	Q624j4_caenorhabdi	348	35	74.5	306	2	Q9M9C9_ARATH	Q9m9c9_arabidopsis
276	36	76.6	1257	2	Q4SKR6_DROVI	Q4skrf6_drosophila	349	35	74.5	325	2	Q7QSH9_GITAI	Q7qsh9_giardia lam
277	36	76.6	1267	2	Q54D51_DICDI	Q54d51_dictyosteli	350	35	74.5	328	2	Q24795_ECHGR	Q24795_echinococcu
278	36	76.6	1292	2	Q6C889_YARLI	Q6c889_yarrowia li	351	35	74.5	342	2	Q7X826_ORYSA	Q7x826_oryza sativ
279	36	76.6	1295	2	Q2RIQ3_ORYSA	Q2riq3_oryza sativ	352	35	74.5	352	2	Q6BWS3_DEBHA	Q6bws3_debaryomyce
280	36	76.6	1303	2	Q86KP3_DICDI	Q86kp3_dictyosteli	353	35	74.5	362	2	Q331B1_RHILE	Q331b1_rhizobium l
281	36	76.6	1310	2	Q7RHN1_PLAYO	Q7rhn1_plasmodium	354	35	74.5	362	2	Q5MB41_BORHE	Q5mb41_borrelia he
282	36	76.6	1310	2	Q86IX0_DICDI	Q86ix0_dictyosteli	355	35	74.5	365	2	Q55G49_DICDI	Q55g49_dictyosteli
283	36	76.6	1328	2	Q4PIU9_CAEEL	Q4piu9_caenorhabdi	356	35	74.5	366	2	Q461U4_9NUCL	Q461u4_trichoplusi
284	36	76.6	1331	2	Q53UB7_CAEEL	Q53ub7_caenorhabdi	357	35	74.5	368	2	Q2KDX0_RHIEF	Q2kdx0_rhizobium e
285	36	76.6	1351	2	Q7RFU8_PLAYO	Q7rf18_plasmodium	358	35	74.5	371	2	Q6NSB1_HUMAN	Q6nse1_homo sapien
286	36	76.6	1357	2	Q556A3_DICDI	Q556a3_dictyosteli	359	35	74.5	374	2	Q41366_SPIOL	Q41366_spinacia ol
287	36	76.6	1363	2	Q81AM5_PLAF7	Q81am5_plasmodium	360	35	74.5	391	2	Q3CRYS_ALUTAT	Q3cry5_pseudalter
288	36	76.6	1369	2	Q69Z18_MOUSE	Q69z18_mus musculus	361	35	74.5	396	2	Q5KG90_CRYNE	Q5kg90_cryptococcu
289	36	76.6	1419	2	Q54HA0_DICDI	Q54ha0_dictyosteli	362	35	74.5	410	2	Q02327_CAEEL	Q02327_caenorhabdi
290	36	76.6	1427	2	Q6FK39_CANGA	Q6fk39_candida gla	363	35	74.5	412	2	Q88X29_IACPL	Q88x29_lactobacilli
291	36	76.6	1446	2	Q57G11_DICDI	Q57g11_dictyosteli	364	35	74.5	413	2	Q6BQ56_DEBHA	Q6bq56_debaryomyce
292	36	76.6	1476	2	Q4DE53_TRYCR	Q4de53_trypanosoma	365	35	74.5	416	2	Q55RT7_CRYNE	Q55rt7_cryptococcu
293	36	76.6	1484	2	Q4D8L4_TRYCR	Q4d8l4_trypanosoma	366	35	74.5	416	2	Q5KG91_CRYNE	Q5kg91_cryptococcu
294	36	76.6	1570	2	Q389Q3_9TRYR	Q389q3_trypanosoma	367	35	74.5	420	2	Q4HYO2_GIBRE	Q4hyo2_gliborella
295	36	76.6	1571	2	Q81JF5_PLAF7	Q81jf5_plasmodium	368	35	74.5	422	2	Q9FKX8_ARATH	Q9fkx8_arabidopsis
296	36	76.6	1590	2	Q67WV4_ORYSA	Q67wv4_oryza sativ	369	35	74.5	423	2	Q9FW47_ARATH	Q9fw47_arabidopsis
297	36	76.6	1641	2	Q54BH0_DICDI	Q54bh0_dictyosteli	370	35	74.5	427	2	Q2M184_DROPS	Q2m184_drosophila
298	36	76.6	1657	2	Q51C65_ENTHI	Q51c65_entamoeba h	371	35	74.5	430	2	Q08729_YEAST	Q08729_saccharomyc
299	36	76.6	1943	2	Q54G63_DICDI	Q54g63_dictyosteli	372	35	74.5	439	2	Q3LIB9_HUMAN	Q3lib9_homo sapien
300	36	76.6	1972	1	BAZ2B_HUMAN	Q9uif8_homo sapien	373	35	74.5	445	2	Q96OP3_DROME	Q96op3_drosophila
301	36	76.6	1973	2	Q7NP45_GLOVI	Q7np45_gloeobacter	374	35	74.5	447	2	Q61X96_CAEER	Q61x96_caenorhabdi
302	36	76.6	2130	1	BAZ2B_CHICK	Q9del1_gallus galli	375	35	74.5	451	1	LSB3_YEAST	P43603_saccharomyc
303	36	76.6	2249	2	Q811Y8_PLAF7	Q811y8_plasmodium	376	35	74.5	455	2	Q4UIB5_THENM	Q4uib5_theliera a
304	36	76.6	2295	2	Q81ER2_PLAF7	Q81er2_plasmodium	377	35	74.5	460	2	Q9VF39_DROME	Q9vfc9_arabidopsis
305	36	76.6	2295	2	Q9TY98_PLAF7	Q9ty98_plasmodium	378	35	74.5	464	2	Q3ECN7_ARATH	Q3ecn7_arabidopsis
306	36	76.6	2379	2	Q81JQ2_PLAF7	Q81jq2_plasmodium	379	35	74.5	469	2	Q5BEM1_BRAHE	Q5bem1_brachydanio
307	36	76.6	2457	2	Q97375_PLAF7	Q97375_plasmodium	380	35	74.5	471	2	P87360_BRAHE	P87360_brachydanio
308	36	76.6	2706	2	Q97292_PLAF7	Q97292_plasmodium	381	35	74.5	472	2	Q07962_CARUB	Q07962_carassius a
309	36	76.6	2773	2	Q81BR4_PLAF7	Q81br4_plasmodium	382	35	74.5	506	2	Q43HK4_9CHUB	Q43hk4_chlorobium
310	36	76.6	2814	2	Q81C15_PLAF7	Q81c15_plasmodium	383	35	74.5	517	2	Q3EBB5_ARATH	Q3ebb5_arabidopsis
311	36	76.6	2868	2	Q4QDV7_LEIMA	Q4qdv7_leishmania	384	35	74.5	523	2	Q7RME4_PLAYO	Q7rme4_plasmodium
312	36	76.6	2994	2	Q95ZG5_DICDI	Q95zgs_dictyosteli	385	35	74.5	550	2	Q4YR25_PLAEE	Q4yxr25_plasmodium
313	36	76.6	3328	2	Q81JG6_PLAF7	Q81jg6_plasmodium	386	35	74.5	575	2	Q4XX79_PLACH	Q4xx79_plasmodium
314	36	76.6	5910	2	Q81AP1_PLAF7	Q81ap1_plasmodium	387	35	74.5	581	2	Q59UG5_CANAL	Q59ug5_candida alb
315	36	74.5	78	2	Q3MDP4_ANAVT	Q3mdp4_anabaena sp	388	35	74.5	585	2	Q59UL8_CANAL	Q59ul8_tetradodon n
316	36	74.5	78	2	Q8YPP2_ANASP	Q8ypp2_anabaena sp	389	35	74.5	592	2	Q4RRD5_TETNG	Q4rrd5_tetradodon n
317	36	74.5	82	2	Q4QD67_9RHO8	Q4qd67_jannaschia	390	35	74.5	617	2	Q5B4Q0_EMENT	Q5b4q0_aspergillus
318	36	74.5	87	2	Q6J3Q8_CANFA	Q6j3q8_canis famill	391	35	74.5	635	2	Q82253_ARATH	Q82253_arabidopsis
319	36	74.5	97	2	Q4XC35_PLACH	Q4xc35_plasmodium	392	35	74.5	647	2	Q4FW53_LEIMA	Q4fw53_leishmania
320	36	74.5	97	2	Q4B995_BURVI	Q4b995_burkholderi	393	35	74.5	658	2	Q5NVJ2_FONYF	Q5nvj2_pongo pygma
321	36	74.5	117	2	Q9LJEL_ARATH	Q9lje1_arabidopsis	394	35	74.5	664	2	Q4E4V1_TRYCR	Q4e4v1_trypanosoma
322	36	74.5	136	2	Q45UK5_SHIVL	Q45uk5_human immun	395	35	74.5	679	2	Q96176_PLAF7	Q96176_plasmodium
323	36	74.5	150	2	Q2U900_ASPOR	Q2u900_aspergillus	396	35	74.5	680	1	PIT_DROME	Q9v451_drosophila

397	35	74.5	681	2	06A809_PROAC	06A8g9	propionibac	470	34	72.3	125	2	09NH0_PLAFA	09nh0	plasmodium
398	35	74.5	682	2	057T26_9TRYE	057t26	trypanosoma	471	34	72.3	131	2	08STF4_PLAFA	08stf4	plasmodium
399	35	74.5	685	2	07ZWP4_BRARE	07zwp4	brachydanio	472	34	72.3	132	2	08AA71_BACTN	08aa71	bacteroides
400	35	74.5	715	2	069Q4_ORYSA	069q4	oryza sativ	473	34	72.3	134	2	0868X1_PLAFA	0868x1	plasmodium
401	35	74.5	716	2	086HD4_DICDI	086hd4	dictyosteli	474	34	72.3	135	2	05M0X9_STRT1	05m0x9	streptococc
402	35	74.5	724	2	06MWT1_NEUCR	06mwt1	neutrospora	475	34	72.3	135	2	05M5G6_STRT2	05m5g6	streptococc
403	35	74.5	724	2	02MNX3_FLOBE	02mnx3	clostridial	476	34	72.3	136	2	0590Y2_CANAL	0590y2	candida alb
404	35	74.5	724	2	03IF93_PSEHT	03if93	pseudotaller	477	34	72.3	136	2	077177_PLAFA	077177	plasmodium
405	35	74.5	734	2	06Z7V1_ORYSA	06z7v1	oryza sativ	478	34	72.3	136	2	03BHK9_PLAFA	03bhk9	plasmodium
406	35	74.5	738	2	05XX08_MONO	05xx08	sudan ebola	479	34	72.3	136	2	03BUL6_PLAFA	03bul6	plasmodium
407	35	74.5	774	2	094170_PNECA	094170	pneumocysti	480	34	72.3	137	2	03BFS8_PLAFA	03bfs8	plasmodium
408	35	74.5	791	2	09VTC1_PNECA	09vtc1	dictyostella	481	34	72.3	137	2	08T513_PLAFA	08t513	plasmodium
409	35	74.5	793	2	021053_CAEEL	021053	caenorhabdi	482	34	72.3	138	2	03BRG7_PLAFA	03brg7	plasmodium
410	35	74.5	798	2	08SP32_DICDI	08sp32	dictyosteli	483	34	72.3	138	2	03B132_PLAFA	03b132	plasmodium
411	35	74.5	810	2	07SC92_NEUCR	07sc92	neutrospora	484	34	72.3	139	2	03B165_PLAFA	03b165	plasmodium
412	35	74.5	812	2	02LZX7_DROPS	02lzx7	trypanosoma	485	34	72.3	139	2	02ZY49_STRSU	02zy49	streptococc
413	35	74.5	813	2	0584Y5_9TRYE	0584y5	trypanosoma	486	34	72.3	139	2	017393_CAREL	017393	caenorhabdi
414	35	74.5	816	2	05M1X1_STRT1	05m1x1	streptococc	487	34	72.3	140	2	017393_CAREL	017393	caenorhabdi
415	35	74.5	816	2	05M6G1_STRT2	05m6g1	streptococc	488	34	72.3	144	2	0330E3_9GAMM	0330e3	shewanella
416	35	74.5	825	2	055CM6_DICDI	055cm6	dictyosteli	489	34	72.3	147	2	06FVN4_CANGA	06fyn4	candida gla
417	35	74.5	833	1	SPB1_KLUDA	06cvi1	kluyveromyc	490	34	72.3	148	2	060UTC3_CABER	060utc3	caenorhabdi
418	35	74.5	844	2	0553N1_DICDI	055n1	dictyosteli	491	34	72.3	151	2	05ANM5_CANAL	05anm5	candida alb
419	35	74.5	845	1	SPB1_ASHGO	0751n1	ashbya goss	492	34	72.3	152	2	03CPH0_THRET	03cph0	thermoanaeae
420	35	74.5	873	2	04RGS2_USTMA	04rgs2	neutrospora	493	34	72.3	163	2	03T1L4_MOUSE	03t1l4	mus musculul
421	35	74.5	888	2	07RXL7_NEUCR	07rxl7	neutrospora	494	34	72.3	163	2	093VF4_ARATH	093vf4	arabidopsis
422	35	74.5	960	2	09V5L1_DROME	09v5l1	dirosophila	495	34	72.3	165	1	MCH_RAT	mch_rat	rattus norv
423	35	74.5	962	2	04Z8K6_DROME	04z8k6	dirosophila	496	34	72.3	165	2	0816F7_BACCR	0816f7	bacillus ce
424	35	74.5	972	2	054F86_DICDI	054f86	dictyosteli	497	34	72.3	168	2	03ERM0_BACTA	03erm0	bacillus th
425	35	74.5	985	2	04DTD3_TRYCR	04dtd3	trypanosoma	498	34	72.3	169	2	075HG1_ORYSA	075hg1	oryza sativ
426	35	74.5	1006	2	08EMF6_MYCPE	08emf6	mycoplasma	499	34	72.3	177	1	ARGR1_YEAST	argr1	saccharomyc
427	35	74.5	1018	2	07S706_NEUCR	07s706	neutrospora	500	34	72.3	212	2	0541N9_DICDI	0541n9	dictyostelli
428	35	74.5	1026	2	086B03_DICDI	086b03	dictyosteli								
429	35	74.5	1037	2	05CGQ8_CRYHO	05cgq8	cryptospori								
430	35	74.5	1038	2	09P4C6_PICPA	09p4c6	pichia past								
431	35	74.5	1040	2	05CSD0_CRYPY	05csd0	cryptospori								
432	35	74.5	1046	2	054118_DICDI	054118	dictyosteli								
433	35	74.5	1047	2	07RPJ9_PLAYO	07rpj9	plasmodium								
434	35	74.5	1054	2	04D0T2_TRYCR	04d0t2	trypanosoma								
435	35	74.5	1055	2	055G65_DICDI	055g65	dictyosteli								
436	35	74.5	1172	2	07S592_NEUCR	07s592	neutrospora								
437	35	74.5	1199	2	054Q41_DICDI	054q41	dictyosteli								
438	35	74.5	1345	1	YHO0_YEAST	Y88800	saccharomyc								
439	35	74.5	1349	2	05OYB8_ENTHI	05oyb8	entamoeba h								
440	35	74.5	1349	2	06RCM0_ENTHI	06rcm0	entamoeba h								
441	35	74.5	1442	2	0815V9_PLAFA	0815v9	plasmodium								
442	35	74.5	1469	2	05SVU9_CRYNE	05svu9	cryptococcu								
443	35	74.5	1469	2	05KKR0_CRYNE	05kke0	cryptococcu								
444	35	74.5	1559	2	08IDC3_PLAFA	08idc3	plasmodium								
445	35	74.5	1671	2	054M02_DICDI	054m02	dictyosteli								
446	35	74.5	1726	1	SPT6H_BRARE	08hvK2	brachydanio								
447	35	74.5	2039	2	0658K1_HUMAN	0658k1	homo sapien								
448	35	74.5	2062	1	ANR12_HUMAN	06ub98	homo sapien								
449	35	74.5	2122	2	054EA3_DICDI	054ea3	dictyosteli								
450	35	74.5	2169	2	097312_PLAFA	097312	plasmodium								
451	35	74.5	2452	1	RPB1_PLAFA	Pl4248	plasmodium								
452	35	74.5	2461	2	03AR75_CHLCH	03ar75	chlorobium								
453	35	74.5	2573	2	096185_PLAFA	096185	plasmodium								
454	35	74.5	2594	2	07RJKA_PLAYO	07rjka	plasmodium								
455	35	74.5	4507	2	07RRG7_PLAYO	07rrg7	plasmodium								
456	35	74.5	4805	2	07RRM5_PLAYO	07rrm5	plasmodium								
457	34	72.3	61	2	03ITV8_NATPD	03itv8	nationomona								
458	34	72.3	69	2	07XPYA_ORYSA	07xpy4	oryza sativ								
459	34	72.3	74	2	04YEG5_PLABE	04yeg5	plasmodium								
460	34	72.3	85	2	08DPF8_VIRBU	08dpf8	vibrio vuln								
461	34	72.3	101	2	04NCX5_9MICC	04ncx5	arthrobacte								
462	34	72.3	104	2	09XG51_LYCES	09xg51	lycoperstico								
463	34	72.3	113	2	041VN3_DESHA	041vn3	desulfotoba								
464	34	72.3	114	2	086HP6_DICDI	086hp6	dictyosteli								
465	34	72.3	115	2	03BHE1_PLAFA	03bhe1	plasmodium								
466	34	72.3	123	2	09SW71_PLAFA	09sw71	plasmodium								
467	34	72.3	124	2	081G20_BACCR	081g20	bacillus ce								
468	34	72.3	125	2	03BWS5_PLAFA	03bws5	plasmodium								
469	34	72.3	125	2	095VW2_PLAFA	095vw2	plasmodium								

RESULT 1																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
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RESULT 1				
SCKA_PANIM	STANDARD;	PRT;	47 AA.	
ID_SCKA_PANIM				
AC	P55927;			
DT	01-NOV-1997, integrated into UniProtKB/Swiss-Prot.			
DT	15-DEC-1998, sequence version 2.			
DT	07-FEB-2006, entry version 47.			
DE	Potassium channel-blocking toxin PiTX-K-alpha precursor (Pandinotoxin alpha) (Potassium channel-blocking toxin 2) (Pi2) (Pi-2) (Alpha-KTX 7.1) (Fragment).			
GN	Name=PiTX-1;			
OS	Pandinus imperator (Emperor scorpion).			
CC	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones			
CC	Inulida; Scorpimorda; Scorpimidae; Scorpioninae; Pandinus.			
OX	NCBI_TaxId=55084;			
RA	NUCLEOTIDE SEQUENCE [MRNA].			
RA	Rogowski R.S., Collins J.H., O'Neill T.J., Gustafson T.A.,			
RA	Wexman T.R., Rogawski M.A., Tenenholz T.C., Weber D.J.,			
RA	Blaustein M.P.;			
RL	Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	PROTEIN SEQUENCE OF 13-47.			
RC	TISSUE=Venom;			
RC	MEDLINE=97070422; PubMed=8913348;			
EX	Rogowski R.S., Collins J.H., O'Neill T.J., Gustafson T.A.,			
RA	Wexman T.R., Rogawski M.A., Tenenholz T.C., Weber D.J.,			
RA	Blaustein M.P.;			
RT	"Three new toxins from the scorpion Pandinus imperator selectively			
RT	block certain voltage-gated K+ channels.";			
RL	Mol. Pharmacol. 50:1167-1177(1996).			
RP	[3]			
RP	PROTEIN SEQUENCE OF 13-47, AND FUNCTION.			
RC	TISSUE=Venom;			
EX	MEDLINE=96304303; PubMed=8660410; DOI=10.1007/s002329900084;			
RA	Gomez-Lagunas F., Olamendi-Portugal T., Zamudio F.Z., Possas L.D.			
RT	"Two novel toxins from the venom of the scorpion Pandinus imperator			



```

RT show that the N-terminal amino acid sequence is important for their
RT affinities towards Shaker B K+ channels."
RL J. Membr. Biol. 152:49-56(1996).
[4]
RN STRUCTURE BY NMR.
RX MEDLINE=97215813; PubMed=9062103; DOI=10.1021/bj9628432;
RA Tenenholz T.C., Rogowski R.S., Collins J.H., Blaustein M.P.,
RA Weber D.J.;
RT "Solution structure for Pandinus toxin K-alpha (Pitx-K alpha), a
RT selective blocker of A-type potassium channels."
RL Biochemistry 36:2763-2771(1997).
CC -1- FUNCTION: Potent inhibitor of the A-type voltage-gated potassium
CC channels. Most potent inhibitor of Kv1.2/KCNA2 channels.
CC Reversibly block the Shaker B potassium-channels (Kv1.1 sub-
CC family).
CC -1- SUBCELLULAR LOCATION: Secreted protein.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- SIMILARITY: Belongs to the short scorpion toxin family. Potassium
CC channel inhibitor subfamily.
CC -----
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CC
CC EMBL; U79579; AA852576.1; -; mRNA.
CC PIR; T10471; T10471.
CC DR PDB; 2PTA; NMR; @=13-47.
CC DR Linkhub; P55927; -
CC DR InterPro; IPR001947; Scorpion_toxins.
CC DR Pfam; PF00451; Toxin_2; 1.
CC DR PRINTS; PR00286; CHARYBOTOXIN.
CC DR ProDom; PD003586; Scorpion_toxins; 1.
CC DR PROSITE; PS01138; SCORP_SHORT_TOXIN; 1.
CC KW 3D-structure; Direct protein sequencing; Ionic channel inhibitor;
CC Neurotoxin; Potassium channel inhibitor; Signal; Toxin.
CC FT SIGNAL <1 12
CC FT PEPIDE 13 47 Potassium channel-blocking toxin Pitx-K-
CC alpha.
CC /FTid=PRO_0000035328.
CC
CC FT DISULFID 16 37
CC FT DISULFID 22 42
CC FT DISULFID 26 44
CC FT NON_TER 1 1
CC FT STRAND 17 18
CC FT HELIX 19 29
CC FT TURN 30 30
CC FT STRAND 31 31
CC FT STRAND 35 38
CC FT TURN 39 40
CC FT STRAND 41 45
CC SQ SEQUENCE 47 AA; 5434 MW; 2188BF110A37BD7C CRC64;
Query Match 100.0%; Score 47; DB 1; Length 47;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYKDDDDK 8
Db 5 DYKDDDDK 12

```

```

RESULT 2
Q8NFNG HUMAN PRELIMINARY; PRT; 319 AA.
AC Q8NFNG;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DE RGS3 isoform RGS3S.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2203288; PubMed=12036301; DOI=10.1006/geno.2002.6773;
RA Kehl J.H., Srikumar D., Harrison K., Wilson G.L., Shi C.S.;
RT "Additional 5' exons in the RGS3 locus generate multiple mRNA
RT transcripts, one of which accounts for the origin of human PDZ-RGS3."
RL Genomics 79:860-868(2002).
CC -1- SIMILARITY: Contains 1 RGS domain.
CC -----
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CC
CC EMBL; AF490838; AA033253.1; -; mRNA.
CC DR HSSP; P49799; IAGR.
CC DR EMBL; ENSG00000158935; Homo sapiens.
CC DR GO; GO:0004871; F:signal transducer activity; IEA.
CC DR InterPro; IPR000342; RGS.
CC DR Pfam; PF00615; RGS; 1.
CC DR PRINTS; PR01301; RGS_PROTEIN.
CC DR ProDom; PD001580; Reg1_Gproteins; 1.
CC DR SMART; SM00315; RGS; 1.
CC DR PROSITE; PS0132; RGS; 1.
CC SQ SEQUENCE 319 AA; 36094 MW; 998632C6E9B1F0F3 CRC64;
Query Match 100.0%; Score 47; DB 2; Length 319;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYKDDDDK 8
Db 312 DYKDDDDK 319

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RESULT 3
Q36Q46 MARRY PRELIMINARY; PRT; 246 AA.
ID Q36Q46;
AC Q36Q46;
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 06-DEC-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Uncharacterized conserved membrane or secreted protein precursor.
GN ORFNames=MaquDRAPT_1112;
OS Marinobacter aquaeolei VT8.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Marinobacter.
OC NCBI_TaxID=351348;
OX [1]
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VT8;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome of Marinobacter aquaeolei VT8."
RT Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC
CC EMBL; AL001000011; EAO98985.1; -; Genomic_DNA.
CC SIGNAL 1 22 Potential.
FT

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SQ SEQUENCE 246 AA; 26731 MW; C1CCEPE80E0E24EA CRC64;
Query Match 91.5%; Score 43; DB 2; Length 246;
Best Local Similarity 87.5%; Pred. No. 58;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
Db 223 DYEDDDDK 230

RESULT 4
Q4X9J6 PLACH PRELIMINARY; PRT; 154 AA.
ID Q4X9J6 PLACH PRELIMINARY; PRT; 154 AA.
AC Q4X9J6;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Hypochemical protein (Fragment).
GN ORFNames=PC404555.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
RA Britman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Church C.M.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Batwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Stinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
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CC -----
DR EMBL: CAJ01008539; CAH86427.1; -; Genomic_DNA.
DR InterPro: IPR006484; PIST-B; 1.
DR TrEMBL: TIGR01597; PIST-B; 1.
KW Hypochemical protein.
FT NON TER 154
SQ SEQUENCE 154 AA; 18627 MW; 3CC4FE0E30746F404 CRC64;

Query Match 89.4%; Score 42; DB 2; Length 154;
Best Local Similarity 87.5%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
Db 76 DYNDDDDK 83

RESULT 5
Q7Y283 PLACH PRELIMINARY; PRT; 284 AA.
ID Q7Y283 PLACH PRELIMINARY; PRT; 284 AA.
AC Q7Y283;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE PC10106C.
GN ORFNames=PC10106C;
OS Plasmodium chabaudi chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=31271;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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RC STRAIN=AS;
RX MEDLINE=22672904; PubMed=12787350;
RX DOI=10.1046/j.1365-2958.2003.03491.x;
RA Fischer K., Chavich M., Huestis R., Wilson D.W., Kemp D.J., Saul A.;
RT "Ten families of variant genes encoded in subtelomeric regions of
RT multiple chromosomes of Plasmodium chabaudi, a malaria species that
RT undergoes antigenic variation in the laboratory mouse.";
RL Mol. Microbiol. 48:1209-1223(2003).
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CC -----
DR EMBL: AY149028; AAC06133.1; -; Genomic_DNA.
DR InterPro: IPR006484; PIST-B.
DR TrEMBL: TIGR01597; PIST-B; 1.
SQ SEQUENCE 284 AA; 34079 MW; 31EE4D0DF6243FAC CRC64;

Query Match 89.4%; Score 42; DB 2; Length 284;
Best Local Similarity 87.5%; Pred. No. 97;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
Db 72 DYNDDDDK 79

RESULT 6
Q6FN57 CANGA PRELIMINARY; PRT; 586 AA.
ID Q6FN57 CANGA PRELIMINARY; PRT; 586 AA.
AC Q6FN57;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Similar to sp|P38748 Saccharomyces cerevisiae YHL010C.
GN OrdereducusNames=CAGC0K02563;
OS Candida glabrata (Yeast) (Totipotopsis glabrata); Saccharomycetes;
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5478;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=ATCC 2001 / CBS 138;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durand P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Geoffard N., Frangeul L., Aigle M., Anboudar V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boissame A., Boyer J., Cartolico L., Contandriou F., de Darvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantaye F., Hennequin C., Jaumaux N., Joyet P., Kachouri R.,
RA Karrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicoud J.-M., Nikolski M., Ortiz S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Sureau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
-!- SIMILARITY: Contains 1 RING-type zinc finger.
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CC -----
DR EMBL: CR380957; CAG61298.1; -; Genomic_DNA.
DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO: GO:0046872; F:metal ion binding; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0016567; F:protein ubiquitination; IEA.
DR InterPro: IPR011422; BRAP2.
DR InterPro: IPR001841; ZnF_RING.
DR InterPro: IPR001607; ZnF_UBP.

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DR Pfam: PF07576; BRAP2.1.  
 DR Pfam: PF00097; zF-C3HC4.1.  
 DR Pfam: PF02148; zF-UBP.1.  
 DR SMART: SM00184; RING.1.  
 DR SMART: SM00290; ZNF\_UBP.1.  
 DR PROSITE: PS50089; zF\_RING\_2.1.  
 DR Complete proteome; Metal-binding; Zinc; Zinc-finger.  
 SW SEQUENCE 586 AA; 68333 MW; 550DFA56268A1321 CRC64;

Query Match 89.4%; Score 42; DB 2; Length 586;  
 Best Local Similarity 87.5%; Pred. No. 2.1e+02;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDD 8  
 Db 401 NYKDDDDK 408

RESULT 7  
 ID Q2PEW5 TRIPR PRELIMINARY; PRT; 603 AA.  
 AC Q2PEW5  
 DT 07-FEB-2006, integrated into UniProtKB/TrEMBL.  
 DT 07-FEB-2006, sequence version 1.  
 DE Putative phosphoinositide specific phospholipase C.  
 OS Trifolium pratense (Red clover).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 OC Rosids; eutrosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
 OC Trifolium.  
 OC NCBI\_TaxID=57577;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed:13679984; DOI=10.1007/s00122-003-1412-z;  
 RA Isobe S., Kikmenko I., Iwashita S., Gau M., Kozlov N.N.;  
 RT "First RFLP linkage map of red clover (Trifolium pratense L.) based on  
 RT cDNA probes and its transferability to other red clover germplasm.",  
 RL Theor. Appl. Genet. 108:105-112(2003).  
 RL [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Sato S., Isobe S., Asamizu E., Nakamura Y., Ohmido N., Sakurai N.,  
 RA Kikmenko I., Sasamoto S., Wada T., Watanabe A., Tabata S.;  
 RT "Comprehensive structural analysis of the genome of red clover  
 RT (Trifolium pratense).";  
 RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.  
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 CC -----  
 DR EMBL: AB36785; BAE71237.1; -; mRNA.  
 SQ SEQUENCE 603 AA; 68714 MW; FA71D84631E30A31 CRC64;

Query Match 89.4%; Score 42; DB 2; Length 603;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDD 7  
 Db 311 DYKDDDD 317

RESULT 8  
 ID Q6FK24 CANGA PRELIMINARY; PRT; 1385 AA.  
 AC Q6FK24  
 DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.  
 DT 19-JUL-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 13.  
 DE Similar to ap1p5177 Saccharomyces cerevisiae YBR081c SPT7  
 DE Transcriptional activator.  
 GN OrderdLocustNames=CAGL0M017389;  
 OS Candida glabrata (Yeast) (Torulopsis glabrata).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; mitospotic Saccharomycetales; Candida.  
 OC NCBI\_TaxID=5478;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).  
 RC STRAIN=ATCC 2001 / CBS 138;  
 RX PubMed:15229592; DOI=10.1038/nature02579;  
 RA Dujon B., Sherman D., Fischer G., Durieux P., Casaregola S.,  
 RA Lafontaine I., de Montigny J., Marc C., Neuvéglise C., Talla E.,  
 RA Goffard N., Frangeul L., Aigle M., Anhouard V., Babor A., Barde V.,  
 RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,  
 RA Boissarie A., Boyer J., Catolico L., Confantolero F., de Darvar A.,  
 RA Despons L., Fabre E., Fairhead C., Ferry-Dunazet H., Groppi A.,  
 RA Hantreay F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Miller H.,  
 RA Nicoud J.-M., Nikolski M., Oztas S., Ozler-Kalogeropoulos O.,  
 RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,  
 RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
 RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,  
 RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,  
 RA Wincker P., Souciet J.-L.,  
 RL "Genome evolution in yeasts."  
 RL Nature 430:35-44(2004).  
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 CC -----  
 DR EMBL: CR380959; CAG62396.1; -; Genomic DNA.  
 DR InterPro: IPR001487; Bromodomain.  
 DR Pfam: PF00439; Bromodomain.1.  
 DR PRINTS: PR00503; BROMODOMAIN.  
 DR SMART: SMO0297; BROMO.1.  
 DR PROSITE: PS00633; BROMODOMAIN\_1; 1.  
 DR PROSITE: PS50014; BROMODOMAIN\_2; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 1385 AA; 157899 MW; E722C657091CE53E CRC64;

Query Match 89.4%; Score 42; DB 2; Length 1385;  
 Best Local Similarity 87.5%; Pred. No. 5.2e+02;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDD 8  
 Db 546 DYKDDNDK 553

RESULT 9  
 ID Q91BJ4 NPVST PRELIMINARY; PRT; 399 AA.  
 AC Q91BJ4  
 DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.  
 DT 01-DEC-2001, sequence version 1.  
 DT 07-FEB-2006, entry version 10.  
 DE Hypothetical protein.  
 OS Spodoptera litura multicausid nucleopolyhedrovirus (SplmNPV).  
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;  
 OC Nucleopolyhedrovirus.  
 OC NCBI\_TaxID=46242;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RP STRAIN=G2;  
 RX MEDLINE=21425398; PubMed=11531416; DOI=10.1006/viro.2001.1056;  
 RA Yang Y., Yu J., Wang L., Hu X., Bao W., Li G., Chen C., Han H., Hu S.,  
 RA Yang H.;  
 RT "Sequence analysis of the Spodoptera litura multicausid  
 RT nucleopolyhedrovirus genome.";  
 RL Virology 287:391-404(2001).  
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 CC -----  
 DR EMBL: AF25155; AA010710.1; -; Genomic DNA.  
 DR Hypothetical protein.

SQ SEQUENCE 399 AA; 47305 MW; 877F2E6A5DE0E1E1 CRC64;  
 Query Match 87.2%; Score 41; DB 2; Length 399;  
 Best Local Similarity 87.5%; Pred. No. 2e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DYKDDDDK 8  
 DB 360 DYKDDDDK 367  
 RESULT 10  
 SPR28 YEAST STANDARD; PRT; 423 AA.  
 ID 004921;  
 DT 26-APR-2004, integrated into UniProtKB/Swiss-Prot.  
 DT 01-NOV-1996, sequence version 1.  
 DT 07-MAR-2006, entry version 33.  
 DE Sporulation-regulated protein 28.  
 GN Name=SPR28; Ordered locus names=YDR218C; ORF names=YD9934.03C;  
 OS *Saccharomyces cerevisiae* (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=5288C / AB972;  
 RX MEDLINE=97313263; PubMed=9169867;  
 RA Jacq C., Alt-Moerle J., Andre B., Arnold W., Bahr A., Ballista J.P.G.,  
 RA Barges M., Baron L., Becker A., Bileau N., Bloeker H., Blugeon C.,  
 RA Boskovic J., Brandt P., Bruckner M., Buitrago M.J., Coester F.,  
 RA Delaveau T., del Rey F., Dujon B., Eide L.G., Garcia-Cantalejo J.M.,  
 RA Goffeau A., Gomez-Perez A., Granotier C., Hanemann V., Hankeln T.,  
 RA Hohnes J.D., Jaeger W., Jimenez A., Joniaux J.-L., Kraemer C.,  
 RA Kuester H., Laamanen P., Legros Y., Louis E.J., Moeller-Rieker S.,  
 RA Monnet A., Moro M., Mueller-Auer S., Nussbaumer B., Paricio N.,  
 RA Paulin L., Perea J., Perez-Alonso M., Perez-Ortin J.E., Pohl T.M.,  
 RA Puydt H., Purnelle B., Raemussen S.W., Remacha M.A., Revuelta J.L.,  
 RA Rieger M., Salom D., Saluz H.P., Saiz J.B., Saren A.-M., Schaefer M.,  
 RA Scharfe M., Schmidt E.R., Schneider C., Scholler P., Schwarz S.,  
 RA Soler-Mita A., Urtizteazu L.A., Verhasselt P., Vissers S., Voet M.,  
 RA Volckaert G., Wagner G., Wambutt R., Wedler E., Wiesler H., Woelfl S.,  
 RA Harris D.E., Bowman S., Brown D., Churcher C.M., Connor R., Dedman K.,  
 RA Gentles S., Hamlin N., Hunt S., Jones L., McDonald S., Murphy L.D.,  
 RA Niblett D., Odell C., Oliver K., Rajandream M.A., Richards C.,  
 RA Shore L., Walsh S.V., Bartell B.G., Dietrich F.S., Molligan J.T.,  
 RA Allen E., Araujo R., Aviles E., Berro A., Carpenter J., Chen E.,  
 RA Cherry J.M., Chung E., Duncan M., Hunkle-Smith S., Hyman R.W.,  
 RA Komp C., Lahekari D., Lew H., Lin D., Mosedale D., Nakahara K.,  
 RA Namach A., Oefner P., Oh C., Petel F.X., Roberts D., Schramm S.,  
 RA Schroeder M., Shogren T., Shroff N., Minant A., Yelton M.A.,  
 RA Botstein D., Davis R.W., Johnston M., Andrews S., Brinkman R.,  
 RA Cooper J., Ding H., Du Z., Favell A., Fulton L.W., Gattung S.,  
 RA Greco T., Hallsworth K., Hawkins J., Haller L.W., Jier M.,  
 RA Johnson D., Johnston L., Kirsten J., Kucaba T., Langston Y.,  
 RA Latreille P., Le T., Mardis E., Menezes S., Miller N., Nhan M.,  
 RA Pauley A., Peluso D., Rifkin L., Riles L., Taich A., Trevaekis E.,  
 RA Vignati D., Wilcox L., Wohlman P., Vaudin M., Wilson R.,  
 RA Waterston R., Alberman K., Han J., Heumann K., Kleine K.,  
 RA Mewes H.-W., Zollner A., Zaccaria P.;  
 RT "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome IV.";  
 RN Nature 387:75-78(1997).  
 RP SUBCELLULAR LOCATION, DEVELOPMENTAL STAGE, AND INTERACTIONS WITH CDC11  
 AND SPR3.  
 RP MEDLINE=97039860; PubMed=8885406;  
 RA de Virgilio C., Dewarini D.J., Pringle J.R.;  
 RT "SPR28, a sixth member of the septin gene family in *Saccharomyces*  
 CC *cerevisiae* that is expressed specifically in sporulating cells.";  
 CC Microbiology 147:2897-2905(1996).  
 CC -!- FUNCTION: Septins are GTPases involved in cytokinesis that  
 CC assemble into filaments and form a ring at the cleavage site. May  
 CC act by recruiting MYO1 and HOF1, a protein involved in septation,

CC to the site of cleavage. Septins are also involved in cell  
 CC morphogenesis, bud site selection, chitin deposition, cell cycle  
 CC regulation, cell compartmentalization and spore wall formation  
 CC (By similarity).  
 CC -!- SUBUNIT: Interacts with itself. Interacts with CDC11 and SPR3;  
 CC probably to form a ring at the bud neck.  
 CC -!- INTERACTION:  
 CC P32458: CDC11; NbExp=2; Interact=EBI-38416, EBI-4178;  
 CC -!- SUBCELLULAR LOCATION: Membrane-associated. Present at the bud neck  
 CC during cell division. Probably interacts with phosphatidylinositol 5-  
 CC as phosphatidylinositol 4-phosphate or phosphatidylinositol 5-  
 CC phosphate (By similarity). Localizes to ring-like structures  
 CC around each of the four nuclear lobes at the onset and during  
 CC meiosis II. Concentrated initially at the leading edge of the  
 CC developing prospore wall.  
 CC -!- DEVELOPMENTAL STAGE: Expressed during meiosis and ascospore  
 CC formation. First expressed at the beginning of meiosis I, and is  
 CC highly expressed prior meiosis II.  
 CC -!- SIMILARITY: Belongs to the septin family.  
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 CC -----  
 CC EMBL; Z48612; CA88498.1; -; Genomic DNA.  
 CC PIR; S59425; S59425.  
 CC Inact; Q04921; -.  
 CC DR Ensembl; YDR218C; *Saccharomyces cerevisiae*.  
 CC DR GenomeReviews; Z71256.GR; YDR218C.  
 CC SGD; S000002626; SPR28.  
 CC BioCyc; SCER-S28-01:SCER-S28-01-001235-MONOMER; -.  
 CC Linkhub; Q04921; -.  
 CC DR GO; GO:0000144; C:septin ring (sensu *Saccharomyces*); TAS.  
 CC DR GO; GO:0005515; F:structural constituent of cytoskeleton; TAS.  
 CC DR GO; GO:0007047; P:cell wall organization and biogenesis; TAS.  
 CC DR GO; GO:0009022; P:cellular morphogenesis; TAS.  
 CC DR InterPro; IPR000038; Cell Div GTP Bd.  
 CC DR PANTHER; PTHR18884; GTP Cell Div; 2.  
 CC DR Pfam; PF00735; GTP CDC; 1.  
 CC DR Prodom; PD002565; GTP Cell Div; 1.  
 CC KM Cell cycle; Cell division; Coiled coil; Complete proteome;  
 CC GTP-binding; Membrane; Nucleotide-binding.  
 CC FT CHAIN 1 423  
 FT NP\_BIND 38 45 /FTID=PRO\_0000173501.  
 FT FT COILED 384 417 GTP (Potential).  
 FT COMPBIAS 60 68 Poly-Asp.  
 SQ SEQUENCE 423 AA; 48193 MW; EB8D3C0F47CD41DB CRC64;  
 Query Match 87.2%; Score 41; DB 1; Length 423;  
 Best Local Similarity 87.5%; Pred. No. 2.2e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DYKDDDDK 8  
 DB 62 DYKDDDDK 69  
 RESULT 11  
 Q21W25\_RHOA PRELIMINARY; PRT; 452 AA.  
 AC Q21W25;  
 DT 07-MAR-2006, integrated into UniProtKB/TrEMBL.  
 DT 07-MAR-2006, entry version 1.  
 DE Trigger factor.  
 GN ORFNames=RPB\_2562;  
 OS *Rhodospseudomonas palustris* Haa2.  
 CC Bacteriia; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 CC Bradyrhizobiaceae; Rhodospseudomonas.  
 OX NCBI\_TaxID=316058;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Ha2;  
 RA US DOE Joint Genome Institute;  
 RA Copeland A., Lucas S., Lapidus A., Barry K., Deter J.C., Glavina T.,  
 RA Hammon N., Istrani S., Plitnick S., Chain P., Malatki S., Shin M.,  
 RA Vergez L., Schmutz J., Larimer F., Land M., Hauser L., Pelletier D.A.,  
 RA Kyriakides N., Anderson I., Oda Y., Harwood C.S., Richardson P.,  
 RT "Complete sequence of Rhodopseudomonas palustris Ha2.",  
 RL Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.  
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 CC -----  
 DR EMBL: CP000250; ABD07265.1; -; Genomic DNA.  
 CC  
 DR SEQUENCE 452 AA; 5011 MW; 4F805CD3AC1A2E5D CRC64;

Query Match 87.2%; Score 41; DB 2; Length 452;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDDK 8  
 DB 443 YKDDDDK 449

RESULT 12  
 ID Q6VZM2 CNPV PRELIMINARY; PRT; 1767 AA.  
 AC Q6VZM2-  
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
 DT 05-JUL-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 8.  
 DE CNPVI25 variola B22R-like protein.  
 GN Name=CNPVI25;  
 OS Canarypox virus (CNPV).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Avipoxvirus.  
 OC NCBI\_TaxID=44088;  
 RX NCB1 [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=ATCC VR-111;  
 RX PubMed14671117; DOI=10.1128/JVI.78.1.353-366.2004;  
 RA Tulman E.R., Afonso C.L., Lu Z., Zsak L., Kutish G.F., Rock D.L.,  
 RT "The genome of canarypox virus."  
 RL J. Virol. 78:353-366(2004).  
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 CC -----  
 DR EMBL: AY318871; AAR83471.1; -; Genomic DNA.  
 DR InterPro: IPR007490; Poxvirus\_B22R.  
 DR Pfam: PF04395; Poxvirus\_B22R; 1.  
 SO SEQUENCE 1767 AA; 195286 MW; 1408E4F8C52547A5 CRC64;

Query Match 85.1%; Score 40; DB 2; Length 1767;  
 Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
 DB 1680 DYKDDDK 1687

RESULT 13  
 ID Q8UKJ5 GVIRU PRELIMINARY; PRT; 322 AA.  
 AC Q8UKJ5;  
 DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.  
 DT 01-OCT-2002, sequence version 1.  
 DT 07-FEB-2006, entry version 8.  
 DE Orf118.  
 GN Name=orf118;  
 OS Helicobacter zea virus 1.  
 OC Viruses; dsDNA viruses, no RNA stage; unclassified dsDNA viruses.

OX NCBI\_TaxID=29250;  
 RN [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22174892; PubMed=12186886;  
 RA DOI=10.1128/JVI.76.18.9024-9034.2002;  
 RA Cheng C.H., Liu S.M., Chow T.Y., Hsiao Y.Y., Wang D.P., Huang J.J.,  
 RA Chen H.H.,  
 RT "Analysis of the complete genome sequence of the Hs-1 virus suggests  
 that it is related to members of the Baculoviridae";  
 RL J. Virol. 76:9024-9034(2002).  
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 CC -----  
 DR EMBL: AF451898; AAN04411.1; -; Genomic DNA.  
 SO SEQUENCE 322 AA; 36706 MW; 22B5C1209717A90 CRC64;

Query Match 83.0%; Score 39; DB 2; Length 322;  
 Best Local Similarity 75.0%; Pred. No. 3.4e+02;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
 DB 271 DYKDDDK 278

RESULT 14  
 ID Q4N797 THEPA PRELIMINARY; PRT; 432 AA.  
 AC Q4N797;  
 DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.  
 DT 02-AUG-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 8.  
 DE ATP-dependent helicase, putative.  
 GN ORFNames=rp01\_0923;  
 OS Theileria parva.  
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;  
 OC Theileria.  
 OC NCBI\_TaxID=5875;  
 RX NCB1 [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Muguga;  
 RX PubMed=15994558; DOI=10.1126/science.1110439;  
 RA Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,  
 RA Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.,  
 RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,  
 RA Jiang L., Lynn J., Weaver B., Shoabai A., Domingo A.R., Maasouk D.,  
 RA Creditre J., Wortman J.R., Haas B., Anguioni S.V., Creasy T.H., Lu C.,  
 RA Sun B., Silva J.C., Uteback T.R., Feldblyum T.V., Perera M.,  
 RA Allen J., Nieman W.C., Taracha E.L., Salzberg S.L., White O.R.,  
 RA Fitzhugh H.A., Morzaria S., Venter J.C., Fraser C.M., Nene V.,  
 RT "Genome Sequence of Theileria parva, a Bovine Pathogen That Transforms  
 Lymphocytes";  
 RL Science 309:134-137(2005).  
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 CC -----  
 RN [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Muguga;

RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,  
 RA Ren O., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,  
 RA Ralph S.A., Mann D.J., Xiong Z., Shallow S., Midman J., Jiang L.,  
 RA Lynn J., Weaver B., Shoabi A., Waswo D., Crabtree J., Wotman J.R.,  
 RA Haas B., Anguoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,  
 RA Uteback T., Feldblum T., Petrea M., Allen J., Taracha E.L.,  
 RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,  
 RA Fraser C.M., Nene V.;  
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
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DR EMBL, AAGK01000001, EAM34161.1, -, Genomic DNA.  
 DR GO, GO:0005524, F:ATP binding; IEA.  
 DR GO, GO:0008026, F:ATP-dependent helicase activity; IEA.  
 DR GO, GO:0016787, F:hydrolyase activity; IEA.  
 DR GO, GO:0003676, F:nucleic acid binding; IEA.  
 DR GO, GO:0001656, F:nucleotide binding; IEA.  
 DR InterPro: IPR001410, DEAD.  
 DR InterPro: IPR011545, DEAD/DEAH\_N.  
 DR InterPro: IPR001650, Helicase\_C.  
 DR Pfam: PF00270, DEAD; 1.  
 DR Pfam: PF00271, Helicase\_C; 1.  
 DR SMART: SM00487, DEXDC; 1.  
 DR SMART: SM00490, HELIC\_C; 1.  
 DR ATP-binding; Helicase; Hydrolyase.  
 KW SEQUENCE 432 AA; 49387 MW; 02F0BE597876EE1E CRC64;  
 SQ

Query Match 83.0%; Score 39; DB 2; Length 432;  
 Best Local Similarity 75.0%; Pred. No. 4.6e+02;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDX 8  
 Db 264 NYKDDDDR 271

RESULT 15  
 ID Q7UQZ7 RHOBA  
 AC Q7UQZ7;  
 DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.  
 DT 01-OCT-2003, sequence version 1.  
 DT 07-FEB-2006, entry version 10.  
 DE Probable acetylornithine aminotransferase (EC 2.6.1.11).  
 GN OrderedLocustNames=RB5984;  
 OS Rhodopirella baltica.  
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;  
 OC Planctomycetaceae; Pirellula.  
 OC NCBI\_TaxID=117;  
 RN [1]  
 RP NCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=1;  
 RX MEDLINE=22735913; Pubmed=12835416; DOI=10.1073/pnas.1431443100;  
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,  
 RA Ludwig W., Gade D., Beck A., Borzym K., Hellmann K., Rabus R.,  
 RA Schlesner H., Amann R., Reinhardt R.;  
 RT "Complete genome sequence of the marine planctomycete Pirellula sp.  
 strain 1.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).  
 CC -1- SIMILARITY: Belongs to the class-III pyridoxal-phosphate-dependent  
 CC aminotransferase family.  
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DR EMBL, BX94143, CAD74545.1, -, Genomic DNA.  
 DR GO, GO:0003992, F:acetylornithine transaminase activity; IEA.  
 DR GO, GO:0030170, F:pyridoxal phosphate binding; IEA.

DR GO, GO:0016740, F:transferase activity; IEA.  
 DR InterPro: IPR005814, AminoTrans\_3.  
 DR PANTHER: PTHR11986; AminoTrans\_3; 1.  
 DR Pfam: PF00202; AminoTrans\_3; 1.  
 KW AminoTransferase; Complete proteome; Pyridoxal phosphate; Transferase.  
 SQ SEQUENCE 506 AA; 54062 MW; 49F0AC9D3C4272C1 CRC64;  
 SQ

Query Match 83.0%; Score 39; DB 2; Length 506;  
 Best Local Similarity 75.0%; Pred. No. 5.5e+02;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDX 8  
 Db 439 DYEDDDDE 446

RESULT 16  
 ID CWC25\_YARLI  
 AC CWC25\_YARLI STANDARD; PRT; 561 AA.  
 DT 22-NOV-2005, integrated into UniProtKB/Swiss-Prot.  
 DT 16-AUG-2004, sequence version 1.  
 DT 07-MAR-2006, entry version 14.  
 DE Pre-mRNA-splicing factor CWC25.  
 GN Name=CWC25; OrderedLocustNames=YAL10F13057g;  
 OS Yarrowia lipolytica (Candida lipolytica).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Dipodascaceae; Yarrowia.  
 OC NCBI\_TaxID=4952;  
 RN [1]  
 RP NCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=CLIB 122 / B 150;  
 RX Pubmed=15229592; DOI=10.1038/nature02579;  
 RA Dujon B., Sherman D., Fischer G., Durans P., Casaregola S.,  
 RA Lafontaine I., de Montigny J., Marck C., Neugeglise C., Talla E.,  
 RA Goffard N., Frangoul L., Aigle M., Antouard V., Babour A., Barbe V.,  
 RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,  
 RA Boissame A., Boyer J., Catolico L., Confanioleri F., de Daruvar A.,  
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Giropi A.,  
 RA Hantreay F., Hennequin C., Janniaux N., Joyet P., Kachouri R.,  
 RA Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,  
 RA Nicoud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,  
 RA Pellenz S., Potier S., Richard G.-F., Strub M.-L., Suleau A.,  
 RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
 RA Zenou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,  
 RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,  
 RA Wincker P., Souciet J.-L.;  
 RT "Genome evolution in yeasts.";  
 RL Nature 430:35-44(2004).  
 CC -1- FUNCTION: Involved in pre-mRNA splicing (By similarity).  
 CC -1- SUBUNIT: Associated with the spliceosome (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Nucleus (By similarity).  
 CC -1- SIMILARITY: Belongs to the CWC25 family.  
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DR EMBL, CR382132, CAG78163.1, -, Genomic DNA.  
 KW Coiled coil; Complete proteome; mRNA processing; mRNA splicing;  
 KW Nuclein protein; Spliceosome.  
 FT CHAIN 1 561  
 FT FTID=PRO.0000079595.  
 FT COILED 22 64  
 FT COILED 495 545  
 FT COILED 166 353  
 FT COMPBIAS 166 353 Arg-rich.  
 SQ SEQUENCE 561 AA; 66044 MW; 61374B600C4CB6B CRC64;  
 SQ

Query Match 83.0%; Score 39; DB 1; Length 561;  
 Best Local Similarity 75.0%; Pred. No. 6.1e+02;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDX 8

Db 419 EYKDEDDK 426

RESULT 17

OS4DNA\_DICDI PRELIMINARY; PRT; 648 AA.

AC OS4DNA;

DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.

DT 24-MAY-2005, sequence version 1.

DT 07-FEB-2006, entry version 4.

DE Hypothetical protein.

GN ORFNames=DD80184366;

OS Dictyostelium discoideum (Slime mold).

OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.

NCBI\_TaxID=44689;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=AX4;

RX PubMed=15875012; DOI=10.1038/nature03481;

RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.A.,

RA Sugang R., Berriman M., Song J., Olsen R., Szatranski K., Xu Q.,

RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,

RA Bankier A.T., Lehman R., Hamlin N., Davies R., Gaudet P., Fey P.,

RA Pilcher K., Chen G., Saunders D., Sodergren E.J., Davis P.,

RA Karhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,

RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.M.,

RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,

RA Muzny D.M., Moutier T., Pain A., Lu M., Harper D., Lindsay R.,

RA Hauser H., James K.D., Quiles M., Madan Babu M., Saito T.,

RA Buchrieser C., Wardrop A., Felder M., Thangavelu M., Johnson D.,

RA Knights A., Louiseged H., Mungall K.L., Oliver K., Price C.,

RA Quail M.A., Urushihara H., Hernandez J., Rabinowitsch E., Steffen D.,

RA Sanders M., Ma J., Kohara Y., Sharp S., Simmonds M.N., Spiegler S.,

RA Tivey A., Sgano S., White B., Walker D., Woodward J.R., Winckler T.,

RA Tanaka Y., Shaulsky G., Schleicher M., Weinstock G.M., Rosenthal A.,

RA Cox E.C., Chisholm R.L., Gibbs R.A., Loomis W.F., Platzer M.,

RA Kay R.R., Williams J.G., Dear P.H., Noegel A.A., Barrell B.G.,

RA Kuspa A.;

RT "The genome of the social amoeba Dictyostelium discoideum.";

RL Nature 435:43-57(2005).

CC -1- CAUTION: The sequence shown here is derived from an

CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

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CC -----

DR EMBL; AAF10100268; EAL61185.1; -; Genomic DNA.

DR GO; GO:0008324; F: cation transporter activity; IEA.

DR GO; GO:0006812; P: cation transport; IEA.

DR InterPro: IPR008262; Lipase\_AS.

DR InterPro: IPR006162; Pfamne\_S.

DR Pfam; PF02386; TrkH; 1.

DR POSITIVE; PS00120; LIPASE\_SER; UNKNOWN\_1.

DR POSITIVE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN\_1.

DR KW Hypothetical protein.

SO SEQUENCE 648 AA; 73510 MW; 32A77CDBDE84E505 CRC64;

Query Match 83.0%; Score 39; DB 2; Length 648;

Best Local Similarity 75.0%; Pred. No. 7.1e+02;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDDK 8

Db 107 DFKDDDD 114

RESULT 18

OSXMT9\_CLOPE PRELIMINARY; PRT; 706 AA.

AC OSXMT9;

DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.

DT 01-MAR-2002, sequence version 1.

Db 419 EYKDEDDK 426

RESULT 19

OS4UVU\_DICDI PRELIMINARY; PRT; 1254 AA.

AC OS4UVU;

DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.

DT 24-MAY-2005, sequence version 1.

DT 07-FEB-2006, entry version 3.

DE Hypothetical protein.

GN ORFNames=DD80204740;

OS Dictyostelium discoideum (Slime mold).

OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.

NCBI\_TaxID=44689;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=AX4;

RX PubMed=15875012; DOI=10.1038/nature03481;

RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.A.,

RA Sugang R., Berriman M., Song J., Olsen R., Szatranski K., Xu Q.,

RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,

RA Bankier A.T., Lehman R., Hamlin N., Davies R., Gaudet P., Fey P.,

RA Pilcher K., Chen G., Saunders D., Sodergren E.J., Davis P.,

RA Karhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,

RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,

RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,

RA Muzny D., Moutier T., Pain A., Lu M., Harper D., Lindsay R.,

RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,

RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,

RA Louiseged H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,

RA Urushihara H., Mungall K., Oliver K., Price C., Quail M.A.,

RA Tivey A., Sgano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,

RA Sugano S., Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,

RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,

DT 07-FEB-2006, entry version 19.

DE Hypothetical protein CPE0599.

GN OrderedLocusNames=CPE0599;

OS Clostridium perfringens.

OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;

OC Clostridium.

NCBI\_TaxID=1502;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=13 / Type A;

RX MEDLINE=21664373; PubMed=11792842; DOI=10.1073/pnas.022493799;

RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,

RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;

RT "Complete genome sequence of Clostridium perfringens, an anaerobic

RT flesh-eater";

RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).

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CC -----

DR EMBL; BA000016; BAB80305.1; -; Genomic DNA.

DR Biocyc; CPE0599; CPE0599-MONOMER; --

DR LinkHub; OSXMT9; --

DR GO; GO:0005524; F: ATP binding; IEA.

DR GO; GO:0004003; F: ATP-dependent DNA helicase activity; IEA.

DR GO; GO:0003677; F: DNA binding; IEA.

DR GO; GO:0006281; P: DNA repair; IEA.

DR InterPro: IPR00212; UVRD\_helicase.

DR PANTHER; PTHR11070; UVRD\_helicase; 1.

DR Pfam; PF00580; UVRD\_helicase; 2.

DR Complete proteome; Hypothetical protein.

SO SEQUENCE 706 AA; 82992 MW; 85B3A4EB1B35478A CRC64;

Query Match 83.0%; Score 39; DB 2; Length 706;

Best Local Similarity 75.0%; Pred. No. 7.8e+02;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDDK 8

Db 51 EYKDEDDK 58

RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,  
 RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;  
 RT "The genome of the social amoeba *Dictyostelium discoideum*.";  
 RL Nature 0:0-0(2005).  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
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 CC -----  
 CC EMBL; AAFI01000069; EAL67058.1; -; Genomic\_DNA.  
 DR Hypochemical protein.  
 KM SEQUENCE 1254 AA; 146907 MW; A53C93E69754EC61 CRC64;  
 SQ

Query Match 83.0%; Score 39; DB 2; Length 1254;  
 Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDDK 8  
 Db 880 DYEDDDK 887

RESULT 20  
 ID 046YH5\_RALEJ PRELIMINARY; PRT; 110 AA.  
 AC 046YH5;  
 DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.  
 DT 13-SEP-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 4.  
 DE Probable signal peptide protein.  
 GN OrderedlocusNames=Reut\_A2446;  
 OS *Ralstonia eutropha* (strain JMP134) (*Alcaligenes eutrophus*).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Burkholderiaceae; Cupriavidus.  
 NCBI\_TaxID=264198;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RA Copeland A., Lucas S., Lapidus A., Barry K., Deter J.C., Glavina T.,  
 RA Hammon N., Israni S., Pitluck S., Goltzman E., Martinson P.,  
 RA Schmutz J., Latimer F., Land M., Lykidis A., Richardson P.;  
 RT "Complete sequence of chromosome 1 of *Ralstonia eutropha* JMP134.";  
 RL Submitted (MUG-2005) to the EMBL/GenBank/DBJ databases.  
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 CC -----  
 CC EMBL; CP000090; AA261808.1; -; Genomic\_DNA.  
 DR Complete proteome.  
 KM SEQUENCE 110 AA; 11880 MW; AC13E71F3914FF89 CRC64;  
 SQ

Query Match 80.9%; Score 38; DB 2; Length 110;  
 Best Local Similarity 75.0%; Pred. No. 1.6e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DYKDDDDK 8  
 Db 83 DYDDDDK 90

RESULT 21  
 ID 05COA2\_CRYPV PRELIMINARY; PRT; 125 AA.  
 AC 05COA2;  
 DT 12-APR-2005, integrated into UniProtKB/TrEMBL.  
 DT 12-APR-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 5.  
 DE Hypochemical protein.  
 GN ORFNames=cg4d\_1500;  
 OS *Cryptosporidium parvum*.  
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;  
 OC Cryptosporididae; Cryptosporidium.

OX NCBI\_TaxID=5807;  
 [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC SRRAIN-Iowa type II;  
 RX PubMed=15044751; DOI=10.1126/science.1094786;  
 RA Abrahamson M.S., Templeton T.J., Enomoto S., Abraham J.E., Zhu G.,  
 RA Lianco C.A., Deng M., Liu C., Widmer G., Tzipori S., Buck G.A., Xu P.,  
 RA Banker A.T., Dear P.H., Konfortov B.A., Spriggs H.F., Iyer L.,  
 RA Anantharaman V., Aravind L., Kapur V.;  
 RT "Complete genome sequence of the apicomplexan, *Cryptosporidium*  
 RT parvum".;  
 RL Science 304:441-445(2004).  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
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 CC -----  
 CC EMBL; AAE01000009; EAK87605.1; -; Genomic\_DNA.  
 DR EMBL; AAE01000009; EAK87605.1; -; Genomic\_DNA.  
 KM Hypochemical protein.  
 SQ SEQUENCE 125 AA; 14670 MW; 77D0BDCEB44094A CRC64;  
 SQ

Query Match 80.9%; Score 38; DB 2; Length 125;  
 Best Local Similarity 85.7%; Pred. No. 1.8e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDD 7  
 Db 60 DYKDDDD 66

RESULT 22  
 ID 09FM73\_ARATH PRELIMINARY; PRT; 154 AA.  
 AC 09FM73;  
 DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.  
 DT 01-MAR-2001, sequence version 1.  
 DT 07-FEB-2006, entry version 11.  
 DE Arabidopsis thaliana genomic DNA, chromosome 5, p1 clone:MDF20.  
 GN OrderedlocusNames=At5g55650;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsie.  
 NCBI\_TaxID=3702;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA MEDLINE=98290546; PubMed=9628582; DOI=10.1093/dnares/5.1.41;  
 RA Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,  
 RA Tabata S.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. IV.  
 RT Sequence features of the regions of 1,456,315 bp covered by nineteen  
 RT physically assigned p1 and TAC clones.";  
 RL DNA Res. 5:41-54(1998).  
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 CC -----  
 CC EMBL; AB009050; BAB09232.1; -; Genomic\_DNA.  
 DR TAIR; At5g55650; -;  
 SQ SEQUENCE 154 AA; 17650 MW; 7A4C895328B7E2DC CRC64;  
 SQ

Query Match 80.9%; Score 38; DB 2; Length 154;  
 Best Local Similarity 85.7%; Pred. No. 2.2e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDD 7  
 Db 84 DYEDDD 90

RESULT 23



Q8D4G1 VIBVU  
ID Q8D4G1 VIBVU PRELIMINARY; PRT; 171 AA.  
AC Q8D4G1  
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.  
DT 01-MAR-2003, sequence version 1.  
DT 07-FEB-2006, entry version 8.  
DE Hypothetical protein.  
GN OrderedLocustNames=VV21340; ORFNames=VV2\_1340;  
OS Vibrio vulnificus.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrrio.  
OX NCBI\_TaxID=672;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=CMCP6;  
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,  
Choy H.E.,  
RT "Complete genome sequence of Vibrio vulnificus CMCP6,"  
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
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CC  
DR EMBL; AE016796; AA008227.1; -; Genomic DNA.  
DR BioCyc; VVUL216895:VV21340-MONOMER; -;  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 171 AA; 20363 MW; 985FABC9C2C0A875 CRC64;

Query Match 80.9%; Score 38; DB 2; Length 171;  
Best Local Similarity 75.0%; Pred. No. 2.5e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 DYKDDDK 8  
Db 54 DYSDDEK 61

RESULT 24  
076542 DICDI  
ID 076542 DICDI PRELIMINARY; PRT; 235 AA.  
AC 076542;  
DT 01-NOV-1998, integrated into UniProtKB/TrEMBL.  
DT 01-NOV-1998, sequence version 1.  
DT 21-FEB-2006, entry version 36.  
DE Ubiquitin-conjugating enzyme protein Ubcc.  
GN Name=ubcc; ORFNames=DB0219926;  
OS Dictyostelium discoideum (Slime mold).  
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.  
OX NCBI\_TaxID=44689;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Iranfar N., Loomis W.F.;  
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=AX4;  
RX PubMed=15875012; DOI=10.1038/nature03481;  
RA Elchinger L., Pachbat J.A., Gloeckner G., Rajandream M.A.,  
Sugand R., Berriman M., Song J., Olsen R., Szafianski K., Xu Q.,  
Tunggal B., Kummerfeld S., Madera M., Kontorov B.A., Rivero F.,  
Bankler A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,  
Pillcher K., Chen G., Saunders D., Sodergren E.J., Davis P.,  
Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,  
Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.M.,  
Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,  
Munzy D.M., Moutier T., Pain A., Harper D., Lindsay R.,  
Hanser H., James K.D., Quiles M., Madan Babu M., Saito T.,  
Bachreiser C., Wardrop A., Felder M., Thangavelu M., Johnson D.,  
Knights A., Louised H., Mungall K.L., Oliver K., Price C.,  
Quail M.A., Urushihara H., Hernandez J., Rabinowitsch E., Steffen D.,  
Sanders M., Ma J., Kohara Y., Sharp S., Simmonds M.N., Spiegler S.,  
Tivey A., Sugano S., White B., Walker D., Woodward J.R., Winckler T.,  
Tanaka Y., Shatsky G., Schleicher M., Weinstock G.M., Rosenthal A.,

RA Cox E.C., Chisholm R.L., Gibbs R.A., Loomis W.F., Platzter M.,  
Kay R.R., Williams J.G., Dear P.H., Noegel A.A., Barrell B.G.,  
RA Kuapa A.;  
RT "The genome of the social amoeba Dictyostelium discoideum,"  
RL Nature 435:43-57(2005).  
CC -1- SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family.  
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CC  
DR EMBL; AAF1000097; EAI65437.1; -; Genomic DNA.  
DR EMBL; AF076597; AAC27763.1; -; mRNA.  
DR HSSP; P34477; 1PZV.  
DR DICTYBASE; DB0219926; ubcc.  
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.  
DR GO; GO:0006512; P:ubiquitin cycle; IEA.  
DR InterPro; IPR000608; UBQ-conjugat\_E2.  
DR SMART; SM00212; UBCC; 1.  
DR PROSITE; PS00183; UBIQUITIN CONJUGAT 1; 1.  
DR PROSITE; PS50127; UBIQUITIN CONJUGAT\_2; 1.  
KW ligase; ubi conjugation pathway.  
SQ SEQUENCE 235 AA; 27224 MW; F4914E867359700 CRC64;

Query Match 80.9%; Score 38; DB 2; Length 235;  
Best Local Similarity 75.0%; Pred. No. 3.5e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 DYKDDDK 8  
Db 220 DYNDDEK 227

RESULT 25  
Q8L7V6 ARATH  
ID Q8L7V6 ARATH PRELIMINARY; PRT; 242 AA.  
AC Q8L7V6;  
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.  
DT 01-OCT-2002, sequence version 1.  
DT 07-FEB-2006, entry version 9.  
DE AT3G29075/MX2\_1 (Fragment).  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Shin P., Chen H., Cheuk R., Kim C.J., Banh J., Bowser L.,  
RA Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,  
Ishida J., Jones T., Kamiya A., Karlín-Neumann G., Kawai J., Lam B.,  
Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,  
Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,  
Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,  
Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
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CC  
DR EMBL; AY125517; AAM78108.1; -; mRNA.  
FT NON TER 242  
SQ SEQUENCE 242 AA; 27898 MW; 500C97B9FE5D754A CRC64;

Query Match 80.9%; Score 38; DB 2; Length 242;  
Best Local Similarity 75.0%; Pred. No. 3.6e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 DYKDDDK 8  
Db 211 DYNDDEK 218

```

RESULT 26
O4X8B5_PLACH PRELIMINARY; PRT; 265 AA.
AC O4X8B5;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DE Hypoetical protein (Fragment).
GN ORFNames=PC405060.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
-1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
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CC -----
DR EMBL; CAJ01008940; ECH86861.1; -; Genomic_DNA.
KM Hypoetical protein.
FT NON_TER 265
SQ SEQUENCE 265 AA; 29964 MW; BD11AB5B5085C4CF CRC64;

Query Match 80.9%; Score 38; DB 2; Length 265;
Best Local Similarity 85.7%; Pred. No. 4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
Db 103 DFKDDDD 109

RESULT 27
O9LJV8_ARATH PRELIMINARY; PRT; 294 AA.
AC O9LJV8;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DE 07-FEB-2006, entry version 15.
DE GB|AA16629.1.
GN OrderedLocustNames=At3g29075;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20363099; PubMed=10907853; DOI=10.1093/dnares/7.3.217;
RA Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the 4,251,695 bp regions covered by 90 P1, TAC
RT and BAC clones.";
RL DNA Res. 7:217-221(2000).
[2]
RP NUCLEOTIDE SEQUENCE.
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -----

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CC -----
DR EMBL; AP000388; BAB02950.1; -; Genomic_DNA.
DR EMBL; AB018121; BAB02950.1; JOINED; Genomic_DNA.
DR TAIR; At3g29075; -.
SQ SEQUENCE 294 AA; 34452 MW; 98164D6FAFD1533F CRC64;

Query Match 80.9%; Score 38; DB 2; Length 294;
Best Local Similarity 75.0%; Pred. No. 4.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDX 8
Db 211 DYVDDDEK 218

RESULT 28
O54YA8_DICDI PRELIMINARY; PRT; 301 AA.
ID O54YA8_DICDI
AC O54YA8;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DE 07-FEB-2006, entry version 3.
DE Hypoetical protein.
GN ORFNames=DBG0205379;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RX PubMed=15875012; DOI=10.1038/nature03481;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.A.,
RA Sugang R., Berriman M., Song J., Olsen R., Szafanski K., Xu O.,
RA Tunggal B., Kummerfeld S., Madera M., Kontorov B.A., Riveo F.,
RA Bankler A.T., Lehmann R., Hamlin N., Davies R., Gaut P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E.J., Davis P.,
RA Karhoun A., Nie X., Hall N., Anjard C., Hemphill L., Bacon N.,
RA Farbrother P., Desany B., Just B., Morio T., Rost R., Churcher C.M.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D.M., Moutier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K.D., Quiles M., Madan Babu M., Salto T.,
RA Buchrieser C., Wardrop A., Felder M., Thangavelu M., Johnson D.,
RA Knights A., Loulseg H., Mungall K.L., Oliver K., Price C.,
RA Quail M.A., Urushihara H., Hernandez J., Rabinowitsch E., Steffen D.,
RA Sanders M., Ma J., Kohara Y., Sharp S., Simmonds M.N., Spiegler S.,
RA Tivey A., Sugano S., White B., Walker D., Woodward J.R., Winckler T.,
RA Tanaka Y., Shaulsky G., Schleicher M., Weinstock G.M., Rosenthal A.,
RA Cox E.C., Chisholm R.L., Gibbs R.A., Loomis W.F., Platzer M.,
RA Kay R.R., Williams J.G., Dear P.H., Noegel A.A., Barrell B.G.,
RA Kuapa A.;
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 435:43-57(2005).
-1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC -----
DR EMBL; AAF101000052; EAL68337.1; -; Genomic_DNA.
KM Hypoetical protein.
SQ SEQUENCE 301 AA; 35014 MW; 15B6A20128BCF37 CRC64;

Query Match 80.9%; Score 38; DB 2; Length 301;
Best Local Similarity 75.0%; Pred. No. 4.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDX 8
Db 112 DYSDDDDE 119

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RESULT 29
VHCG_METVO STANDARD; PRT; 306 AA.
ID VHCG_METVO
AC Q00406;
DT 16-JAN-2004, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 30.
DE F420-non-reducing hydrogenase vhc subunit G (EC 1.1.2.99.-).
GN Name=vhcg.
OS Methanococcus voltae.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanococcaceae; Methanococcus.
OX NCBI_TaxID=2188;
RN [1]
RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).
RC STRAIN=DSM 1537 / PS;
RX MEDLINE=92293118; PubMed=1603063;
RA Halboch S., Klein A.;
RT "Methanococcus voltae harbors four gene clusters potentially encoding
RT two [NiFe] and two [NiFeSe] hydrogenases, each of the cofactor F420-
RT reducing or F420-non-reducing types.";
RL Mol. Gen. Genet. 233:217-224(1992).
RN [2]
RP TRANSCRIPTIONAL REGULATION.
RC STRAIN=DSM 1537 / PS;
RX PubMed=8121392; DOI=10.1007/BF00281785;
RA Berghoefer Y., Agha-Amiri K., Klein A.;
RT "Selenium is involved in the negative regulation of the expression of
RT selenium-free [NiFe] hydrogenases in Methanococcus voltae.";
RL Mol. Gen. Genet. 242:369-373(1994).
CC -1- SUBUNIT: The F420-non-reducing hydrogenase vhc is composed of
CC three subunits: vhcA, vhcD and vhcg (By similarity).
CC -1- SIMILARITY: Belongs to the [NiFe]/[NiFeSe] hydrogenase small
CC subunit family.
CC
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CC
DR EMBL, X61203; CAA43505.1; -; Genomic_DNA.
DR PIR, S32834; S32834.
DR InterPro: IPR006137; Oxidored_g6.
DR Pfam: PF01058; Oxidored_g6; 1.
KW Oxidoreductase.
FT CHAIN 1 306 F420-non-reducing hydrogenase vhc subunit
FT G.
FT SEQUENCE 306 AA; 33636 MW; 2A88AC3EAE194DB8 CRC64;
SQ
Query Match 80.9%; Score 38; DB 1; Length 306;
Best Local Similarity 87.5%; Pred. No. 4.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 DYKDDDD 8
DB 260 DYKDDDD 267

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RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.040168101;
RA Jones T., Federle N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of Candida albicans.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC
DR EMBL, AAC0100025; EAL01427.1; -; Genomic_DNA.
DR EMBL, AAC0100023; EAL01667.1; -; Genomic_DNA.
DR GO, GO:0005489; F:electron transporter activity; IEA.
DR GO, GO:0006118; P:electron transport; IEA.
DR InterPro: IPR012336; Thioresdn-like_fd.
DR InterPro: IPR006662; Thioresd.
DR InterPro: IPR006663; Thioresdn_dom2.
DR InterPro: IPR012335; Thioresdn_fold.
DR Pfam: PF00085; Thioresdn_1.
DR PRINTS, PR00421; THIOREDOXIN.
KW Hypothetical protein; Redox-active center.
SQ SEQUENCE 332 AA; 39236 MW; 94A2A754F3DBF5EB CRC64;
QY 1 DYKDDDD 7
DB 318 DYEDDD 324

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RESULT 31
Q4XYM1_PLACH PRELIMINARY; PRT; 369 AA.
ID Q4XYM1_PLACH
AC Q4XYM1;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Hypothetical protein (Fragment).
GN ORFNames=PC000687.02.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Truman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carnucci D.J., Yates J.R. III,
RA Karatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC
DR EMBL, CAJ01002240; CAJ77989.1; -; Genomic_DNA.
DR InterPro: IPR000436; Sush1_SCR_CCP.
DR Pfam: PF00084; Sush1_1.
DR SMART, SM00032; CCP; 1.

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DR PROSITE; PS50923; SUSHI; 1.
KM Hypochemical protein.
FT NON_TER 1
SQ SEQUENCE 369 AA; 41722 MW; 8C620622D1F15895 CRC64;

Query Match
Best Local Similarity 80.9%; Score 38; DB 2; Length 369;
Pred. No. 5.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
DB 35 DYEDDDD 41

RESULT 32
Q5F360.CHICK
ID Q5F360.CHICK PRELIMINARY; PRT; 416 AA.
AC Q5F360;
DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 15-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Hypochemical protein.
GN ORFNames=RCJMB04_33c19;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NCLEOTIDE SEQUENCE.
RC STRAIN=CB; TISSUE=Bursa;
RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezubov Y., Zaim J.,
RA Fiedler P., Kuter S., Blagodatki A., Kostovska D., Koter M.,
RA Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
RT "Full-length cDNAs from chicken bursal lymphocytes to facilitate
RT gene function analysis."
RL Genome Biol. 6:R6-R6(2005).
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DR EMBL; A0851790; CAH65424.1; -; mRNA.
KM Hypochemical protein.
SQ SEQUENCE 416 AA; 46132 MW; BAA049E45C2918B1 CRC64;

Query Match
Best Local Similarity 80.9%; Score 38; DB 2; Length 416;
Pred. No. 6.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
DB 321 DYEDDDD 327

RESULT 33
Q5ZKN5.CHICK
ID Q5ZKN5.CHICK PRELIMINARY; PRT; 418 AA.
AC Q5ZKN5;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Hypochemical protein.
GN ORFNames=RCJMB04_9015;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NCLEOTIDE SEQUENCE.
RC STRAIN=CB; TISSUE=Bursa;
RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezubov Y., Zaim J.,
RA Fiedler P., Kuter S., Blagodatki A., Kostovska D., Koter M.,
RA Fiedler P., Kuter S., Blagodatki A., Kostovska D., Koter M.,

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RA Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
RT "Full-length cDNAs from chicken bursal lymphocytes to facilitate
RT gene function analysis."
RL Genome Biol. 6:R6-R6(2005).
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DR EMBL; A0720049; CAG31708.1; -; mRNA.
KM Hypochemical protein.
SQ SEQUENCE 418 AA; 46233 MW; AAE8909BBE729CC0 CRC64;

Query Match
Best Local Similarity 80.9%; Score 38; DB 2; Length 418;
Pred. No. 6.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
DB 323 DYEDDDD 329

RESULT 34
Q8QHJ7.CHICK
ID Q8QHJ7.CHICK PRELIMINARY; PRT; 418 AA.
AC Q8QHJ7;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Dorsal neural tube nuclear protein.
GN Name=DNTNP;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NCLEOTIDE SEQUENCE.
RX MEDLINE=22021057; PubMed=11984880; DOI=10.1002/dvdy.10090;
RA Ju L., Balboni A.L., Laitman J.T., Bergemann A.D.;
RT "Isolation of DNTNP, which encodes a potential nuclear protein that is
RT expressed in the developing, dorsal neural tube."
RL Dev. Dyn. 224:116-123(2002).
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DR EMBL; AF396666; AA176115.1; -; mRNA.
DR Ensembl; ENSGALG00000015713; Gallus gallus.
DR GO; GO:0005634; C:nucleus; IEA.
KM Nuclear protein.
SQ SEQUENCE 418 AA; 46233 MW; 80994AAFFBED372F CRC64;

Query Match
Best Local Similarity 80.9%; Score 38; DB 2; Length 418;
Pred. No. 6.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
DB 323 DYEDDDD 329

RESULT 35
Q4X0R6.PLACH
ID Q4X0R6.PLACH PRELIMINARY; PRT; 475 AA.
AC Q4X0R6;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 21-FEB-2006, entry version 7.
DE Hypochemical protein.
GN ORFNames=PC000206_04.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;

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RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooli T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Omond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carnucci D.J., Yates J.R. III,
RA Karafos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86 (2005).
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DDJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
CC EMBL: CAJ01003901; CAH80746.1; -; Genomic_DNA.
CC
CC DR GO: GO:0005615; C:extracellular space; IEA.
CC DR GO: GO:0005125; F:cyclin activity; IEA.
CC DR InterPro: IPR012351; Cyclin_4_hlx.
CC KW Cyclin; Hypothetical protein.
SQ SEQUENCE 475 AA; 56352 MW; 1F1E3BBA3CE8829 CRC64;

Query Match 80.9%; Score 38; DB 2; Length 475;
Best Local Similarity 75.0%; Pred. No. 7.4e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DYKDDDK 8
Db 369 DYKDDDK 376

RESULT 36
MAOL YERPS STANDARD; PRT; 565 AA.
ID MAOL YERPS STANDARD; PRT; 565 AA.
AC Q8ZG09; Q7AVB1; Q7CHQ5;
DT 06-DEC-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2002, sequence version 1.
DT 07-MAR-2006, entry version 27.
DE NAD-dependent malic enzyme (EC 1.1.1.38) (NAD-ME).
GN Name=afa; OrderedLocNames=YPO1511.y2658.y11401;
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OC NCBI_TaxID=632;
[1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Pakhili J., Wren B.W., Thomson N.R., Tibball R.W., Holden M.T.G.,
RA Penrice M.B., Sebailia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Baaham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Katiryahev A.V.,
RA Leach S., Mout S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527 (2001).
[2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
DOI=10.1126/SCIENCE.1197.16.4601-4611.2002;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Niles M.L., Watson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM.";

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RL J. Bacteriol. 184:4601-4611 (2002).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=91001 / Biovar Mediaevalis;
RX PubMed=15568893; DOI=10.1093/dnares/11.3.179;
RA Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,
RA Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,
RA Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,
RA Yang H., Wang J., Huang P., Yang R.;
RT "Complete genome sequence of Yersinia pestis strain 91001, an isolate
RT avirulent to humans.";
RL DNA Res. 11:179-197 (2004).
CC -! CATALYTIC ACTIVITY: (S)-malate + NAD(+) = pyruvate + CO(2) + NADH.
CC -! COPACITOR: Divalent cations, magnesium or manganese (By
CC similarity).
CC -! SUBUNIT: Homotrimer (By similarity).
CC -! SIMILARITY: Belongs to the malic enzymes family.
CC -----
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CC -----
CC EMBL: AJ414148; CAC90334.1; -; Genomic_DNA.
CC DR EMBL: AE013868; AAM86211.1; -; Genomic_DNA.
CC DR EMBL: AE017132; AAS61642.1; -; Genomic_DNA.
CC DR PIR: AC0184; AC0184.
CC DR HSP: P40927; IGO2.
CC
CC DR GenomeReviews: AE009952.GR.y2658.
CC DR GenomeReviews: AE017042.GR.y11401.
CC DR GenomeReviews: AL590842.GR.yPO1511.
CC DR BiOCyc: YPES187410.y2658-MONOMER; -.
CC DR BiOCyc: YPES229193.y11401-MONOMER; -.
CC DR BiOCyc: YPES632.yPO1511-MONOMER; -.
CC DR HAMAP: MF_01619; -.
CC DR InterPro: IPR012301; Malic_N.
CC DR InterPro: IPR012302; Malic_NAD_bd.
CC DR InterPro: IPR001891; Malic_oxred.
CC DR PANTHER: PTHR10893; Malic_oxred; 1.
CC DR Pfam: PF00390; malic_1.
CC DR Pfam: PF03949; malic_M_1.
CC DR PIRSF: PIRSF000106; ME; 1.
CC DR PRINTS: PR00072; MALOXRDYASE.
CC DR PROSITE: PS00331; MALIC_ENZYMES; 1.
CC KW Complete proteome; Metal-binding; NAD; Oxidoreductase.
CC CHAIN 1 565
FT FT 104 104 /FTID=PRO_0000160240.
FT ACT SITE 175 175 Proton donor (By similarity).
FT ACT SITE 175 175 Proton acceptor (By similarity).
FT METAL 246 246 Divalent metal cation (By similarity).
FT METAL 247 247 Divalent metal cation (By similarity).
FT METAL 247 247 Divalent metal cation (By similarity).
FT BINDING 157 157 NAD (By similarity).
FT BINDING 270 270 NAD (By similarity).
FT BINDING 270 270 NAD (By similarity).
FT BINDING 418 418 NAD (By similarity).
FT SITE 270 270 Important for activity (By similarity).
SQ SEQUENCE 565 AA; 62828 MW; F57C1183ECAA3D CRC64;

Query Match 80.9%; Score 38; DB 1; Length 565;
Best Local Similarity 75.0%; Pred. No. 8.9e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DYKDDDK 8
Db 66 DYKDDDK 73

RESULT 37
MAOL YERPS STANDARD; PRT; 565 AA.
ID MAOL YERPS STANDARD; PRT; 565 AA.
AC Q6C8D0;
DT 06-DEC-2005, integrated into UniProtKB/Swiss-Prot.
DT 11-OCT-2004, sequence version 1.
DT 07-MAR-2006, entry version 12.
DE NAD-dependent malic enzyme (EC 1.1.1.38) (NAD-ME).

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GN Name=sfca; OrderedLocusNames=YPTB1526;  
 OS Yersinia pseudotuberculosis.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Yersinia.  
 NCBI\_TaxID=633;  
 [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=IP32953 / Serotype I;  
 RX PubMed=1535858; DOI=10.1073/pnas.0404012101;  
 RA Chain P.S.G., Carniel E., Larimer F.W., Lamezin J., Stoutland P.O.,  
 RA Regala W.M., Georgescu A.M., Verges L.M., Land M.L., Motin V.L.,  
 RA Brubaker R.R., Fowler J., Himebusch U., Marceau M., Medigue C.,  
 RA Smoot M., Chantal-Francoise V., Souza B., Dacheux D., Elliott J.M.,  
 RA Derbise A., Hauser J.J., Garcia E.;  
 RA "Insights into the evolution of Yersinia pests through whole-genome  
 RT comparison with Yersinia pseudotuberculosis.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).  
 CC -1- CATALYTIC ACTIVITY: (S)-malate + NAD(+) = pyruvate + CO(2) + NADH.  
 CC -1- COFACTOR: Divalent cations, magnesium or manganese (By  
 similarity).  
 CC -1- SUBUNIT: Homotetramer (By similarity).  
 CC -1- SIMILARITY: Belongs to the malic enzymes family.  
 CC  
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 CC  
 CC EMBL: BX936398; CAH20765.1; -; Genomic DNA.  
 CC GenomeReviews; BX936398\_CR; YPTB1526.  
 CC HAMAP; MF\_01619; -; 1.  
 CC InterPro; IPR012301; Malic\_N.  
 CC InterPro; IPR012302; Malic\_NAD\_Bd.  
 CC InterPro; IPR001891; Malic\_oxred.  
 CC PANTHER; PTHR10893; Malic\_oxred; 1.  
 CC Pfam; PF00390; malic; 1.  
 CC Pfam; PF03949; Malic\_M; 1.  
 CC PRINTS; PR00072; MALOXRDTSASE.  
 CC DR PIRSF; PIRSF00106; ME; 1.  
 CC DR PIRSF; PR00072; MALOXRDTSASE.  
 CC DR PROSITE; PS00331; MALIC ENZYMES; 1.  
 CC KM Complete proteome; Metal-binding; NAD; Oxidoreductase.  
 CC FT CHAIN 1 565 NAD-dependent malic enzyme.  
 FT ACT SITE 104 104 /FTID=PRO\_0000160241.  
 FT ACT SITE 175 175 Proton donor (By similarity).  
 FT METAL 246 246 Proton acceptor (By similarity).  
 FT METAL 247 247 Divalent metal cation (By similarity).  
 FT METAL 270 270 Divalent metal cation (By similarity).  
 FT BINDING 157 157 Divalent metal cation (By similarity).  
 FT BINDING 270 270 NAD (By similarity).  
 FT BINDING 418 418 NAD (By similarity).  
 FT SITE 270 270 Important for activity (By similarity).  
 SQ SEQUENCE 565 AA; 62828 MW; F57C1183ECC4AAAD3 CRC64;  
 Query Match 80.9%; Score 38; DB 1; Length 565;  
 Best Local Similarity 75.0%; Pred. No. 8.9e+02;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Db 66 DFKNDK 73  
 1 DYKDDDK 8  
 |:::|  
 DPH2\_KLUUA STANDARD; PRT; 587 AA.  
 AC QGCS50;  
 DT 20-DEC-2005, integrated into UniProtKB/Swiss-Prot.  
 DT 16-AUG-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 14.  
 DE Diphthamide biosynthesis protein 2.  
 GN Name=DPH2; OrderedLocusNames=KLU002948g;  
 OS Kluyveromyces lactis (Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.

OX NCBI\_TaxID=28985;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=CBS 2359 / IFO 1267 / NRL Y-1140 / WM37;  
 RX PubMed=1529592; DOI=10.1038/nature02579;  
 RA Dujon B., Sherman D., Fischer G., Durieux P., Casaregola S.,  
 RA Lafontaine I., de Montigny J., Marck C., Neveglise C., Talla E.,  
 RA Goffard N., Frangoul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
 RA Barray S., Blanchot S., Beckerich J.-M., Beyne E., Bleykarsen C.,  
 RA Bistrane A., Boyer J., Cattolico L., Confenietti F., de Darvar A.,  
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,  
 RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
 RA Kerest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,  
 RA Nicand J.-M., Nikolski M., Oztas S., Olier-Kalogeropoulos O.,  
 RA Pellanz S., Porter S., Richard G.-F., Strub M.-L., Suleau A.,  
 RA Swennen D., Tekala F., Wesolowski-Jouvel M., Westhof E., Wirth B.,  
 RA Zenou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,  
 RA Bouchier C., Caudron B., Scarpelli C., Galliard C., Weissendach J.,  
 RA Winkler P., Souciet J.-L.;  
 RA "Genome evolution in Yeasts.";  
 RL Nature 430:35-44(2004).  
 CC -1- FUNCTION: Required for the first step of diphthamide biosynthesis,  
 CC the transfer of 3-amino-3-carboxypropyl from S-adenosyl-L-  
 CC methionine to a histidine residue. Diphthamide is a post-  
 CC translational modification of histidine which occurs in elongation  
 CC factor 2 (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasm (By similarity).  
 CC -1- SIMILARITY: Belongs to the DPH2 family.  
 CC  
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 CC  
 CC EMBL: CR382124; CAH00295.1; -; Genomic DNA.  
 CC InterPro; IPR002728; diphthamide\_syn.  
 CC InterPro; IPR010014; DPH2.  
 CC PANTHER; PTHR10762; Diphthamide\_syn; 2.  
 CC Pfam; PF01866; Diphthamide\_syn; 1.  
 CC TRIPFAMS; TRIPR00272; DPH2; 1.  
 CC KM Complete proteome.  
 CC FT CHAIN 1 587 Diphthamide biosynthesis protein 2.  
 FT SEQUENCE 587 AA; 66189 MW; 4F51D875B767EC1A CRC64;  
 SQ  
 Query Match 80.9%; Score 38; DB 1; Length 587;  
 Best Local Similarity 85.7%; Pred. No. 9.3e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Db 553 DYKDDK 559  
 1 DYKDDK 7  
 |:::|  
 Q55CB4\_DICDI PRELIMINARY; PRT; 588 AA.  
 ID Q55CB4\_DICDI  
 AC Q55CB4;  
 DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.  
 DT 24-MAY-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 4.  
 DE Hypothetical protein.  
 GN ORFNames=DD80190829;  
 OS Dictyostelium discoideum (Slime mold).  
 CC Eukaryota; Eukaryota; Dictyosteliales; Dictyostelium.  
 CC NCBI\_TaxID=44689;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=AX4;  
 RX PubMed=15875012; DOI=10.1038/nature03481;  
 RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandran M.A.,  
 RA Sengang R., Berriman M., Song J., Olsen R., Szafranski K., Xu O.,  
 RA Tunggal B., Kummerfeld S., Madera M., Kontorov B.A., Rivero F.,  
 RA Bankler A.T., Lehmann R., Hamlin N., Davis R., Gaudet P., Fey P.,  
 RA Pilcher K., Chen G., Saunders D., Sodergren E.J., Davis P.,

RA Kethornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,  
 RA Fadrocher P., Desany B., Just E., Morio T., Rose R., Chuchard C.M.,  
 RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,  
 RA Muzny D.M., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,  
 RA Hauser H., James K.D., Quiles M., Madan Babu M., Saito T.,  
 RA Buchrieser C., Wadrop A., Felder M., Thangavelu M., Johnson D.,  
 RA Knights A., Louieged H., Mungall K.L., Oliver K., Pirce C.,  
 RA Quail M.A., Urushihara H., Hernandez J., Rabinowitsch E., Steffen D.,  
 RA Sanders M., Ma J., Kohata Y., Sharp S., Simmonds M.N., Spiegel S.,  
 RA Tivey A., Sugano S., White B., Walker D., Woodward J.R., Winkler T.,  
 RA Tanaka Y., Shaulsky G., Schleicher M., Mainstock G.M., Rosenthal A.,  
 RA Cox E.C., Chisholm R.L., Gibbs R.A., Loomis W.F., Platzner M.,  
 RA Kay R.R., Williams J.G., Dear P.H., Noegel A.A., Barrell B.G.,  
 RA Kuypa A.,  
 RA "The genome of the social amoeba *Dictyostelium discoideum*."  
 RL Nature 435:43-57(2005).  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
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EMBL: AAF10100011; EAL72415.1; -; Genomic\_DNA.  
 DR InterPro: IPR006575; RMD.  
 DR InterPro: IPR002867; Znf\_C6HC.  
 DR Pfam: PF01485; IIR; 1.  
 DR Pfam: PF05773; RMD; 1.  
 DR SMART: SM00647; IIR; 1.  
 DR SMART: SM00591; RMD; 1.  
 DR PROSITE: PS50908; RMD; 1.  
 DR Hypothetical protein.  
 SQ SEQUENCE 588 AA; 67624 MW; 8AD824B3BD6F07A CRC64;

Query Match 80.9%; Score 38; DB 2; Length 588;  
 Best Local Similarity 85.7%; Pred. No. 9.3e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
 |||  
 Db 101 DYEDDD 107

RESULT 40  
 G6BYDO DEBHA PRELIMINARY; PRT; 590 AA.  
 ID G6BYDO DEBHA  
 AC Q6BYDO  
 DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.  
 DT 16-AUG-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 10.  
 DE Debaryomyces hansenii chromosome A of strain CBS767 of Debaryomyces  
 DE hansenii.  
 GN OrderedLocustNames=DEBHA0108689;  
 OS Debaryomyces hansenii (Yeast) (Torulaspora hansenii).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.  
 OX NCBI\_TaxID=4959;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).  
 RC STRAIN=ATCC 36239 / CBS 767;  
 RX PubMed=15229592; DOI=10.1038/nature02579;  
 RA Lafontaine I., de Montigny J., Marc C., Neuvéglise C., Talla E.,  
 RA Goffard N., Frangoul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
 RA Barney S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,  
 RA Boissière A., Boyer J., Cattolico L., Confiantoleri F., de Daruvar A.,  
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Gropi A.,  
 RA Hantuya F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
 RA Nicand J.-M., Nikolski M., Ozias S., Ozier-Kalogeropoulos O.,  
 RA Pellenz S., Potter S., Richard G.-F., Strand M.-L., Suleau A.,  
 RA Svenen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
 RA Zenitov-Meyer M., Zivanovic Y., Boločin-Fukuhara M., Thierry A.,

RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,  
 RA Winkler P., Souciet J.-L.,  
 RT "Genome evolution in yeasts."  
 RL Nature 430:35-44(2004).  
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EMBL: CR382133; CAG84758.1; -; Genomic\_DNA.  
 DR GO: GO:0016020; C:membrane; IEA.  
 DR GO: GO:0004377; F:glycolipid 2-alpha-mannosyltransferase acti. .; IEA.  
 DR GO: GO:0006486; P:protein amino acid glycosylation; IEA.  
 DR InterPro: IPR002685; Glyco\_transf\_15.  
 DR Pfam: PF01793; Glyco\_transf\_15; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 590 AA; 69412 MW; A3762251468590F1 CRC64;

Query Match 80.9%; Score 38; DB 2; Length 590;  
 Best Local Similarity 75.0%; Pred. No. 9.3e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 8  
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 Db 27 DYSDDD 34

RESULT 41  
 Q2UGP9 ASPOR PRELIMINARY; PRT; 629 AA.  
 ID Q2UGP9 ASPOR  
 AC Q2UGP9  
 DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.  
 DT 24-JAN-2006, sequence version 1.  
 DT 07-MAR-2006, entry version 3.  
 DE Predicted protein.  
 GN ORFNames=A0909023000761;  
 OS Aspergillus oryzae.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Eurotiiales; Trichocommataceae; mitosporic Trichocommataceae; Aspergillaceae;  
 OX NCBI\_TaxID=5062;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=RIB 40;  
 RX PubMed=16372010; DOI=10.1038/nature04300;  
 RA Machida M., Asai K., Sano M., Tanaka T., Kumagai T., Terai G.,  
 RA Kusumoto K., Arima T., Akita O., Kashiwagi Y., Aoe K., Gomi K.,  
 RA Horituchi H., Kitamoto K., Kodayashi T., Takeuchi M., Denning D.W.,  
 RA Galagan J.E., Nieman W.C., Yu J., Archer D.B., Bennett J.W.,  
 RA Bhattacharya D., Cleveland T.E., Fedorova N.D., Gotch O., Horikawa H.,  
 RA Hosoyama A., Ichinomiya M., Igataishi R., Washita K., Jurvadi P.R.,  
 RA Kato M., Kato Y., Kiri T., Kokubun A., Maeda H., Maeyama N.,  
 RA Maruyama Y., Nagasaki H., Nakajima T., Oda K., Okada K., Paulsen I.,  
 RA Sakamoto K., Sawano T., Takahashi M., Takase K., Terabayashi Y.,  
 RA Wortman J.R., Yamada O., Yamagata Y., Anazawa H., Hata Y., Koide Y.,  
 RA Morita T., Koyama Y., Minetoki T., Suharnan S., Tanaka A., Isono K.,  
 RA Kubara S., Ogatawara N., Kikuchi H.,  
 RT "Genome sequencing and analysis of *Aspergillus oryzae*."  
 RL Nature 438:1157-1161(2005).

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EMBL: AP007157; BA559266.1; -; Genomic\_DNA.  
 SQ SEQUENCE 629 AA; 68502 MW; 5821BD26BB21145F CRC64;

Query Match 80.9%; Score 38; DB 2; Length 629;  
 Best Local Similarity 85.7%; Pred. No. 1e+03;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
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 Db 182 DYEDDD 188

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RESULT 42
Q2UF79 ASPOR PRELIMINARY; PRT; 782 AA.
AC Q2UF79;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DE Phosphatidylinositol 4-kinase.
GN ORFNames=A0090026000314;
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RIB 40;
RX PubMed=16372010; DOI=10.1038/nature04300;
RA Machida M., Asai K., Sano M., Tanaka T., Kumagai T., Terai G.,
RA Kusumoto K., Atima T., Akita O., Kashiwagi Y., Abe K., Gomi K.,
RA Horuchi H., Kitamoto K., Kobayashi T., Takeuchi M., Denning D.W.,
RA Galagan J.E., Niernan W.C., Yu J., Archer D.B., Bennett J.W.,
RA Bhattacharjee D., Cleveland T.E., Fedorova N.D., Gotch O., Horikawa H.,
RA Hosoyama A., Ichinomiya M., Igarashi R., Iwashita K., Urvashi P.R.,
RA Kato M., Kato Y., Kin T., Kokubun A., Maeda H., Maeyama N.,
RA Maruyama J., Nagasaki H., Nakajima T., Oda K., Okada K., Paulsen I.,
RA Sakamoto K., Sawano T., Takahashi M., Takase K., Terabayashi Y.,
RA Mortman J.R., Yamada O., Yamagata Y., Anazawa H., Hata Y., Koide Y.,
RA Komori T., Koyama Y., Minetoki T., Suharnan S., Tanaka A., Isono K.,
RA Kihara S., Ogasawara N., Kikuchi H.;
RT "Genome sequencing and analysis of Aspergillus oryzae.";
RL Nature 438:1157-1161(2005).
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CC -----
DR EMBL; AP007159; BAE59786.1; -; Genomic DNA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR KM
SQ SEQUENCE 782 AA; 89076 MW; B35FPBD2EA712335 CRC64;

Query Match 80.9%; Score 38; DB 2; Length 782;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 27 DYSDDDQ 34

RESULT 43
Q3QJ20 GRHOB PRELIMINARY; PRT; 804 AA.
AC Q3QJ20;
DT 23-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2005, sequence version 1.
DE 07-FEB-2006, entry version 3.
DE Hypothetical protein precursor.
GN ORFNames=RosedRAFT_1857;
OS Silicibacter sp. TM1040.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Silicibacter.
OX NCBI_TaxID=292414;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=TM1040;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pittluck S., Richardson P.,
RT "Sequencing of the draft genome and assembly of Silicibacter sp.
RT TM1040.";
RU Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.

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RC STRAIN=TM1040;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Silicibacter sp. TM1040.";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=TM1040;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pittluck S., Richardson P.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAFG02000004; EAN57069.1; -; Genomic DNA.
DR KM
FT SIGNAL 1 21 Potential.
SQ SEQUENCE 804 AA; 87577 MW; 7132035950682D7C CRC64;

Query Match 80.9%; Score 38; DB 2; Length 804;
Best Local Similarity 87.5%; Pred. No. 1.3e+03;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 207 DYKDDDDK 214

RESULT 44
O96505 DROME PRELIMINARY; PRT; 823 AA.
ID O96505;
AC O96505;
DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1999, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE STR2.
GN Name=Str2; ORFNames=CG5216;
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=22549451; PubMed=12663533;
RX Astrom S.U., Cline T.W., Rine J.;
RT "The Drosophila melanogaster str2(+) Gene Is Nonessential and Has Only
RT Minor Effects on Position-Effect Variegation.";
RL Genetics 163:931-937(2003).
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CC -----
DR EMBL; AF068758; AAC79684.1; -; mRNA.
DR HSSP; P5386; I01A.
DR FLYBase; FBgn0024291; Str2.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0017136; F:NAD-dependent histone deacetylase activity; IDA.
DR INTERPRO; IPR003000; STR2.
DR PANTHER; PTHR11085; STR2; 1.
DR Pfam; PF02146; Str2; 1.
DR PROSITE; PSS0305; STRUTIN; 1.
SQ SEQUENCE 823 AA; 92024 MW; 5EF09F1A46235E7F CRC64;

Query Match 80.9%; Score 38; DB 2; Length 823;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 DYKDDDDK 8  
 DB 698 DYSDDDE 705

RESULT 45  
 Q9VK34 DROME PRELIMINARY; PRT; 823 AA.  
 ID Q9VK34 DROME  
 AC Q9VK34  
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.  
 DT 01-MAY-2000, sequence version 1.  
 DT 07-FEB-2006, entry version 28.  
 DE CG5216-PA.  
 GN Name=Sir2; ORFNames=Dmel CG5216;  
 OS Drosophila melanogaster (fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NC NCBI\_TaxID=7227;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20196006; PubMed=10731132, DOI=10.1126/science.287.5461.2185;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotlier P.,  
 RA Buttle K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferreira C., Ferreira S., Fleischmann W.,  
 RA Foeller C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodde A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibbegan C.,  
 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA LaJoie P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
 RA Liu X., Matrei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Mekulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,  
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Spier B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Svirskas R., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster."  
 RL Science 287:2185-2195 (2000).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22426065; PubMed=12537568;  
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,  
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise B., Hodgson A.,  
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,  
 RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
 RA Weinstein G., Scher S.E., Myers E.W., Rubin G.M., Rubin G.M.;  
 RT "Finishing a whole-genome shotgun: release 3 of the Drosophila  
 melanogaster euchromatic genome sequence."  
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).

RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22426070; PubMed=12537573;  
 RA Celniker S.E., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,  
 RA Patel S., Frise B., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.;  
 RT "The transposable elements of the Drosophila melanogaster euchromatin:  
 a genomic perspective."  
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20 (2002).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22426069; PubMed=12537572;  
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,  
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
 RA Betencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,  
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.;  
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
 systematic review."  
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RG Berkeley Drosophila Genome Project;  
 RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise B., George R.,  
 RA Hoskins R., Stapleton M., Pacle J., Park S., Svirskas R., Smith E.,  
 RA Yu C., Rubin G.;  
 RT "Drosophila melanogaster release 4 sequence."  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE.  
 RG FlyBase;  
 RL Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.  
 CC CC  
 CC -i- INTERACTION:  
 CC Q9V860:CG6459; NBExp=1; Intact=EBI-83837, EBI-151216;  
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DR EMBL: AE003639; AAF53248.1; -; Genom1C\_DNA.  
 DR HSSP: P53686; 1Q1A.  
 DR InFrac: Q9VK34; -;  
 DR FlyBase: FBgn004291; Sir2.  
 DR GO: GO:0005737; C:cytoplasm; IDA.  
 DR GO: GO:0005634; C:nucleus; IDA.  
 DR GO: GO:0017136; F:NAD-dependent histone deacetylase activity; IDA.  
 DR GO: GO:0005515; F:protein binding; IPI.  
 DR InterPro: IPR003000; SIR2.  
 DR PANTHER: PTHR11085; SIR2; 1.  
 DR Pfam: PF02146; SIR2; 1.  
 DR PROSITE: PS50363; SIRTUIN; 1.  
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 DB 698 DYSDDDE 705

RESULT 46  
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 AC Q4Y026  
 DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.  
 DT 05-JUL-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 4.  
 DE Apoptosome-rich antigen Pfafs-14, putative (Fragment).  
 GN ORFNames=PC000038.02.0;  
 OS Plasmodium chabaudi.

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OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCB1_TaxID=5825;
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RP NUCLEOTIDE SEQUENCE.
RX PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
RA Bertram M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA Kafatos F.C., Jansse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Stinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC
CC
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CC
CC EMBL, CAJ01001857, CAH77164.1; -, Genomic DNA.
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378 DFNDDDDK 385
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ID Q6CG65_YARLI PRELIMINARY; PRT; 926 AA.
AC Q6CG65;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, entry version 1.
DE Yarrowia lipolytica chromosome B of strain CLIB122 of Yarrowia
DE lipolytica.
GN OrderedLocustNames=YALI10B005289;
OS Yarrowia lipolytica (Candida lipolytica).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCB1_TaxID=4952;
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RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durieux P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangoul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckrich J.-M., Beyne B., Bleykasten C.,
RA Boismarie A., Boyer J., Cartolico L., Confarioleri F., de Darvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Giropi A.,
RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire X., Lesur I., Ma L., Muller H.,
RA Nicand J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Porter S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekia F., Wesolowski-Louvel M., Weshof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic Y., Bolocin-Fukuhara C., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
CC -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
CC -----
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CC distributed under the Creative Commons Attribution-NonDerivs license
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CC EMBL, CR382128, CAG82561.1; -, Genomic DNA.
DR GO: GO:0005488; F-binding; IEA.
DR InterPro: IPR011990; TPR-like_helical.
DR InterPro: IPR001440; TPR_1.
DR InterPro: IPR013105; TPR_2.
DR InterPro: IPR013026; TPR_region.
DR Pfam: PF00515; TPR_1; 4.
DR SMART: SM00028; TPR; 3.
DR PROSITE: PSS0005; TPR; 7.
DR PROSITE: PSS0293; TPR_REGION; 3.
KM Complete proteome; Repeat; TPR repeat.
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12 DYEDDD 18
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AC Q416J9;
DT 16-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein.
DE ORFNames=FG07159.1;
GN Gibberella zeae (Fusarium graminearum).
OS Gibberella zeae (Fusarium graminearum).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
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RX STRAIN=PH-1 / NRRL 31084;
RA Birren B.W., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,
RA Boukhalil B., Butler J., Calvo S.E., Canarata U., Chang J.,
RA Choepel Y., Collimore A., Cook A., Cooke P., Corum B., Deatellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D.,
RA Hagagan J.E., Gardyna S., Gierre S., Graham L., Grand-Pierre N.,
RA Hafez N., Haggopian D., Hagos B., Hall J., Horton L., Hulme W.,
RA Iliev I., Uafte D., Johnson R., Jones C., Kamai M., Kanat A.,
RA Karatas A., Kells C., Landers T., Levine R., Linblad-Toh K., Liu G.,
RA Lui A., Ma L.-J., Mabbitt R., Maclean C., MacDonald P., Major J.,
RA Manning J., Matthews C., Mauceli E., McCarthy M., Meldrum J.,
RA Menes L., Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C.,
RA O'Neil D., Nielsen C.B., Norbu C., O'Connor T., O'Donnell P.,
RA O'Neil D., Oliver J., Peterson K., Phunkhang P., Pierre N.,
RA Percell S., Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C.,
RA Rogov P., Roman J., Schauer S., Schuback R., Seaman S., Severy P.,
RA Shtinov S., Smith C., Spencer B., Stange-Thomann N., Stojanovic N.,
RA Stribos M., Talmas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zairoun U., Zembek L., Zimmer A., Zody M.,
RA Lander E.S.;
RT "Fusarium graminearum genome sequence.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC
CC
CC EMBL, AAC01000301, EAA76618.1; -, Genomic DNA.
DR Complete proteome; Hypothetical protein.
SQ SEQUENCE 1018 AA; 114167 MW; 07DFCD7B0F0A11F4 CRC64;
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QY 1 DYKDDDD 7  
 DB 545 DYEDDDD 551

RESULT 49  
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 AC P39520;  
 DT 01-FEB-1995, integrated into UniProtKB/Swiss-Prot.  
 DT 01-FEB-1995, sequence version 1.  
 DT 07-MAR-2006, entry version 38.  
 DE Protein IFH1 (Protein RRP3).  
 GN Name=IFH1; Synonyms=RRP3; Ordered locus names=YLR223C; ORFNames=L8083.9;  
 OS *Saccharomyces cerevisiae* (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 CC *Saccharomycetales*; *Saccharomycetaceae*; *Saccharomyces*.  
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[1]  
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 RC STRAIN=ATCC 28383 / FL100;  
 RX MEDLINE=95304839; PubMed=7785326;  
 RA Chereil I., Thuriaux P.,  
 RT "The IFH1 gene product interacts with a fork head protein in  
 RT *Saccharomyces cerevisiae*.";  
 RL Yeast 11:261-270(1995).  
 [2]  
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 RP STRAIN=S288c / AB972;  
 RX MEDLINE=9733267; PubMed=9169871;  
 RA Johnston M., Hillier L.W., Riles L., Albermann K., Andre B.,  
 RA Ansorge W., Benes V., Bruckner M., Delius H., Dubois E.,  
 RA Duescherhoef A., Entian K.-D., Floeth M., Goffeau A., Hebling U.,  
 RA Heumann K., Heuss-Neitzel D., Hilbert H., Hilger F., Klatte K.,  
 RA Koetter P., Louis E.J., Messenguy F., Mewes H.-W., Miosga T.,  
 RA Moestl D., Mueller-Auer S., Nentwich U., Odermatt B., Piravandi E.,  
 RA Pohl T.M., Portetelle D., Purnelle B., Rechmann S., Rieger M.,  
 RA Rinke M., Rose M., Scharfe M., Scherens B., Scholler P., Schwager C.,  
 RA Schwarz S., Underwood A.P., Urestarazu L.A., Vandenbol M.,  
 RA Vershaesselt P., Vierendeels F., Voet M., Voickert G., Voss H.,  
 RA Wambutt R., Wedler E., Weller H., Zimmermann F.K., Zollner A.,  
 RA Hani U., Hohlmeier J.D.;  
 RT "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome XII.";  
 RL Nature 387:87-90(1997).  
 [3]  
 LEVEL OF PROTEIN EXPRESSION.  
 RP MEDLINE=22933965; PubMed=14562106; DOI=10.1038/nature02046;  
 RA Chaemugarnam S., Huu W.-K., Bower K., Howson R.W., Belle A.,  
 RA Dephoure N., O'Shea E.K., Weissman J.S.;  
 RT "Global analysis of protein expression in yeast.";  
 RL Nature 425:737-741(2003).  
 CC -1- FUNCTION: Controls the pre-rRNA processing machinery in  
 CC conjunction with FHL1. Could convert FHL1 from a repressor to an  
 CC activator.  
 CC -1- INTERACTION: NDBxp=1; Intact=EBI-9054, EBI-38337;  
 CC Q08673:SRIL; NDBxp=1; Intact=EBI-9054, EBI-38337;  
 CC -1- SUBCELLULAR LOCATION: Nucleus (Probable).  
 CC -1- MISCELLANEOUS: Present with 1430 molecules/cell.  
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 CC EMBL: Z29488; CA82624.1; -; Genomic DNA.  
 CC EMBL: U19027; AAB67412.1; -; Genomic DNA.  
 CC PIR: S55352; S55352.  
 CC Inactive; P39520; -;  
 CC Germline; YLR223C; *Saccharomyces cerevisiae*.  
 DR

DR GenomeReviews; Y13138 GR; YLR223C.  
 DR SGD; S000004213; IFH1-  
 DR BiOCC; SCER-S28-01:SCER-S28-01-004107-MONOMER; -  
 DR LinkDb; P39520; -;  
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 DR GO; GO:0005515; F:protein binding; IPI.  
 DR GO; GO:0003700; F:transcription factor activity; IGI.  
 DR GO; GO:0006348; P:chromatin silencing at telomere; IMP.  
 DR GO; GO:0006363; P:rRNA processing; IGI.  
 DR GO; GO:0006383; P:transcription from RNA polymerase III promoter; IGI.  
 KW Complete proteome; Nuclear protein; Transcription;  
 KW Transcription regulation.  
 FT CHAIN 1 1085 Protein IFH1.  
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 FT Asp/Glu-rich (highly acidic).  
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QY 1 DYKDDDD 7  
 DB 612 DYEDDDD 618

RESULT 50  
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 DT 19-JUL-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 5.  
 DE Hypothetical protein.  
 GN ORFNames=UM04235.1;  
 OS *Ustilago maydis* 521.  
 CC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;  
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 RC STRAIN=521;  
 RA Alt-Zahra M., Allen C., Abebe A., Abouelleil A., Adekoya E.,  
 RA Biren B.W., Nuebaum C., Allen T., An P., Anderson M., Anderson S.,  
 RA Arachchi H.M., Armbruster J., Bachantsang P., Baldwin J., Barry A.,  
 RA Bayul T., Bittensteyn B., Bloom T., Bye J., Boguslavsky L.,  
 RA Bowocky M., Bouhgalter B., Brunache A., Butler J., Calixte N.,  
 RA Calvo S.E., Camarata J., Campo K., Chang J., Cheahatsang Y.,  
 RA Clitroen M., Collymore A., Considine T., Cook A., Cooke P., Corum B.,  
 RA Chomo C., David R., Dawoe T., Degray S., Dodge S., Dooley K.,  
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 RA Hognan D., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,  
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 RA Kells C., Kieu A., Kisher P., Kodira C., Kulbokas E., Labutti K.,  
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 RA Lindblad-Toh K., Liu X., Lokysang T., Lokysang Y., Lucien O.,  
 RA Lui A., Ma L.-J., Mabbitt R., MacDonald J., Maclean C., Mayor J.,  
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 RA Mesitov J., Mihalay A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,  
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RA Venkataraman V.S., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,  
RA Wangli T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,  
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,  
RA Zimmer A., Zody M., Lander E.S.;  
RT "The genome sequence of Ustilago maydis.";  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
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CC -----  
CC EMBL: AACP01000150; EAK85284.1; -; Genomic_DNA.  
DR GO: GO:0005634; C:nucleus; IEA.  
DR GO: GO:0046872; F:metal ion binding; IEA.  
DR GO: GO:0003700; F:transcription factor activity; IEA.  
DR GO: GO:0008270; F:zinc ion binding; IEA.  
DR GO: GO:0006355; P:regulation of transcription; DNA-dependent; IEA.  
DR GO: GO:0006350; P:transcription; IEA.  
DR InterPro: IPR001138; Funct_Trcscp_N.  
DR Pfam: PF04082; Fungal_trans; 1.  
DR SMART: SM00066; GAL4; 1.  
DR PROSITE: PS00463; ZN2_CY6_FUNGAL_1; UNKNOWN_1.  
DR PROSITE: PS0048; ZN2_CY6_FUNGAL_2; 1.  
KW DNA-binding; Hypothetical protein; Metal-binding; Nuclear protein;  
KW Transcription; Transcription regulation; Zinc.  
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Best Local Similarity 85.7%; Pred. No. 2e+03;  
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QY 1 DYKDDDD 7  
Db 851 DYEDDD 857  
  
RESULT 51  
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AC Q7MKW4;  
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.  
DT 15-DEC-2003, sequence version 1.  
DT 21-FEB-2006, entry version 22.  
DE DNA polymerase III, alpha subunit.  
GN Name:dnai3; Ordered locus names=PG0035; ORFNames=PG_0035;  
OS Porphyromonas gingivalis (Bacteroides gingivalis).  
OC Bacteria; Bacteroidetes; Bacteroidales (class); Bacteroidales;  
OC Porphyromonadaceae; Porphyromonas.  
OX NCBI_TaxID=837;  
[1]  
RA NCBILOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RP STRAIN=W83;  
RX MEDLINE=22829867; PubMed=12949112;  
RX DOI=10.1128/JB.185.18.5591-5601.2003;  
RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,  
RA Bisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,  
RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,  
RA Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,  
RA Dewhirst F.E., Fraser C.M.;  
RT "Complete genome sequence of the oral pathogenic bacterium  
RT Porphyromonas gingivalis strain W83.";  
RL J. Bacteriol. 185:5591-5601(2003).  
CC -!- CATALYTIC ACTIVITY: Deoxynucleoside triphosphate + DNA(n) =  
CC diphosphate + DNA(n+1).  
CC -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).  
CC -----  
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DR TRIGR; PG0035;  
DR BiotCyc; PG1242619; PG0035-MONOMER; -.  
DR GO: GO:0057377; C:cytoplasm; IEA.  
DR GO: GO:0004808; F:3',5'-5' exonuclease activity; IEA.  
DR GO: GO:0003889; F:alpha DNA polymerase activity; IEA.  
DR GO: GO:0003677; F:DNA binding; IEA.  
DR GO: GO:0016740; F:transferase activity; IEA.  
DR GO: GO:0006260; F:DNA replication; IEA.  
DR InterPro: IPR011708; DNA_pol3_alpha.  
DR InterPro: IPR004365; OB_RNA_NA_bd.  
DR InterPro: IPR003141; Pesterase_PHP_N.  
DR InterPro: IPR004013; PHP_C.  
DR InterPro: IPR004805; PolC_alpha.  
DR Pfam: PF07733; DNA_pol3_alpha; 1.  
DR Pfam: PF02811; PHP; 1.  
DR Pfam: PF01336; tRNA_anti; 1.  
DR SMART: SM00481; POLITAC; 1.  
DR TIGRFAMs; TIGR00594; polC; 1.  
KW Complete proteome; DNA replication; DNA-directed DNA polymerase;  
KW Nucleotidyltransferase; Transferase.  
SQ SEQUENCE 1228 AA; 139197 MW; 39B848DEFC7783 CRC64;  
  
Query Match 80.9%; Score 38; DB 2; Length 1228;  
Best Local Similarity 85.7%; Pred. No. 2e+03;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DYKDDDD 7  
Db 357 EYKDDDD 363  
  
RESULT 52  
Q81LD1_P1AF7 PRELIMINARY; PRT; 1267 AA.  
ID Q81LD1_P1AF7  
AC Q81LD1;  
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.  
DT 01-MAR-2003, sequence version 1.  
DT 07-FEB-2006, entry version 14.  
DE Hypothetical protein.  
GN ORFNames=PF14_0313;  
OS Plasmodium falciparum (Isolate 3D7).  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI_TaxID=36329;  
[1]  
RA NCBILOTIDE SEQUENCE.  
RP STRAIN=3D7;  
RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;  
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,  
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,  
RA Bisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,  
RA Chan W.-S., Nene V., Shallow S.J., Sun B., Peterson J., Angiuoli S.,  
RA Pereira M., Allen J., Selengut J., Haft D., Mather M.W., Valdivia A.B.,  
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,  
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,  
RA Fraser C.M., Barrett B.G.;  
RT "Genome sequence of the human malaria parasite Plasmodium  
RT falciparum.";  
RL Nature 419:498-511(2002).  
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CC -----  
CC EMBL: AE014821; AAN36926.1; -; Genomic_DNA.  
DR InterPro: IPR002048; EF_hand_Ca_bd.  
DR PROSITE: PS00018; EF_HAND_1; UNKNOWN_1.  
KW Hypothetical protein.  
SQ SEQUENCE 1267 AA; 152262 MW; 239F91EBBD942C80 CRC64;  
  
Query Match 80.9%; Score 38; DB 2; Length 1267;
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Best Local Similarity 75.0%; Pred. No. 2.1e+03;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 855 NYKDDDEK 862

## RESULT 53

PDS5\_YEAST

ID\_PDS5\_YEAST STANDARD; PRT: 1277 AA.

AC Q04264; Q04780;

DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.

DT 01-NOV-1997, sequence version 1.

DT 07-MAR-2006, entry version 35.

DE Sister chromatid cohesion protein PDS5 (Precocious dissociation of

DE sisters protein 5).

GN Name=PDS5; OrderedLocustNames=YMR076C; ORFNames=YM9582.01C, YM9916.15C;

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OX NCBI\_TaxID=4932; Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

RN Nucleotide sequence [LARGE SCALE GENOMIC DNA].

RC STRAIN=S288c / AB972;

RX MEDLINE=97313268; PubMed=9169872;

RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,

RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,

RA Jagsels K., Iye G., Moutle S., Odell C., Pearson D., Rajandream M.A.,

RA Rice F., Skelton J., Walsh S.V., Whitehead S., Barrrell B.G.;

RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome

XII."

RL Nature 387:90-93(1997).

RN FUNCTION AND SUBCELLULAR LOCATION.

RX MEDLINE=20517447; PubMed=11062262; DOI=10.1083/jcb.151.3.613;

RA Hartman T., Stead K., Koshland D., Guacci V.;

RT "Pds5 is an essential chromosomal protein required for both sister

RT chromatid cohesion and condensation in Saccharomyces cerevisiae."

RL J. Cell Biol. 151:613-626(2000).

RN CURR. BIOL. 10:1557-1564(2000).

RL ACETYLATION.

RX PubMed=11864574; DOI=10.1016/S0960-9822(02)00681-4;

RA Ivanov D., Schleiffer A., Eisenhaber F., Mechtler K., Haering C.H.,

RA Nasmyth K.;

RT "Pds5 is a novel acetyltransferase that can acetylate proteins

RT involved in cohesion."

RL Curr. Biol. 12:323-328(2002).

RN LEVEL OF PROTEIN EXPRESSION.

RX MEDLINE=22923965; PubMed=14562106; DOI=10.1038/nature02046;

RA Gaemmaghami S., Huh W.-K., Bower K., Howson R.W., Belle A.,

RA Dephoure N., O'Shea E.K., Weissman J.S.;

RT "Global analysis of protein expression in yeast."

RL Nature 425:737-741(2003).

RT FUNCTION: Essential for the establishment and maintenance of

RT sister chromatid cohesion at centromere proximal and distal

RT regions during S phase. Also required for chromosomal

RT condensation.

RT INTERACTION: Self; NDCxp-1; InAct=EBI-13077, EBI-13077;

RT PTM: Acetylated by ECO1.

RT MISCELLANEOUS: Present with 7720 molecules/cell.

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CC EMBL: Z49259; CAA89322.1; -; Genomic DNA.  
DR EMBL: Z49952; CAA88801.1; -; Genomic DNA.  
DR PIR: S54451, S54451.

DR InAct: Q04264; -;

DR GERMOnline: 142743; -;

DR Ensemble: YMR076C; Saccharomyces cerevisiae.

DR GenomeReviews: Z71257 GR; YMR076C.

DR SGD: S000004681; PDS5\_

DR BioCyc: SCER-528-01:SCER-528-01-004587-MONOMER; -;

DR LinkHub: Q04264; -;

DR GO: GO:0000794; C:condensed nuclear chromosome; IDA.

DR GO: GO:0042802; F:protein self binding; IPI.

DR GO: GO:0007076; P:mitotic chromosome condensation; IMP.

DR GO: GO:0006473; P:protein amino acid acetylation; IDA.

DR InterPro: IPR011989; ARM-1like.

DR InterPro: IPR000357; HEAT\_1.

DR Pfam: PF02985; HEAT\_1.

DR Acetylation: Cell cycle; Cell division; Complete proteome; Mitosis;

KW Nuclear protein.

FT CHAIN 1 1277 Sister chromatid cohesion protein PDS5.

FT /FTID=PRO\_000058280.

SQ SEQUENCE 1277 AA; 147041 MW; 9DF40A5274FD9623 CRC64;

Query Match 80.9%; Score 38; DB 1; Length 1277;

Best Local Similarity 85.7%; Pred. No. 2.1e+03;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 7

Db 1265 DYKDDDDK 1271

RESULT 54

Q6FNZ8 CANGA

ID\_Q6FNZ8 CANGA PRELIMINARY; PRT: 1305 AA.

AC Q6FNZ8;

DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.

DT 19-JUL-2004, sequence version 1.

DT 21-FEB-2006, entry version 20.

DE Similar to sp|P12753 Saccharomyces cerevisiae YNL250w DNA repair

DE protein.

GN OrderedLocustNames=CAGLOJ077889;

OS Candida glabrata (Yeast) (Torulopsis glabrata).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; mitosporic Saccharomycetales; Candida.

OX NCBI\_TaxID=5478;

RN Nucleotide sequence [LARGE SCALE GENOMIC DNA].

RC STRAIN=ATCC 2001 / CBS 138;

RX PubMed=15229592; DOI=10.1038/nature02579;

RA Dujon B., Sherman D., Fischer G., Durieux P., Casaregola S.,

RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,

RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Babe V.,

RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,

RA Bostrame A., Boyer J., Cartolico L., Confanioli F., de Darvar A.,

RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppl A.,

RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,

RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,

RA Nicand J.-M., Nikolski M., Octas S., Olier-Kalogeropoulos O.,

RA Pellens S., Potier S., Richard G.-F., Strub M.-L., Suleau A.,

RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,

RA Zenou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,

RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,

RT "Genome evolution in yeasts."

RT Nature 430:35-44(2004).

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CC EMBL: CR380956; CAG60997.1; -; Genomic DNA.

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DR GO: GO:0005694; C:chromosome; IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0030870; C:miR1 complex; IEA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0016887; F:ATPase activity; IEA.
DR GO: GO:0004518; F:nuclease activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0051276; P:chromosome organization and biogenesis; IEA.
DR GO: GO:0006281; P:DNA repair; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR003439; ABC_transp_like.
DR InterPro: IPR004584; Rad50.
DR InterPro: IPR007517; Rad50_Zn_hook.
DR InterPro: IPR003395; SMC_N.
DR InterPro: IPR013134; Zn_hook_Rad50.
DR Pfam: PF04423; Rad50_zn_hook; 1.
DR Pfam: PF02463; SMC_N; 1.
DR TIGRPFAM: TIGR00606; rad50; 1.
DR Complete proteome.
SQ SEQUENCE 1305 AA; 150668 MW; 7489860D317CEFB80 CRC64;

Query Match      80.9%; Score 38; DB 2; Length 1305;
Best Local Similarity 87.5%; Pred. No. 2.2e+03;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 8
DB 1095 DYKDDDD 1102

RESULT 55
Q81B1 PLAF7 PRELIMINARY; PRT; 1523 AA.
ID Q81B1 PLAF7 PRELIMINARY; PRT; 1523 AA.
AC Q81B1;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Hypothetical protein PF10185w.
GN Name=PF10185w;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
RX MEDLINE=22255708; PubMed=12368867; DOI=10.1038/nature01095;
RA Hall N., Pain A., Berriman M., Churcher C.M., Harris B., Harris D.,
RA Mungall K.L., Bowman S., Ackin R., Baker S., Barron A., Brooks K.,
RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
RA Cronin A., Davies R.M., Davis P., Dear P., Dearden F., Doggett J.,
RA Felwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
RA Humphray S., Jagers K., James K.D., Johnson D., Kerhornou A.,
RA Knights A., Kontorov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E.,
RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders S., Simmonds M.,
RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
RA Sulston J.E., Craig A., Newbold C., Barrell B.G.;
RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13."
RL Nature 419:527-531(2002).
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DR EMBL: AL929355; CAD51723.1; -; Genomic_DNA.
DR InterPro: IPR013320; ConA_like_subgrp.
DR InterPro: IPR004043; LCCL.
DR InterPro: IPR000772; Ricin_B_lectin.
DR Pfam: PF03815; LCCL; 1.
DR PROSITE: PS50820; LCCL; 1.
DR PROSITE: PS50231; RICIN_B_LLECTIN; 1.

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KW Hypothetical protein; Repeat.
SQ SEQUENCE 1523 AA; 178335 MW; DAAD8056B3C97C7D CRC64;

Query Match      80.9%; Score 38; DB 2; Length 1523;
Best Local Similarity 75.0%; Pred. No. 2.5e+03;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 8
DB 809 DYKDDDD 816

RESULT 56
Q81B8 PLAF7 PRELIMINARY; PRT; 1687 AA.
ID Q81B8 PLAF7 PRELIMINARY; PRT; 1687 AA.
AC Q81B8;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 21-FEB-2006, entry version 13.
DE Hypothetical protein MAL8P1.18.
GN Name=MAL8P1.18;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
RX MEDLINE=22255708; PubMed=12368867; DOI=10.1038/nature01095;
RA Hall N., Pain A., Berriman M., Churcher C.M., Harris B., Harris D.,
RA Mungall K.L., Bowman S., Ackin R., Baker S., Barron A., Brooks K.,
RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
RA Cronin A., Davies R.M., Davis P., Dear P., Dearden F., Doggett J.,
RA Felwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
RA Humphray S., Jagers K., James K.D., Johnson D., Kerhornou A.,
RA Knights A., Kontorov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E.,
RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders S., Simmonds M.,
RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
RA Sulston J.E., Craig A., Newbold C., Barrell B.G.;
RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13."
RL Nature 419:527-531(2002).
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DR EMBL: AL844507; CAD51099.1; -; Genomic_DNA.
DR GO: GO:0003723; F:RNA binding; IEA.
DR InterPro: IPR000804; Clat_adaptor_s.
DR InterPro: IPR012340; OB_NA_bd_sub.
DR InterPro: IPR003029; S1_RNA_bd.
DR SMART: SM00316; S1; 2.
DR PROSITE: PS00989; Clat_ADAPTOR_S; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 1687 AA; 203792 MW; C850B170184C0467 CRC64;

Query Match      80.9%; Score 38; DB 2; Length 1687;
Best Local Similarity 85.7%; Pred. No. 2.8e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
DB 315 DYKDDDD 321

RESULT 57
Q4XUN1 PLAF7 PRELIMINARY; PRT; 1818 AA.
ID Q4XUN1 PLAF7 PRELIMINARY; PRT; 1818 AA.
AC Q4XUN1;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein (fragment).
GN ORFNames=PC000259.03.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5825;
RX MEDLINE=15637271; PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karas M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Truman H.B., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,

```

RA Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,  
RA Sinden R.S.;  
RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
RT transcriptomic, and proteomic analyses.";  
RL Science 307:82-86(2005).  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.

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CC  
CC EMBL, CAJ01003023; CAJ79380.1; -; Genomic\_DNA.  
CC Hypothetical protein.  
CC NON TER 1818 1818  
SQ SEQUENCE 1818 AA; 212574 MW; 66385CDD5FBE512C CRC64;

Query Match 80.9%; Score 38; DB 2; Length 1818;  
Best Local Similarity 75.0%; Pred. No. 3.1e+03;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8  
Db 1693 DYSDDEK 1700

## RESULT 58

Q4UBC4 THEAN PRELIMINARY; PRT; 1921 AA.  
AC Q4UBC4;  
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2005, sequence version 1.  
DT 07-FEB-2006, entry version 3.  
DE Hypothetical protein.  
GN ORFNames-TA18820;  
OS Theileria annulata.  
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;  
OC Theileria.  
OX NCBI\_TaxID=5874;

OC [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Ankara isolate clone C9;  
RX PubMed=1594597; DOI=10.1258/jrem.98.7.320;  
RA Pain A., Renaud H., Berriman M., Murphy L., Yeats C.A., Weir W.,  
RA Kerhoun A., Aletti M., Bishop R., Bouchier C., Cochet M.,  
RA Coulson R.M.R., Cronin A., de Villiers E.P., Frazer A., Foster N.,  
RA Gardner M., Goble A., Griffiths-Jones S., Harris D.E., Katzer F.,  
RA Larke N., Lord A., Maier P., McKellar S., Mooney P., Morton F.,  
RA Nene V., O'Neill S., Price C., Quail M.A., Rabinowitch E.,  
RA Rawlings N.D., Rutter S., Saunders D., Seeger K., Shah T., Squares R.,  
RA Squares S., Tivey A., Walker A.R., Woodward J., Dobbelaere D.A.E.,  
RA Langley G., Rajandream M.A., McKeever D., Shiels B., Tait A.,  
RA Barrell B., Hall N.;  
RT "Genome of the host-cell transforming parasite *Theileria annulata*  
RT compared with *T. parva*.";  
RL Science 309:131-133(2005).  
CC -----  
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CC  
CC EMBL, CR940352; CAI75877.1; -; Genomic\_DNA.  
CC  
CC Hypothetical protein.  
SQ SEQUENCE 1921 AA; 225331 MW; C15605816DA5711C CRC64;

Query Match 80.9%; Score 38; DB 2; Length 1921;  
Best Local Similarity 85.7%; Pred. No. 3.3e+03;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDD 7  
Db 155 DYEDDD 161

RESULT 59  
Q5ASE7 EMENI PRELIMINARY; PRT; 2051 AA.  
AC Q5ASE7;  
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.  
DT 26-APR-2005, sequence version 1.  
DT 07-MAR-2006, entry version 10.  
DE B1MB EMENI CELL DIVISION-ASSOCIATED PROTEIN B1MB.  
GN ORFNames=AN9783.2;  
OS Aspergillus nidulans F5SC A4.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
OC Eurotiales; Trichocomaceae; Emericella.  
OX NCBI\_TaxID=227321;

OX [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=F5SC 4;  
RX PubMed=16372000; DOI=10.1038/nature04341;  
RA Galagan J.E., Calvo S.E., Cuomo C., Ma L.-J., Wortman J.R.,  
RA Batzoglou S., Lee S.-I., Basten C., Spevak C.C., Clutterbuck J.,  
RA Kapitonov V., Jurka J., Scanzocchio C., Farmer M., Butler J.,  
RA Purcell S., Harris S., Bruns G.H., Drant O., Busch S., D'Entert C.,  
RA Boucher C., Goldman G.H., Bell-Pedersen D., Griffiths-Jones S.,  
RA Doonan J.H., Yu J., Vlenken K., Pain A., Freitag M., Selker E.U.,  
RA Archer D.B., Penhaly M.A., Oakley B.R., Momany M., Tanaka T.,  
RA Kumagai T., Asai K., Machida M., Niernan W.C., Denning D.W.,  
RA Caddick M., Hynes M., Paolletti M., Fischer R., Miller B.L., Dyer P.S.,  
RA Sachs M.S., Osmani S.A., Birren B.W.;  
RT "Sequencing of *Aspergillus nidulans* and comparative analysis with *A. fumigatus* and *A. oryzae*.";  
RL Nature 438:1105-1115(2005).  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.

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CC  
CC EMBL, AACD01000161; BAA60576.1; -; Genomic\_DNA.  
CC  
CC GO: GO:0005634; C:nucleus; IEA.  
CC GO: GO:0005488; F:binding; IEA.  
CC GO: GO:0008233; F:peptidase activity; IEA.  
CC GO: GO:0051301; P:cell division; IEA.  
CC GO: GO:0006508; P:proteolysis; IEA.  
CC InterPro: IPR005314; Peptidase\_C50.  
CC InterPro: IPR011990; TPR-like helical.  
CC PANTHER: PTHR12792; Peptidase\_C50; 1.  
CC Pfam: Pf03568; Peptidase\_C50; 1.  
CC Cell division; Hydrolase.

SQ SEQUENCE 2051 AA; 225809 MW; 97E9C0EC70590464 CRC64;  
Query Match 80.9%; Score 38; DB 2; Length 2051;  
Best Local Similarity 85.7%; Pred. No. 3.5e+03;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYQDDDD 7  
Db 883 DYQDDDD 889

RESULT 60  
B1MB EMENI STANDARD; PRT; 2067 AA.  
AC P33134;  
DT 01-OCT-1993, integrated into UniProtKB/Swiss-Prot.  
DT 01-OCT-1993, sequence version 1.  
DT 07-FEB-2006, entry version 30.  
DE Separin (EC 3.4.22.49) (Separase) (Cell division-associated protein  
DE b1mb).  
GN Name=b1mb;  
OS Emericella nidulans (*Aspergillus nidulans*).  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
OC Eurotiales; Trichocomaceae; Emericella.  
OX NCBI\_TaxID=162425;

```

RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RP STRAIN=A773; PubMed=1639810;
RX MEDLINE=92348436; Pubmed=1639810;
RA May G.S., McGoldrick C.A., Holt C.L., Denison S.H.;
RT "The blmb3 mutation of Aspergillus nidulans uncouples DNA replication
from the completion of mitosis.";
RL J. Biol. Chem. 267:15737-15743(1992).
CC -1- FUNCTION: Required for nuclear division. Could function in the
mitotic spindle.
CC -1- CATALYTIC ACTIVITY: All bonds known to be hydrolyzed by this
endopeptidase have arginine in P1 and an acidic residue in P4. P6
is often occupied by an acidic residue or by an hydroxy-amino-acid
residue, the phosphorylation of which enhances cleavage.
CC -1- SUBCELLULAR LOCATION: Nucleus.
CC -1- SIMILARITY: Belongs to the peptidase C50 family.
CC -----
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CC -----
DR EMBL: M83232; AAA33297.1; ALT_TPRM; Genomic_DNA.
DR PIR: A42854; A42854.
DR MEROPS: C50.001; -.
DR InterPro: IPR005314; Peptidase_C50.
DR InterPro: IPR011990; TPR-like helical.
DR PANTHER: PTHR12792; Peptidase_C50; 1.
DR Pfam: PF03568; Peptidase_C50_1.
DR Cell cycle; Cell division; Chromosome partition; Hydrolyase; Mitosis;
KW Nuclear protein; Protease; Thiol protease.
FT CHAIN 1 2067
FT Separin.
FT ACT SITE 1964 1964 /Frid=PRO_0000205902.
FT By similarity.
SQ SEQUENCE 2067 AA; 227926 MW; E0655D939EC148DB CRC64;

Query Match 80.9%; Score 38; DB 1; Length 2067;
Best Local Similarity 85.7%; Pred. No. 3.5e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
DB 899 DYQDDDD 905

RESULT 61
ID O97225_PUAF7 PRELIMINARY; PRT; 2226 AA.
AC O97225;
DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 3.
DT 07-FEB-2006, entry version 21.
DE Hypothetical protein MAL3P2.2.
GN Name=MAL3P2.2; Synonyms=PPC0165w;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329; [1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=99376085; Pubmed=10448855; DOI=10.1038/22964;
RX Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
RA Churcher C.M., Craig A., Davies R.M., Devlin K., Feltham T.,
RA Gentsch S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T.,
RA Horrocks P., Jugele K., Jassal B., Kyes S., Molese J., Moulé S.,
RA Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,
RA Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,
RA Whitehead S., Woodward J.R., Newbold C., Barrett B.G.;
RT "The complete nucleotide sequence of chromosome 3 of Plasmodium
falciparum";
RL Nature 400:532-538(1999). [2]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22255708; Pubmed=12368667; DOI=10.1038/nature01095;
RA Hall N., Pain A., Bertram M., Churcher C.M., Harris B., Harris D.,
RA Mungall K.L., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,

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RA Buckee C.O., Burrows C., Cheruvach I., Chillingworth C.,
RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
RA Croft A., Davies R.M., Davis P., Dear P., Dearden F., Doggett J.,
RA Feltham T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
RA Humphray S., Jagers K., James K.D., Johnson D., Kenyon N.,
RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Line A., Maddison M., McLean J., Mooney P., Moulé S., Murphy L.,
RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitch E.,
RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
RA Sulston J.E., Craig A., Newbold C., Barrett B.G.;
RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
RL Nature 419:527-531(2002).
CC -----
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CC -----
DR EMBL: AL034558; CAB38989.3; -. Genomic DNA.
DR GO: GO:0005815; C:microtubule organizing center; IEA.
DR GO: GO:0000922; C:spindle pole; IEA.
DR GO: GO:0002226; P:microtubule cytoskeleton organization and b. .; IEA.
DR InterPro: IPR007259; SPC97_SPC98.
DR PANTHER: PTHR19302; SPC97_SPC98; 1.
DR Pfam: PF04130; SPC97_SPC98; 1.
KW Hypothetical protein.
SQ SEQUENCE 2226 AA; 267976 MW; 8690501ED4994768 CRC64;

Query Match 80.9%; Score 38; DB 2; Length 2226;
Best Local Similarity 85.7%; Pred. No. 3.8e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
DB 218 DYQDDDD 224

RESULT 62
ID O5KID7_CRYNE PRELIMINARY; PRT; 2384 AA.
AC O5KID7;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE 1-phosphatidylinositol-3-phosphate 5-kinase, putative.
GN OrderedNames=CND03330;
OS Cryptococcus neoformans (Filobasidiella neoformans).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=5207; [1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=DEC21;
RX Pubmed=15653466; DOI=10.1126/science.1103773;
RA Loftus B.J., Fung E., Roncaglia P., Rowley D., Amodeo P., Bruno D.,
RA Vamadehyan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,
RA Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,
RA D'Souza C.A., Fox D.S., Grinberg V., Fu U., Fukushima M., Haas B.J.,
RA Huang J.C., Jahnson G., Jones S.J.W., Koo H.L., Krzyzanski M.I.,
RA Kwon-Chung K.J., Lengeler K.B., Maiti R., Maira M.A., Maira R.E.,
RA Matheson C.A., Mitchell T.G., Petrea M., Riggs F.R., Salzberg S.L.,
RA Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,
RA Suh B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,
RA Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,
RA Fraser C.M., Hyman R.W.;
RT "The genome of the basidiomycetous yeast and human pathogen
Cryptococcus neoformans";
RL Science 307:1321-1324(2005).
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DR EMBL: AE017344; AAW43260.1; -; Genomic DNA.  
 DR GO: GO:0016308; F:1-phosphatidylinositol-4-phosphate 5-kinase. .; IEA.  
 DR GO: GO:0005524; F:ATP binding; IEA.  
 DR GO: GO:0016301; F:kinase activity; IEA.  
 DR GO: GO:0005515; F:protein binding; IEA.  
 DR GO: GO:0008270; F:zinc ion binding; IEA.  
 DR GO: GO:0044267; F:cellular protein metabolism; IEA.  
 DR InterPro: IPR002423; Cpn60/TCP-1.  
 DR InterPro: IPR002498; PIP5K.  
 DR InterPro: IPR00306; Znf FYVE.  
 DR Pfam: PF00118; Cpn60\_TCP1; 1.  
 DR Pfam: PF01363; FYVE; 1.  
 DR Pfam: PF01504; PIP5K; 1.  
 DR SMART: SM00064; FYVE; 1.  
 DR PROSITE: PS0178; ZF\_FYVE; 1.  
 KW Complete proteome: Kinase.  
 SO SEQUENCE 2384 AA; 26368 MW; AD29D2B0BF2F793 CRC64;

Query Match 80.9%; Score 38; DB 2; Length 2384;  
 Best Local Similarity 85.7%; Pred. No. 4.1e+03;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DYKDDDD 7  
 Db 429 EYKDDDD 435

RESULT 63  
 OSU02\_CRYNE PRELIMINARY; PRT; 2432 AA.  
 ID 055002\_CRYNE  
 AC 055002;  
 DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.  
 DT 24-MAY-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 3.  
 DE Hypothetical protein.  
 GN ORFNames=CNB03020;  
 OS Cryptococcus neoformans var. neoformans B-3501A.  
 CC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;  
 CC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.  
 CX NCBI\_TaxID=283643;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=B-3501A;  
 RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,  
 RA Wicks B.L., Fu J., Davis R.W.;  
 RT "Cryptococcus neoformans serotype D sequencing."  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
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 CC -----  
 DR EMBL: AAEY0100020; EAL21247.1; -; Genomic DNA.  
 DR GO: GO:0016308; F:1-phosphatidylinositol-4-phosphate 5-kinase. .; IEA.  
 DR GO: GO:0005524; F:ATP binding; IEA.  
 DR GO: GO:0005515; F:protein binding; IEA.  
 DR GO: GO:0008270; F:zinc ion binding; IEA.  
 DR GO: GO:0044267; F:cellular protein metabolism; IEA.  
 DR InterPro: IPR002498; PIP5K.  
 DR InterPro: IPR00306; Znf FYVE.  
 DR Pfam: PF00118; Cpn60\_TCP1; 1.  
 DR Pfam: PF01363; FYVE; 1.  
 DR Pfam: PF01504; PIP5K; 1.  
 DR SMART: SM00064; FYVE; 1.  
 DR PROSITE: PS0178; ZF\_FYVE; 1.  
 KW Hypothetical protein.  
 SO SEQUENCE 2432 AA; 268925 MW; A5A9E486EDC898EE CRC64;

Query Match 80.9%; Score 38; DB 2; Length 2432;  
 Best Local Similarity 85.7%; Pred. No. 4.2e+03;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DYKDDDD 7  
 Db 429 EYKDDDD 435

RESULT 64  
 OS1AM1\_PLAF7 PRELIMINARY; PRT; 2577 AA.  
 ID OS1AM1\_PLAF7  
 AC OS1AM1;  
 DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.  
 DT 01-MAR-2003, sequence version 1.  
 DT 07-FEB-2006, entry version 13.  
 DE Hypothetical protein MAL8P1.153.  
 GN Name=MAL8P1.153;  
 OS Plasmodium falciparum (isolate 3D7).  
 CC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 CX NCBI\_TaxID=36329;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Seeger K., Murphy L., Harris D., Berriman M., Pain A., Hall N.,  
 RA Quail M., Barrell B.;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 CC -----  
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 CC -----  
 DR EMBL: AL844507; CAD51342.1; -; Genomic DNA.  
 DR GO: GO:0046872; F:metal ion binding; IEA.  
 DR GO: GO:0042222; F:metalloendopeptidase activity; IEA.  
 DR GO: GO:0009405; P:patogenesis; IEA.  
 DR GO: GO:0006508; P:proteolysis; IEA.  
 DR InterPro: IPR011591; Botulinum.  
 DR ProDom: PD001963; Botulinum; 1.  
 KW Hypothetical protein.  
 SO SEQUENCE 2577 AA; 299293 MW; 025BBC240587F4D7 CRC64;

Query Match 80.9%; Score 38; DB 2; Length 2577;  
 Best Local Similarity 85.7%; Pred. No. 4.5e+03;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DYKDDDD 7  
 Db 1103 EYKDDDD 1109

RESULT 65  
 OS8786\_PLAFA PRELIMINARY; PRT; 119 AA.  
 ID OS8786\_PLAFA  
 AC OS8786;  
 DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.  
 DT 01-JUN-2002, sequence version 1.  
 DT 07-FEB-2006, entry version 8.  
 DE Erythrocyte membrane protein 1 (Fragment).  
 GN Name=var;  
 OS Plasmodium falciparum.  
 CC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 CX NCBI\_TaxID=5833;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=21839615; PubMed=11849711; DOI=10.1016/S0166-6851(01)00443-1;  
 RA Fowler E.V., Peters J.M., Gatton M.L., Chen N., Cheng O.;  
 RT "Genetic diversity of the DBLalpha region in Plasmodium falciparum var  
 RT genes among Asia-Pacific isolates."  
 RL Mol. Biochem. Parasitol. 120:117-126(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Fowler E., Peters J., Gatton M., Chen N., Cheng O.;  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
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DR EMBL: AY054812; AAL11176.1; -; Genomic DNA.
DR EMBL: AY054843; AAL11207.1; -; Genomic DNA.
FT NON_TER 1 1
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 14141 MW; B4CSEA748DDABBE5 CRC64;

Query Match
Best Local Similarity 78.7%; Score 37; DB 2; Length 119;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDDK 8
Db 45 YKDEDDK 51

RESULT 66
ID Q6S8S9_PLAFA PRELIMINARY; PRT; 132 AA.
AC Q6S8S9;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DE Erythrocyte membrane protein 1 (Fragment).
GN Name=var;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15122533; DOI=10.1086/383250;
RA Kaestli M., Cortes A., Lagog M., Ott M., Beck H.-P.;
RT "Longitudinal Assessment of Plasmodium falciparum var Gene
RT Transcription in Naturally Infected Asymptomatic Children in Papua New
RT Guinea.";
RL J. Infect. Dis. 189:1942-1951(2004).
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CC -----
DR EMBL: AY462771; MAR32011.1; -; mRNA.
FT NON_TER 1 1
FT NON_TER 132 132
SQ SEQUENCE 132 AA; 15767 MW; E1320176782A6AFC CRC64;

Query Match
Best Local Similarity 78.7%; Score 37; DB 2; Length 132;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDDK 8
Db 50 YKDEDDK 56

RESULT 67
ID Q7RB94_PLAYO PRELIMINARY; PRT; 136 AA.
AC Q7RB94;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Hypothetical protein.
GN ORFNames=PY06254;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=17XN1;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlson J.M., Angiuoli S.V., Suh B.B., Kooji T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,

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RA Cho J.K., Quackenbush J., Sedegah M., Shoabli A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,
RA van Lin L.H., Jane C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL: AABL01002092; EAA18432.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 136 AA; 16664 MW; BDF23EE968AD6A27 CRC64;

Query Match
Best Local Similarity 78.7%; Score 37; DB 2; Length 136;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 107 EYDDDDK 114

RESULT 68
ID Q4Y0T6_PLACH PRELIMINARY; PRT; 142 AA.
AC Q4Y0T6;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein.
GN ORFNames=PC103434.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karras M., Raine J.D., Carlson J.M., Kooji T.W.A.,
RA Berrian M., Florens L., Janssen C.S., Pain A., Christopoulos G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Truman H.B., Mendoza U.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
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CC -----
DR EMBL: CAAJ01001887; CAH77226.1; -; Genomic DNA.
KW Hypothetical protein.
SQ SEQUENCE 142 AA; 16322 MW; SCC0816338829E24 CRC64;

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Query Match
Best Local Similarity 78.7%; Score 37; DB 2; Length 142;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 110 DYDDDDK 117

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RESULT 69
OSTKFL1 ORYSA PRELIMINARY; PRT; 164 AA.
ID 05TKFL1_ORYSA
AC 05TKFL1
DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 21-DEC-2004, sequence version 1.
DE 07-FEB-2006, entry version 7.
DE Hypothetical protein OSJNB0030114.15 (Hypothetical protein
OSJNB0086G17.6).
GN Name=OSJNB0030114.15; Synonyms=OSJNB0086G17.6;
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Euphorbiaceae; Oryzae; Oryza.
OX NCBI_TaxID=33947;
RN NUCLEOTIDE SEQUENCE.
RP Chow T.-Y., Haing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C.,
RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RT "Oryza sativa BAC OSJNB0030114 genomic sequence.";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE.
RA Chow T.-Y., Haing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Lee P.-F., Chang S.-J., Chen H.-C., Chen S.-K.,
RA Chen T.-R., Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y.,
RA Hsiao S.-H., Hsiung J.-N., Hsu C.-H., Hsu C.-T., Kau P.-I., Lee H.-F.,
RA Lee M.-C., Leu H.-L., Li Y.-F., Lin S.-J., Lin Y.-C., Lu P.-C.,
RA Wei F.-J., Wu C.-C., Wu S.-W., Yang K.-C., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RT "Oryza sativa BAC OSJNB0086G17 genomic sequence.";
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
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CC
DR EMBL; AC144455; AAW57795.1; -; Genomic_DNA.
DR EMBL; AC136217; AAV59389.1; -; Genomic_DNA.
DR Gramene; Q5TKFL1; -;
KM Hypothetical protein.
SQ SEQUENCE 164 AA; 1818 MW; DE35652258B747CB CRC64;

Query Match 78.7%; Score 37; DB 2; Length 164;
Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
DB 147 DYSDDD 153

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RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carnucci D.J., Yates J.R. III,
RA Kafatos F.C., Janse C.D., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86 (2005).
CC -!- CAUTION: The sequence shown here is derived from an
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CC
DR EMBL; CAJ01001307; CAH76237.1; -; Genomic_DNA.
DR EMBL; CAJ01001307; CAH76237.1; -; Genomic_DNA.
KM Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 168 AA; 20171 MW; AA47045FCABA9057 CRC64;

Query Match 78.7%; Score 37; DB 2; Length 168;
Best Local Similarity 75.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
DB 67 DYKDDDK 74

RESULT 71
02ZA91.9GAMM PRELIMINARY; PRT; 179 AA.
ID 02ZA91.9GAMM
AC 02ZA91.9GAMM
DT 20-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 20-DEC-2005, sequence version 1.
DE 07-FEB-2006, entry version 3.
DE Hypothetical protein.
GN ORFNames=Shewm4DRAFT_1640;
OS Shewanella sp. MR-4;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Shewanellaceae; Shewanella.
OX NCBI_TaxID=60480;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=MR-4;
RC US DOE Joint Genome Institute (JGI-ORNL);
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Shewanella sp. MR-4.";
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=MR-4;
RC US DOE Joint Genome Institute (JGI-ORNL);
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Shewanella sp. MR-4.";
RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
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CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
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CC
DR EMBL; AALX01000008; EAP46635.1; -; Genomic_DNA.
KM Hypothetical protein.
SQ SEQUENCE 179 AA; 20526 MW; BB4A1828BC1F0657 CRC64;

Query Match 78.7%; Score 37; DB 2; Length 179;
Best Local Similarity 85.7%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7

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Db 155 DYSDDDD 161

## RESULT 72

Q35Y65\_9GAMM PRELIMINARY; PRT; 179 AA.

ID Q35Y65\_9GAMM

AC Q35Y65\_9GAMM integrated into UniProtKB/TrEMBL.

DT 06-DEC-2005, sequence version 1.

DT 07-FEB-2006, entry version 3.

DE Hypothetical protein.

GN ORFNames=Shewm7DRAFT\_1872;

OS Shewanella sp. MR-7.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;

OC Shewanellaceae; Shewanella.

NCBI\_TaxID=60481;

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## RESULT 75

Q2M3Y9\_PHYIN PRELIMINARY; PRT; 197 AA.  
 AC Q2M3Y9\_21-FEB-2006, integrated into UniProtKB/TrEMBL.  
 DT 21-FEB-2006, sequence version 1.  
 DT 21-FEB-2006, entry version 1.  
 DE 205 proteasome subunit.  
 OS *Phytophthora infestans* (Potato late blight fungus).  
 OC Eukaryota; stramenopiles; Oomycetes; Peronosporales; Phytophthora.  
 NCBI\_TaxID=4787;  
 [1]  
 NP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=DDR7602;  
 RA Kamoun S., Kanneganti T.-D., Win J.;  
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
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 CC -----  
 DR EMBL; AY961472; AA143418.1; -; mRNA.  
 KW Proteasome.  
 SQ SEQUENCE 197 AA; 22308 MW; C067102DCFB8B1314 CRC64;

Query Match 78.7%; Score 37; DB 2; Length 197;  
 Best Local Similarity 85.7%; Pred. No. 4.2e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 YKDDDD 8  
 Db 28 YKDDDD 34

## RESULT 76

Q42415\_PLABE PRELIMINARY; PRT; 225 AA.  
 AC Q42415\_05-JUL-2005, integrated into UniProtKB/TrEMBL.  
 DT 05-JUL-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 4.  
 DE Hypothetical protein (Fragment).  
 GN ORFNames=PB000975.00.0;  
 OS *Plasmodium berhei*.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.  
 NCBI\_TaxID=5821;  
 [1]  
 NP NUCLEOTIDE SEQUENCE.  
 RX PubMed=15637271; DOI=10.1126/science.1103717;  
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,  
 RA Berrihan M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
 RA James K., Rutherford K., Harris B., Harris J., Trueman H.E., Mendoza J.,  
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,  
 RA Bidwell S.L., Rajadream M.A., Carucci D.J., Yates J.R. III,  
 RA Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,  
 RA Sinden R.S.;  
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
 RT transcriptomic, and proteomic analyses.";  
 RL Science 307:82-86(2005).  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
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 CC -----  
 DR EMBL; CAI01000723; CAH94968.1; -; Genomic\_DNA.  
 KM Hypothetical protein.  
 FT NON TER 1  
 SQ SEQUENCE 225 AA; 27208 MW; 0BEFF4D6B264244 CRC64;

Query Match 78.7%; Score 37; DB 2; Length 225;

Best Local Similarity 75.0%; Pred. No. 4.8e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 8  
 Db 123 DYKDDDD 130

## RESULT 77

Q5CPE3\_CRYPV PRELIMINARY; PRT; 259 AA.  
 AC Q5CPE3\_12-APR-2005, integrated into UniProtKB/TrEMBL.  
 DT 12-APR-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 4.  
 DE Hypothetical protein.  
 GN ORFNames=cgds\_4610;  
 OS *Cryptosporidium parvum*.  
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Bimeriida;  
 OC Cryptosporidiidae; Cryptosporidium.  
 NCBI\_TaxID=5807;  
 [1]  
 NP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Iowa type II;  
 RX PubMed=15044751; DOI=10.1126/science.1094786;  
 RA Abrahamson M.S., Templeton T.J., Enomoto S., Abrahante J.E., Zhu G.,  
 RA Lanco C.A., Deng M., Liu C., Widmer G., Tzipori S., Buck G.A., Xu P.,  
 RA Bankier A.T., Dear P.H., Kontorov B.A., Spriggs H.F., Iyer L.,  
 RA Anantharaman V., Aravind L., Kapur V.;  
 RT "Complete genome sequence of the apicomplexan, *Cryptosporidium*  
 RT *parvum*.";  
 RL Science 304:441-445(2004).  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.

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 CC -----  
 DR EMBL; AAE0100017; EAK87298.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 259 AA; 29923 MW; E37F2455F468CB3B CRC64;

Query Match 78.7%; Score 37; DB 2; Length 259;  
 Best Local Similarity 85.7%; Pred. No. 5.6e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
 Db 175 DYKDDDD 181

## RESULT 78

Q74H22\_LACJO PRELIMINARY; PRT; 268 AA.  
 AC Q74H22\_05-JUL-2004, integrated into UniProtKB/TrEMBL.  
 DT 05-JUL-2004, sequence version 1.  
 DT 07-MAR-2006, entry version 17.  
 DE Hypothetical protein.  
 GN OrderedLocuNames=LJ0673; ORFNames=LJ\_0673;  
 OS *Lactobacillus johnsonii*.  
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;  
 OC Lactobacillus.  
 NCBI\_TaxID=33959;  
 [1]  
 NP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=NCC 533;  
 RX PubMed=14983040; DOI=10.1073/pnas.0307327011;  
 RA Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C.,  
 RA Pitet A.-C., Zwielen M.-C., Rouvet M., Altermann E., Barrangou R.,  
 RA Mollet B., Mercenier A., Kleenhamer T., Arigoni F., Schell M.A.;

RT "The genome sequence of the probiotic intestinal bacterium

RT Lactobacillus johnsonii NCC 533. ";  
 RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).  
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 CC -----  
 DR EMBL: AE017198; AA059548.1; -; Genomic\_DNA.  
 CC GenomeReviews: AE017198 GR; J0673.  
 DR BioCyc: LJOH257314:LJO673-MONOMER; -;  
 DR GO: GO:0003824; F: catalytic activity; IEA.  
 DR InterPro: IPR013094; AB\_Hydrolase\_3.  
 DR InterPro: IPR000379; Ser\_estrs.  
 DR Pfam: PF07859; Abhydrolase\_3; 1.  
 KM Complete proteome: Hypoethetical protein.  
 SQ SEQUENCE 268 AA; 30797 MW; 5319ABECCB19A9F CRC64;  
 QY  
 Db 1 DYKDDDD 8  
 94 DYKDDDD 101  
 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Query Match 78.7%; Score 37; DB 2; Length 268;  
 Best Local Similarity 75.0%; Pred. No. 5.8e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 RESULT 79  
 054U43 D1CD1  
 ID 054U43\_D1CD1 PRELIMINARY; PRT; 299 AA.  
 AC 054U43;  
 DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.  
 DT 24-MAY-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 3.  
 DE Hypoethetical protein.  
 GN ORFNames=DD80204132;  
 OS Dictyostelium discoideum (Slime mold).  
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.  
 NCBI\_TaxID=44689;  
 [1]  
 NP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=AX4;  
 RX PubMed=15875012; DOI=10.1038/nature03481;  
 RA Eichinger L., Pachbat J.A., Gloeckner G., Rajandream M.A.,  
 RA Sungang R., Berriman M., Song J., Olsen R., Safranek K., Xu Q.,  
 RA Tungal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,  
 RA Banker A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,  
 RA Pilcher K., Chen G., Saunders D., Sodergren E.J., Davis P.,  
 RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,  
 RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.M.,  
 RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,  
 RA Muzny D.M., Moutier T., Pain A., Lu M., Harper D., Lindsay R.,  
 RA Hauser H., James K.D., Quiles M., Madan Babu M., Saito T.,  
 RA Buchteser C., Wardrop A., Felder M., Thangavelu M., Johnson D.,  
 RA Knights A., Louisedge H., Mungall K.L., Oliver K., Price C.,  
 RA Quail M.A., Urushihara H., Hernandez J., Rabinowitsch E., Steffen D.,  
 RA Sanders M., Ma J., Kohara Y., Sharp S., Simmonds M.N., Spiegler S.,  
 RA Tivey A., Sigano S., White B., Walker D., Woodward J.R., Winckler T.,  
 RA Tanaka Y., Shatsky G., Gishler M., Weinstein G.M., Rosenthal A.,  
 RA Cox E.C., Chisholm R.L., Gibbs R.A., Loomis W.F., Platzner M.,  
 RA Kay R.R., Williams J.G., Dear P.H., Noegel A.A., Barrell B.G.,  
 RA Kuspa A.;  
 RT "The genome of the social amoeba Dictyostelium discoideum";  
 RL Nature 435:43-57(2005).  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
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 CC -----  
 DR EMBL: AAF101000072; EAL66940.1; -; Genomic\_DNA.  
 KM Hypoethetical protein.  
 SQ SEQUENCE 299 AA; 34386 MW; BEAD000562DC563B CRC64;

Query Match 78.7%; Score 37; DB 2; Length 299;  
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 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DYKDDDD 7  
 252 DYKDDDD 258  
 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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 Best Local Similarity 85.7%; Pred. No. 7.4e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 RESULT 80  
 038D74 9TRYP  
 ID 038D74\_9TRYP PRELIMINARY; PRT; 335 AA.  
 AC 038D74;  
 DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.  
 DT 22-NOV-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 3.  
 DE Hypoethetical protein.  
 GN ORFNames=TB09.211.2220;  
 OS Trypanosoma brucei.  
 OC Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
 NCBI\_TaxID=5691;  
 [1]  
 NP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=927/4 GUTa10.1;  
 RX PubMed=16020724; DOI=10.1126/science.1112812;  
 RA El-Sayed N.M.A., Myler P.J., Blandin G., Berriman M., Crabtree J.,  
 RA Aggarwal G., Caler E., Renaud H., Worthey E.A., Hertz-Fowler C.,  
 RA Chedin E., Peacock C., Bartholomew D.C., Haas B.J., Trn A.-N.,  
 RA Wortman J.R., Alsmark U.C.M., Angiuoli S., Anupama A., Badger J.,  
 RA Bringaud F., Cadag E., Carlton J.M., Cerqueira G.C., Creasy T.,  
 RA Delcher A.L., Djikeng A., Embley T.M., Hauser C., Ivans K.,  
 RA Kummerfeld S.K., Pereira-Leal J.B., Nilsson D., Peterson J.,  
 RA Salzberg S.L., Shallow J., Silva J.C., Sundaram J., Westerberger S.,  
 RA White O., Melville S.E., Donelson J.E., Andersson B., Stuart K.D.,  
 RA Hall N.;  
 RT "Comparative genomics of trypanosomatid parasitic protozoa";  
 RL Science 309:404-409(2005).  
 [2]  
 NP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=927/4 GUTa10.1;  
 RX PubMed=16020726; DOI=10.1126/science.1112642;  
 RA Berriman M., Ghedin E., Hertz-Fowler C., Blandin G., Renaud H.,  
 RA Bartholomew D.C., Lennard N.J., Caler E., Hamlin N.B., Haas B.,  
 RA Bohme U., Hancock L., Aslett M.A., Shallow J., Marcello L., Hou L.,  
 RA Wickstead F., Alsmark U.C.M., Arrowsmith C., Atkin R.J., Barron A.J.,  
 RA Bringaud F., Brooks K., Carrington M., Cherevach I.,  
 RA Chillingworth T.-J., Churcher C., Clark I.N., Corton C.H., Cronin A.,  
 RA Davies R.M., Doggett J., Djikeng A., Feldlyum T., Field M.C.,  
 RA Fraser A., Goodhead I., Hance Z., Harper D., Harris B.R., Hauser H.,  
 RA Hostetler J., Ivans A., Jagels K., Johnson D., Johnson J., Jones K.,  
 RA Kerhornou A.X., Koo H., Larke N., Landfear S., Larkin C., Leech V.,  
 RA Line A., Lord A., Macleod A., Mooney P.J., Moule S., Martin D.M.A.,  
 RA Morgan G.W., Mungall K., Norbertczak H., Ormond D., Pai G.,  
 RA Peacock C.S., Peterson J., Quail M.A., Rabinowitsch E.,  
 RA Rajandream M.-A., Reltter C., Salzberg S.L., Sanders M., Schobel S.,  
 RA Sharp S., Simmonds M., Simpson A.J., Tallon L., Turner C.M.R.,  
 RA Tait A., Tivey A.R., Van Aken S., Walker D., Wanless D., Wang S.,  
 RA White B., White O., Whithead S., Woodward J., Wortman J., Adams M.D.,  
 RA Embley T.M., Gull K., Ullu E., Barry J.D., Fairlamb A.H.,  
 RA Operdoes F., Barrell B.G., Donelson J.E., Hall N., Frazer C.M.,  
 RA Melville S.E., El-Sayed N.M.;  
 RT "The genome of the African trypanosome Trypanosoma brucei";  
 RL Science 309:416-422(2005).  
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 CC -----  
 DR EMBL: CM000207; EANT7036.1; -; Genomic\_DNA.  
 KM Hypoethetical protein.  
 SQ SEQUENCE 335 AA; 38122 MW; AB5C219A51BA4B0 CRC64;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
 |||||  
 Db 13 DYKDDND 19

RESULT 81  
 Q6C9S5\_YARLI PRELIMINARY; PRT; 341 AA.  
 ID Q6C9S5\_YARLI  
 AC Q6C9S5  
 DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.  
 DT 16-AUG-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 12.  
 DE Yarrowia lipolytica chromosome D of strain CLIB122 of Yarrowia  
 DE lipolytica.  
 GN OrderedLocNames=YALI0D08734g;  
 OS Yarrowia lipolytica (Candida lipolytica).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Dipodascaceae; Yarrowia.  
 OX NCBI\_TaxID=4952;  
 RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=CLIB 122 / B 150;  
 RX PubMed=15229592; DOI=10.1038/nature02579;  
 RA Lafontaine I., de Montigny J., Marck C., Neugebauer C., Talla E.,  
 RA Goffard N., Frangoul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
 RA Barny S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,  
 RA Boistrame A., Boyer J., Cattoi L., Confiantoli F., de Daruvar A.,  
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Gropi A.,  
 RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
 RA Nicard J.-M., Nikoleki M., Ortiz S., Ozier-Kalogeropoulos O.,  
 RA Pelienz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,  
 RA Swennen D., Tekala P., Wesolowski-Louvel M., Westhof E., Wirth B.,  
 RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,  
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,  
 RA Wincker P., Souciet J.-L.;  
 RT "Genome evolution in Yeasts."  
 RL Nature 430:35-44(2004).

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DR EMBL: CR382130; CAG80775.1; -; Genomic\_DNA.  
 DR InterPro: IPR013256; Chromatin\_SPT2.  
 KW Complete proteome.  
 SQ SEQUENCE 341 AA; 38489 MW; C7ACBF8F8C3AD0 CRC64;

Query Match 78.7%; Score 37; DB 2; Length 341;  
 Best Local Similarity 85.7%; Pred. No. 7.5e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
 |||||  
 Db 291 DYSDDD 297

RESULT 82  
 BROM1\_ANACO STANDARD; PRT; 351 AA.  
 ID BROM1\_ANACO  
 AC 023791;  
 DT 24-JAN-2006, integrated into UniProtKB/Swiss-Prot.  
 DT 01-JAN-1998, sequence version 1.  
 DT 07-MAR-2006, entry version 30.  
 DE Ananas comosus (Pineapple).  
 OS Ananas comosus (Pineapple).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Bromeliaceae;  
 OC Ananas.  
 OX NCBI\_TaxID=4615;  
 RN [1]

RP NUCLEOTIDE SEQUENCE [mRNA].  
 RC STRAIN=cv. N67-10; TISSUE=fruit;  
 RA Mura E., Aramaki H., Taketa Y., Kono A., Okamoto Y., Ota S.;  
 RT "Cloning and sequencing of fruit bromelain."  
 RL Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.  
 CC -1 CATALYTIC ACTIVITY: Broad specificity for cleavage of proteins,  
 CC but strong preference for Z-Arg-Arg-|-NHMe among small molecule  
 CC substrates.  
 CC -1 ALLERGEN: Causes an allergic reaction in human.  
 CC -1 SIMILARITY: Belongs to the peptidase C1 family.  
 CC  
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DR EMBL: D14059; BAA21849.1; -; mRNA.  
 DR PIR: T10503; T10503.  
 DR HSSP: P07711; ICYL.  
 DR MEROPS: C01.028; -;  
 DR InterPro: IPR000169; Pept. cys. AS.  
 DR InterPro: IPR013128; Peptidase\_C1A.  
 DR InterPro: IPR000668; Peptidase\_C1A.C.  
 DR InterPro: IPR013201; Propeptide\_129.  
 DR PANTHER: PTHR12411; Peptidase\_C1; 1.  
 DR Pfam: PF08246; Inhibitor\_129; 1.  
 DR Pfam: PF00112; Peptidase\_C1; 1.  
 DR PRINTS: PR00705; PAPAIN.  
 DR PRODOM: PD000158; Peptidase\_C1; 1.  
 DR SMART: SM00645; Pept\_C1; 1.  
 DR PROSITE: PS00640; THIOL\_PROTEASE ASN; 1.  
 DR PROSITE: PS00139; THIOL\_PROTEASE CYS; 1.  
 DR PROSITE: PS00639; THIOL\_PROTEASE HIS; 1.  
 KW Allergen; Hydrolase; Protease; Signal; Thiol protease; Zymogen.  
 FT SIGNAL 1 24 Potential.  
 FT PROPEP 25 121 /Ftrd=PRO\_0000045809.  
 FT CHAIN 122 351 Bromelain.  
 FT FT ACT\_SITE 147 147 By similarity.  
 FT FT ACT\_SITE 279 279 By similarity.  
 FT FT DISULFID 144 184 By similarity.  
 FT FT DISULFID 178 217 By similarity.  
 FT FT DISULFID 273 325 By similarity.  
 SQ SEQUENCE 351 AA; 39055 MW; 33781C55144242B0 CRC64;

Query Match 78.7%; Score 37; DB 1; Length 351;  
 Best Local Similarity 85.7%; Pred. No. 7.8e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDK 8  
 |||||  
 Db 48 YKDDDK 54

RESULT 83  
 BMT ANTMA STANDARD; PRT; 364 AA.  
 ID BMT ANTMA  
 AC 09FY29;  
 DT 16-AUG-2005, integrated into UniProtKB/Swiss-Prot.  
 DT 01-MAR-2001, sequence version 1.  
 DT 07-FEB-2006, entry version 15.  
 DE Benzoyl carboxyl methyltransferase (EC 2.1.1.-) (S-adenosyl-L-  
 DE methionine:benzoic acid carboxyl methyltransferase).  
 GN Name=BMT;  
 OS Antirrhinum majus (Garden snapdragon).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 OC asterids; lamiales; Plantaginaceae; Antirrhineae;  
 OC Antirrhinum.  
 OX NCBI\_TaxID=4151;  
 RN [1]

RP NUCLEOTIDE SEQUENCE [mRNA], PARTIAL PROTEIN SEQUENCE, DEVELOPMENTAL  
 RP STAGE, AND TISSUE SPECIFICITY.  
 RX MEDLINE=20312758; PubMed=10852939; DOI=10.1105/epc.12.6.949;

RA Dudareva N., Murfitt L.M., Mann C.J., Gorenstein N., Kolosova N.,  
 RA Kish C.M., Bonham C., Wood K.;  
 RT "Developmental regulation of methyl benzoate biosynthesis and emission  
 in snapdragon flowers.";  
 RL Plant Cell 12:949-961(2000).  
 CC -1- FUNCTION: Converts benzoic acid into the volatile ester methyl  
 benzoates. This scent, mostly produced in a rhythical, diurnal  
 manner, attracts the pollinators.  
 CC -1- TISSUE SPECIFICITY: Expressed only in the upper and lower petal  
 lobes. Not found in the corolla tubes, anthers, pistils, sepals  
 and ovaries.  
 CC -1- DEVELOPMENTAL STAGE: Expressed in mature flowers with a peak 6 to  
 7 days postanthesis.  
 CC -1- PTM: The N-terminus is blocked.  
 CC -1- SIMILARITY: Belongs to the methyltransferase superfamily.  
 CC -----  
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 CC -----  
 DR EMBL: AF198492; AAF98284.1; -; mRNA.  
 DR HSSP: Q9SPV4; 1M6E.  
 DR InterPro: IPR005299; Methyltransf\_6.  
 DR Pfam: PF03492; Methyltransf\_7; 1.  
 DR Direct protein sequencing; Methyltransferase; Transferase.  
 FT CHAIN 1 364  
 FT /FTId=PRO\_0000204466.  
 FT COMPBIAS 292 295 POLY-ASP  
 FT SEQUENCE 364 AA; 41011 MW; C10C8E864581419 CRC64;  
 SQ  
 Query Match 78.7%; Score 37; DB 1; Length 364;  
 Best Local Similarity 75.0%; Pred. No. 8.1e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DYKDDDK 8  
 DB 289 DYTDDDDQ 296  
 RESULT 84  
 ID 053LKL1 ORYSA PRELIMINARY; PRT; 451 AA.  
 AC 053LKL1;  
 DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.  
 DT 24-MAY-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 3.  
 DE P-box domain, putative.  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;  
 OC Eriharoidae; Oryzoae; Oryza.  
 OX NCBI\_TaxID=39947;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Buell C., Yuan Q., Ouyang S., Liu J., Wang A., Maici R., Lin H.,  
 RA Zhu W., Hamilton J., Jones K., Tallon L., Feldblum T., Tsiltris T.,  
 RA Bera J., Kim M., Jin S., Padrosh D., Vuong H., Overton II L.,  
 RA Reardon M., Weaver B., Johri S., Lewis M., Uteback T., Van Aken S.,  
 RA Norton J., Haas B., Koo H., Ziemann V., Hsiao J., Jobst S.,  
 RA de Vazelles A., White O., Salzberg S., Fraser C.;  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Buell R.;  
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
 CC -----  
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 CC -----  
 DR EMBL: AC145321; AA95043.1; -; Genomic\_DNA.  
 DR InterPro: IPR001810; F-box.  
 DR Pfam: PF00646; F-box; 1.  
 DR SMART: SM00256; FBOX; 1.  
 DR PROSITE: PSS0181; FBOX; 1.

SQ SEQUENCE 451 AA; 51414 MW; 53B24E4CE7C6771E CRC64;  
 Query Match 78.7%; Score 37; DB 2; Length 451;  
 Best Local Similarity 85.7%; Pred. No. 1e+03;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 YKDDDDK 8  
 DB 414 YEDDDDK 420  
 RESULT 85  
 ID TIG\_RHOA STANDARD; PRT; 452 AA.  
 AC 06N5L2;  
 DT 07-JUN-2005, integrated into UniProtKB/Swiss-Prot.  
 DT 05-JUL-2004, sequence version 1.  
 DT 07-MAR-2006, entry version 10.  
 DE Trigger factor (TF).  
 GN Name=tig; OrderedLocNames=RPA2962;  
 OS Rhodospseudomonas palustris.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Bradyrhizobiaceae; Rhodospseudomonas.  
 OX NCBI\_TaxID=1076;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RP STRAIN=CGA009 / ATCC BAA-98;  
 RX PubMed=14704707; DOI=10.1038/nbt923;  
 RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,  
 RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,  
 RA Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C.,  
 RA Harrison F.H., Gibson J., Harwood C.S.;  
 RT "Complete genome sequence of the metabolically versatile  
 photosynthetic bacterium Rhodospseudomonas palustris.";  
 Nat. Biotechnol. 22:55-61(2004).  
 RL Nat. Biotechnol. 22:55-61(2004).  
 CC -1- FUNCTION: Involved in protein export. Acts as a chaperone by  
 maintaining the newly synthesized protein in an open conformation  
 (By similarity).  
 CC -1- SIMILARITY: Belongs to the FKBP-type PPIase family. Tig subfamily.  
 CC -1- SIMILARITY: Contains 1 PPIase FKBP-type domain.  
 CC -----  
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 CC -----  
 DR EMBL: BX572602; CAE28403.1; -; Genomic\_DNA.  
 DR GenomeReviews: BX571963 GR; RPA2962.  
 DR BioCyc: RPA2585594.RPA2562-MONOMER; -.  
 DR HAMAP: MF\_00303; -; 1.  
 DR InterPro: IPR001179; FKBP\_PPIase.  
 DR InterPro: IPR005215; Trig\_fac.  
 DR InterPro: IPR008880; Trigger\_C.  
 DR InterPro: IPR008881; Trigger\_N.  
 DR Pfam: PF00254; FKBP\_C; 1.  
 DR Pfam: PF05698; Trigger\_C; 1.  
 DR Pfam: PF05697; Trigger\_N; 1.  
 DR PIRSF: PIRSF03095; Trigger\_factor; 1.  
 DR TRIGFAMS: TIGR00115; tig; 1.  
 DR PROSITE: PSS0059; FKBP\_PPIase; 1.  
 KW Cell cycle; Cell division; Chaperone; Complete proteome; Isomerase;  
 KM Rotamase.  
 FT CHAIN 1 452  
 FT /FTId=PRO\_0000179415.  
 FT DOMAIN 171 256 PPIase FKBP-type.  
 FT SEQUENCE 452 AA; 50097 MW; 9DCE13323A8B5800 CRC64;  
 SQ  
 Query Match 78.7%; Score 37; DB 1; Length 452;  
 Best Local Similarity 85.7%; Pred. No. 1e+03;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 YKDDDDK 8  
 DB 443 YKDDDDK 449



RESULT 86  
Q2R949\_ORYSA PRELIMINARY; PRT; 485 AA.  
ID Q2R949\_ORYSA  
AC Q2R949\_ORYSA  
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.  
DT 24-JAN-2006, sequence version 1.  
DT 07-FEB-2006, entry version 2.  
DE F-box domain, putative.  
GN ORFNames=LOC\_Os11G09970;  
OS Oryza sativa (Japanese cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BDP clade;  
OC Euphorbiaceae; Oryzae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Buell C.R., Wang R.A., McCombie W.A., Ouyang S.;  
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
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DR EMBL; DP000010; ABA91987.1; -; Genomic DNA.  
SQ SEQUENCE 485 AA; 55570 MW; F55EC789BB4635F4 CRC64;  
Query Match 78.7%; Score 37; DB 2; Length 485;  
Best Local Similarity 85.7%; Pred. No. 1.1e+03;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 YKDDDDK 8  
Db 448 YEDDDK 454  
RESULT 87  
Q6BV75\_DEBHA PRELIMINARY; PRT; 487 AA.  
ID Q6BV75\_DEBHA  
AC Q6BV75;  
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.  
DT 16-AUG-2004, sequence version 1.  
DT 07-FEB-2006, entry version 10.  
DE Similarities with CA06121|IP17545 Candida albicans.  
GN OrderedLocNames=DEHAOC054789;  
OS Debaryomyces hansenii (Yeast) (Torulaspora hansenii).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Debaryomyces.  
OX NCBI\_TaxID=4959;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=ATCC 36239 / CBS 767;  
RX PubMed=15229592; DOI=10.1038/nature02579;  
RA Dujon B., Sherman D., Fischer G., Durrens P., Caaregola S.,  
RA Lalontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,  
RA Goffard N., Frangeul J., Aigle M., Anthouard V., Babour A., Barbe V.,  
RA Barney S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,  
RA Boixame A., Boyer J., Cartolico L., Confantieri F., de Daruvar A.,  
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,  
RA Hantreya F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,  
RA Pellenz S., Porter S., Richard G.-F., Straub M.-L., Suleau A.,  
RA Swennen D., Tekala F., Wesolowski-Louvel M., Weshof E., Wirth B.,  
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,  
RA Winkler F., Soulet J.-L.;  
RT Genome evolution in yeasts.";  
RL Nature 430:35-44(2004).  
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DR EMBL; CR382135; CAG85944.1; -; Genomic DNA.

KW Complete proteome.  
SQ SEQUENCE 487 AA; 55772 MW; 1DBDC3E39E4959E3 CRC64;  
Query Match 78.7%; Score 37; DB 2; Length 487;  
Best Local Similarity 85.7%; Pred. No. 1.1e+03;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 DYKDDDD 7  
Db 404 DYSDDDD 410  
RESULT 88  
O56XW8\_ARATH PRELIMINARY; PRT; 487 AA.  
ID O56XW8\_ARATH  
AC O56XW8;  
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.  
DT 10-MAY-2005, sequence version 1.  
DT 07-FEB-2006, entry version 3.  
DE Hypothetical protein At1g48400.  
GN Name=At1g48400;  
OS Arabidopsis thaliana (mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Totoki Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A.,  
RA Narusaka Y., Shin-I T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y.,  
RA Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K.,  
RA Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J.,  
RA Hayashizaki Y., Shinozaki K.;  
RT Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs.";  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
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DR EMBL; AK21555; BAD94953.1; -; mRNA.  
DR InterPro; IPR001810; F-box.  
DR InterPro; IPR006566; FBD.  
DR InterPro; IPR013101; LTR 2.  
DR InterPro; IPR010916; TONB\_Box\_N.  
DR Pfam; PF00646; F-box; 1.  
DR SMART; SM00579; FBD; 1.  
DR SMART; SM00256; FBOX; 1.  
DR PROSITE; PS0181; FBOX; 1.  
DR PROSITE; PS00430; TONB\_DEPENDENT\_REC\_1; UNKNOWN\_1.  
DR PROSITE; PS00430; TONB\_DEPENDENT\_REC\_1; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 487 AA; 55627 MW; 910F4B97D525B818 CRC64;  
Query Match 78.7%; Score 37; DB 2; Length 487;  
Best Local Similarity 85.7%; Pred. No. 1.1e+03;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 DYKDDDD 7  
Db 282 DYSDDDD 288  
RESULT 89  
VE2\_HP20 STANDARD; PRT; 497 AA.  
ID VE2\_HP20  
AC PS0766;  
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.  
DT 01-OCT-1996, sequence version 1.  
DT 07-FEB-2006, entry version 23.  
DE Regulatory protein E2.  
GN Name=E2;  
OS Human papillomavirus type 20.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Betapapillomavirus.

```

OX NCBI_TaxID=31547;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Delius H.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
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CC -----
CC
CC EMBL; U31778; AAA79390.1; -; Genomic_DNA.
CC DR HSSP; P03122; 2BOP.
CC DR InterPro; IPR012677; a_b_pla1c_nuc_bd.
CC DR InterPro; IPR000427; E2_C.
CC DR InterPro; IPR001866; E2_N.
CC DR Pfam; PF00511; PPV_E2_C_1.
CC DR Pfam; PF00508; PPV_E2_N_1.
CC DR ProDom; PD000672; E2_C; 1.
CC DR ProDom; PD000678; E2_N; 1.
CC FT CHAIN 1 497
CC          Regulatory protein E2.
CC          /FTID=PRO_0000133199.
SQ SEQUENCE 497 AA; 56120 MW; 497CA220B3537C85 CRC64;

Query Match      78.7%; Score 37; DB 1; Length 497;
Best Local Similarity 85.7%; Pred. No. 1.le+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 2 YKDDDDK 8
Db 139 YQDDDK 145

RESULT 90
QSXSX72_ARATH PRELIMINARY; PRT; 513 AA.
AC QSXS72;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE F1A17.5 protein.
GN F1A17.5; OrderedLocustNames=At1g48400;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
[1]
RP NUCLEOTIDE SEQUENCE.
RA Vysotskita V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
RA Lee J.M., Li J., Li J., Gonzalez A., Liu A., Liu K., Vaysberg M.,
RA Sakano H., Chin C., Choi E., Chiou J., Altatfi H., Araujo R.,
RA Brooks S., Buehler E., Chao Q., Conn L., Conway A.B., Dunn P.,
RA Hansen N., Hong B., Huizar L., Khan S., Kim C., Palm C., Rowley D.,
RA Shinn P., Walker M., Davis R.W., Ecker J.R., Federspiel N.A.,
RA Theologis A.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
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CC -----
CC
CC EMBL; AC007932; AAD49757.1; -; Genomic_DNA.
CC DR PIR; B96524; B96524.
CC DR TAIR; At1g48400; -.
CC DR InterPro; IPR001810; F-box.
CC DR InterPro; IPR006566; FBD.
CC DR InterPro; IPR013101; LRR_2.
CC DR InterPro; IPR010916; TONB_Box_N.
CC DR Pfam; PF00646; F-box_1.
CC DR SMART; SM00579; FBD; 1.
CC DR SMART; SM00256; FBOX; 1.
CC DR PROSITE; PS00181; FBOX; 1.
CC DR PROSITE; PS00430; TONB_INDEPENDENT_REC_1; UNKNOWN 1.
SQ SEQUENCE 513 AA; 58618 MW; 81A562DBB3DDA0F8 CRC64;

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Query Match	78.7%	Score 37	DB 2	Length 513
Best Local Similarity	85.7%	Pred. No. 1,2e+03		
Matches	6	Conservative	0	Mismatches 1
				Indels 0
				Gaps 0

QY	1 DYKDDDD 7
Db	282 DYSDDD 288

RESULT 91
059MN9 CANAL
AC 059MN9 CANAL PRELIMINARY; PRT; 524 AA.
AC 059MN9
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
DT 26-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Hypothetical protein SRB8 (Fragment).
GN Name=SRB8; ORFNames=CaO19.736, CaO19.8355;
CS Candida albicans SC5314.
CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=237561;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SC5314;
RC PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federicipliel N.A., Chibana H., Dungan J., Kalman S., P.T.,
RA Magee B.B., Newport G., Thorensen Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of Candida albicans.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
CC -!- CAUTION: The sequence shown here is derived from an
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CC -----
CC EMBL; AACQ0100222; EAK91730.1; -; Genomic DNA.
DR EMBL; AACQ0100221; EAK91744.1; -; Genomic DNA.
KW Hypothetical protein.
DR NON TER 524
FT SEQUENCE 524 AA; 60272 MW; 2B051E0F462E7283 CRC64;
SO

Query Match	78.7%	Score 37	DB 2	Length 524
Best Local Similarity	85.7%	Pred. No. 1,2e+03		
Matches	6	Conservative	0	Mismatches 1
				Indels 0
				Gaps 0

QY	1 DYKDDDD 7
Db	392 DYNDDD 398

RESULT 92
08IEG8 PLAF7
AC 08IEG8; PRELIMINARY; PRT; 554 AA.
AC 08IEG8
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Hypothetical protein MAL13P1.75.
GN Name=MAL13P1.75;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=3D7;
RA Harris B., Lennard N., Clark L., Line A., Barron A., Corton C.,
RA Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J.,
RA Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.,
RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -----

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 CC -----  
 DR EMBL: AL844509; CAD52291.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 554 AA; 65670 MW; 332A13B5174CDA85 CRC64;  
 Query Match 78.7%; Score 37; DB 2; Length 554;  
 Best Local Similarity 75.0%; Pred. No. 1.3e+03;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYKDDDDK 8  
 DB 344 DYKDDDDK 351  
 RESULT 93  
 ID Q5JL08 ORYSA PRELIMINARY; PRT; 567 AA.  
 AC Q5JL08;  
 DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.  
 DT 07-FEB-2006, sequence version 1.  
 DE HSV-1 stimulating-related protein-like (HSV-1 stimulation-related 1-like).  
 GN Name=P0459B04.31; Synonyms=P0020E09.1;  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;  
 OC Eriatodeae; Oryzaceae; Oryza.  
 OX NCBI\_TaxID=39947;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA MEDLINE=22337376; PubMed=12447438; DOI=10.1038/nature01184;  
 RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,  
 RA Wu J., Nishimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,  
 RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,  
 RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,  
 RA Hijienita S., Honda M., Ichikawa Y., Ikonuma A., Iijima M., Ikeda M.,  
 RA Ikono M., Ito S., Ito Y., Ito Y., Iwabuchi A., Kamiya K.,  
 RA Karsawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,  
 RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,  
 RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,  
 RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,  
 RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terada K., Tsuji K.,  
 RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,  
 RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.-I., Eun M.-Y.,  
 RA Yano M., Jiang J., Gotohori T.;  
 RT "The genome sequence and structure of rice chromosome 1.";  
 RL Nature 420:312-316(2002).  
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 CC -----  
 DR EMBL: AP003627; BAD87849.1; -; Genomic\_DNA.  
 DR EMBL: AP003228; BAD87032.1; -; Genomic\_DNA.  
 DR GO: GO:0006810; P:transp. IEA.  
 DR InterPro: IPR000005; HTHARC.  
 DR InterPro: IPR004353; Yeast73DUF.  
 DR PANTHER: PTHR13027; Yeast73DUF; 1.  
 DR Pfam: PF03164; DUF254; 1.  
 DR PRINTS: PR01546; YEAST73DUF.  
 DR PROSITE: PS00041; HTH\_ARC\_FAMILY\_1; UNKNOWN\_1.  
 SQ SEQUENCE 567 AA; 63751 MW; 1AB0B30FE1BE148B CRC64;  
 Query Match 78.7%; Score 37; DB 2; Length 567;  
 Best Local Similarity 75.0%; Pred. No. 1.3e+03;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DYKDDDDK 8  
 DB 44 DYKDDDDK 51

RESULT 94  
 ID Q610D3 CAEBR PRELIMINARY; PRT; 664 AA.  
 AC Q610D3;  
 DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.  
 DT 23-NOV-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 11.  
 DE Hypothetical protein CBG07065 (Fragment).  
 GN Name=CBG07065;  
 OS Caenorhabditis briggsae.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6238;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=AF16;  
 RX PubMed=14624247; DOI=10.1371/journal.pbio.0000045;  
 RA Stein L.D., Bao Z., Blasler D., Blumenthal T., Brent M.R., Chen N.,  
 RA Chinwalla A., Clarke L., Clee C., Coghlan A., Coulson A.,  
 RA D'Eustachio P., Fitch D.H.A., Fulton L.A., Fulton R.E.,  
 RA Griffiths-Jones S., Harris T.W., Hillier L.W., Kamath R.,  
 RA Kuwabara P.E., Mardis E.R., Marra M.A., Miner T.L., Mink P.,  
 RA Mullikin J.C., Plumb R.W., Rogers J., Schein J.E., Schumann M.,  
 RA Spieth J., Stajich J.E., Wei C., Willey D., Wilson R.K., Durbin R.,  
 RA Waterston R.H.;  
 RT "The genome sequence of *Caenorhabditis briggsae*: a platform for  
 RT comparative genomics.";  
 RL PLOS Biol. 1:166-192(2003).  
 CC PLOS CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
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 CC -----  
 DR EMBL: CAAC0100031; CA62879.1; -; Genomic\_DNA.  
 DR InterPro: IPR001678; Fmu\_NOL1/Nop2p.  
 DR InterPro: IPR011023; Nop2p.  
 DR InterPro: IPR006174; rRNAsub\_mtfase.  
 DR Pfam: PF01189; NOL1\_Nop2\_Fmu; 1.  
 DR ProDom: PD005242; N5B\_region; 1.  
 DR TIGRFAMs: TIGR00646; nop2p; 1.  
 DR PROSITE: PS01153; NOL1\_Nop2\_SUN; 1.  
 KW Complete proteome; Hypothetical protein.  
 FT NON TER 664  
 SQ SEQUENCE 664 AA; 73746 MW; 67D8CA766879BD3 CRC64;  
 Query Match 78.7%; Score 37; DB 2; Length 664;  
 Best Local Similarity 85.7%; Pred. No. 1.5e+03;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DYKDDDD 7  
 DB 94 DYKDDDD 100  
 RESULT 95  
 ID Q5AAB5 CANAL PRELIMINARY; PRT; 690 AA.  
 AC Q5AAB5;  
 DT 26-APR-2005, integrated into UniProtKB/TrEMBL.  
 DT 26-APR-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 5.  
 DE Hypothetical protein.  
 GN ORNames=Ca019.9993;  
 OS Candida albicans SC5314.  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
 OX NCBI\_TaxID=237561;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=SC5314;

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RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Pederspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S., Thorstenson Y.R., Agabian N., Magee P.T.,
RT "The diploid genome sequence of Candida albicans."
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
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CC -----
DR EMBL; AAC001000040; EAK99642.1; -; Genomic_DNA.
DR InterPro; IPR013154; ADH_N.
KM Hypothetical protein.
SQ SEQUENCE 690 AA; 79582 MW; 6B4989CDDCB7FA0C CRC64;

Query Match 78.7%; Score 37; DB 2; Length 690;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
Db 615 DYKDDND 621

RESULT 96
Q6VZ25_CNPV PRELIMINARY; PRT; 690 AA.
AC Q6VZ25;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DE 07-FEB-2006, entry version 10.
DE CNP322 ankryrin repeat protein.
GN Name=CNP322;
OS Canariyox virus (CNPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Avipoxvirus.
OC NCBI_TaxID=4088;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC VR-111;
RX PubMed=14671117; DOI=10.1128/JVI.78.1.353-366.2004;
RA Tullman E.R., Aconso C.L., Lu Z., Zaak L., Kutish G.F., Rock D.L.;
RT "The genome of canariyox virus."
RL J. Virol. 78:353-366(2004).
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CC -----
DR EMBL; A1318871; AAR83668.1; -; Genomic_DNA.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ANK_6.
DR PRINTS; PRO1415; ANKYRIN.
DR SMART; SM00248; ANK_5.
DR PROSITE; PSS0297; ANK_REPEAT_REGION_2.
DR PROSITE; PSS0088; ANK_REPEAT_3.
KM ANK repeat; Repeat.
SQ SEQUENCE 690 AA; 79416 MW; F279541301AA6310 CRC64;

Query Match 78.7%; Score 37; DB 2; Length 690;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
Db 533 DYSDDDD 539

RESULT 97
Q5AA27_CANAL PRELIMINARY; PRT; 691 AA.
ID Q5AA27_CANAL

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AC Q5AA27;
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
DT 26-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Hypothetical protein.
GN ORFNames=Ca019.2457;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OC NCBI_TaxID=237561;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Pederspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S., Thorstenson Y.R., Agabian N., Magee P.T.,
RT "The diploid genome sequence of Candida albicans."
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
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CC -----
DR EMBL; AAC001000041; EAK99554.1; -; Genomic_DNA.
DR InterPro; IPR013154; ADH_N.
KM Hypothetical protein.
SQ SEQUENCE 691 AA; 79808 MW; 312D03A62F0EF773 CRC64;

Query Match 78.7%; Score 37; DB 2; Length 691;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
Db 616 DYKDDND 622

RESULT 98
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AC Q54D84;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DE 07-FEB-2006, entry version 4.
DE Hypothetical protein.
GN ORFNames=DD80184391;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OC NCBI_TaxID=4689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RX PubMed=15875012; DOI=10.1038/nature03481;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.A.,
RA Sugang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Nadera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E.J., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.M.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Wuzny D.M., Moutier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K.D., Quiles M., Madan Babu M., Saito T.,
RA Buchrieser C., Wardrop A., Felder M., Thangavelu M., Johnson D.,
RA Knights A., Loulsegue H., Mungall K.L., Oliver K., Price C.,
RA Quail M.A., Urushihara H., Hernandez J., Rabinovitch E., Steffen D.,
RA Sanders M., Ma J., Kohara Y., Sharp S., Simmonds M.N., Spiegler S.,
RA Tivey A., Sugano S., White B., Walker D., Woodward J.R., Winckler T.,
RA Tanaka Y., Shaulsky G., Schleicher M., Weinstock G.M., Rosenthal A.,
RA Cox E.C., Chisholm R.L., Gibbs R.A., Loomis W.F., Platzer M.,

```

RA Kay R.R., Williams J.G., Dear P.H., Noegel A.A., Barrel B.G.,  
RA Kuapa A.;  
RT "The genome of the social amoeba *Dictyostelium discoideum*."  
RL Nature 435:43-57(2005).  
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CC -----  
DR EMBL: AAF101000268; EAL61197.1; -; Genomic\_DNA.  
DR GO: GO:0005515; F:protein binding; IEA.  
DR InterPro: IPR00210; BTB.  
DR Pfam: PF00651; BTB; 1.  
DR SMART: SM00225; BTB; 1.  
DR PROSITE: PS00097; BTB; 1.  
KM Hypothetical protein.  
SQ SEQUENCE 697 AA; 79148 MW; FC49F887CE23AC6C CRC64;

Query Match 78.7%; Score 37; DB 2; Length 697;  
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Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DYKDDDDK 8  
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Db 437 DFTDDDDK 444

RESULT 99  
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ID Q5A932 CANAL  
AC Q5A932;  
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.  
DT 26-APR-2005, sequence version 1.  
DT 07-FEB-2006, entry version 7.  
DE Hypothetical protein.  
GN ORENAMES=CaO19.10812, CaO19.3302;  
OS Candida albicans SC5314;  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; mitospotic Saccharomycetales; Candida.  
OX NCBI\_TaxID=237561;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=SC5314;  
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;  
RA Jones T., Federpiel N.A., Chibana H., Dungan J., Kalman S.,  
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,  
RA Davis R.W., Scherer S.;  
RT "The diploid genome sequence of *Candida albicans*."  
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).  
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CC -----  
DR EMBL: AAC001000045; EAK99193.1; -; Genomic\_DNA.  
DR EMBL: AAC001000042; EAK99468.1; -; Genomic\_DNA.  
DR InterPro: IPR005036; CBM\_21.  
DR Pfam: PF03370; CBM\_21; 1.  
KM Hypothetical protein.  
SQ SEQUENCE 700 AA; 78182 MW; E2A5C0C72D41E9F2 CRC64;

Query Match 78.7%; Score 37; DB 2; Length 700;  
Best Local Similarity 85.7%; Pred. No. 1.6e+03;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DYKDDDD 7  
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Db 168 DYSDDD 174

RESULT 100  
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ID Q4N9L1 THEPA  
AC Q4N9L1;  
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.  
DT 02-AUG-2005, sequence version 1.  
DT 07-FEB-2006, entry version 6.  
DE RNA helicase, putative.  
GN ORENAMES=TP01\_0103;  
OS Theileria parva.  
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;  
OC Theileria.  
OX NCBI\_TaxID=5875;  
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RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Muguga;  
RX PubMed=15994558; DOI=10.1126/science.1110439;  
RA Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,  
RA Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.,  
RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,  
RA Jiang L., Lynn J., Weaver B., Shoab B., Anguilo S.V., Creasy T.H., Lu C.,  
RA Crabtree J., Wortman J.R., Felblyum T.V., Pertea M.,  
RA Suh B., Silva J.C., Uteerback T.R., Felblyum T.V., Pertea M.,  
RA Allen J., Nieman W.C., Taracha E.L., Salzberg S.L., White O.R.,  
RA Fitzhugh H.A., Morzaria S., Venter J.C., Fraser C.M., Nene V.;  
RT "Genome Sequence of *Theileria parva*, a Bovine Pathogen That Transforms  
RT Lymphocytes."  
RL Science 309:134-137(2005).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Muguga;  
RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,  
RA Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,  
RA Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L.,  
RA Lynn J., Weaver B., Shoab B., Anguilo S.V., Creasy T.H., Lu C.,  
RA Haas B., Anguilo S., Creasy T.H., Lu C., Suh B., Silva J.C.,  
RA Uteerback T., Felblyum T., Pertea M., Allen J., Taracha E.L.,  
RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,  
RA Fraser C.M., Nene V.;  
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
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CC -----  
DR EMBL: AAGK01000001; EAN33347.1; -; Genomic\_DNA.  
DR GO: GO:0005524; F:ATP binding; IEA.  
DR GO: GO:0008026; F:ATP-dependent helicase activity; IEA.  
DR GO: GO:0000166; F:nucleotide binding; IEA.  
DR InterPro: IPR001410; DEAD.  
DR Pfam: PF07717; DUF1605; 1.  
DR Pfam: PF04408; HA2; 1.  
KM Helicase.  
SQ SEQUENCE 702 AA; 81499 MW; 2924092F65B679AE CRC64;

Query Match 78.7%; Score 37; DB 2; Length 702;  
Best Local Similarity 85.7%; Pred. No. 1.6e+03;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 YKDDDDK 8  
|:|||||  
Db 527 YKDDDDK 533

Search completed: June 29, 2006, 11:40:41  
Job time : 319 secs

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OM protein - protein search, using sw model

Run on: June 29, 2006, 11:40:57 ; Search time 49 Seconds  
(without alignments)  
14.291 Million cell updates/sec

Title: US-10-671-054-2

Perfect score: 47

Sequence: 1 DYKDDDDK 8

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

Issued Patents\_AA:\*

- 1: /EMC\_Celerra\_SIDS3/prodata/2/iaa/5 COMB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/prodata/2/iaa/6 COMB.pep:\*
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- 4: /EMC\_Celerra\_SIDS3/prodata/2/iaa/H COMB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/prodata/2/iaa/CTUS COMB.pep:\*
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- 7: /EMC\_Celerra\_SIDS3/prodata/2/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	47	100.0	8	1 US-08-323-474-4	Sequence 4, Appl1
3	47	100.0	8	1 US-08-225-989-15	Sequence 15, Appl1
4	47	100.0	8	1 US-08-086-335C-12	Sequence 12, Appl1
5	47	100.0	8	1 US-08-265-086-5	Sequence 5, Appl1
6	47	100.0	8	1 US-08-236-918A-16	Sequence 16, Appl1
7	47	100.0	8	1 US-08-570-923-15	Sequence 15, Appl1
8	47	100.0	8	1 US-08-446-908-6	Sequence 6, Appl1
9	47	100.0	8	1 US-08-634-060-25	Sequence 25, Appl1
10	47	100.0	8	1 US-08-231-205A-6	Sequence 6, Appl1
11	47	100.0	8	1 US-08-446-922-1	Sequence 1, Appl1
12	47	100.0	8	1 US-08-430-633-3	Sequence 3, Appl1
13	47	100.0	8	1 US-08-580-014-15	Sequence 15, Appl1
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15	47	100.0	8	1 US-08-442-043A-15	Sequence 15, Appl1
16	47	100.0	8	1 US-08-604-333-5	Sequence 5, Appl1
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171	47	100.0	8	2	US-09-769-482-4	Sequence 4, Appl1	244	47	100.0	8	2	US-09-962-756-1547	Sequence 1547, Ap
172	47	100.0	8	2	US-09-536-201-5	Sequence 5, Appl1	245	47	100.0	8	2	US-09-962-756-1779	Sequence 1779, Ap



246	47	100.0	8	2	US-10-090-365-11	Sequence 11, Appl	319	47	100.0	10	2	US-09-180-167A-18	Sequence 18, Appl
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248	47	100.0	8	2	US-09-060-377-8	Sequence 8, Appl	321	47	100.0	10	2	US-09-631-331-10	Sequence 10, Appl
249	47	100.0	8	2	US-09-065-902-15	Sequence 15, Appl	322	47	100.0	10	2	US-09-545-894-30	Sequence 30, Appl
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253	47	100.0	8	2	US-09-728-911-11	Sequence 11, Appl	326	47	100.0	11	2	US-08-720-565-16	Sequence 16, Appl
254	47	100.0	8	2	US-10-158-925-147	Sequence 147, App	327	47	100.0	11	2	US-09-374-664-1	Sequence 1, Appl
255	47	100.0	8	2	US-10-002-392A-10	Sequence 10, Appl	328	47	100.0	11	2	US-09-964-201A-23	Sequence 23, Appl
256	47	100.0	8	2	US-09-688-286D-6	Sequence 6, Appl	329	47	100.0	11	2	US-08-375-199B-16	Sequence 16, Appl
257	47	100.0	8	2	US-10-340-104B-3	Sequence 3, Appl	330	47	100.0	11	2	US-09-848-616-147	Sequence 147, App
258	47	100.0	8	2	US-09-997-623-47	Sequence 47, Appl	331	47	100.0	12	1	US-10-283-028-16	Sequence 16, Appl
259	47	100.0	8	2	US-10-245-227D-9	Sequence 9, Appl	332	47	100.0	11	3	US-08-963-856-16	Sequence 16, Appl
260	47	100.0	8	2	US-10-284-083-12	Sequence 12, Appl	333	47	100.0	12	1	US-08-350-884-53	Sequence 53, Appl
261	47	100.0	8	2	US-09-092-397A-21	Sequence 21, Appl	334	47	100.0	12	1	US-08-709-173-53	Sequence 53, Appl
262	47	100.0	8	2	US-10-183-770A-16	Sequence 16, Appl	335	47	100.0	12	1	US-08-701-124-23	Sequence 23, Appl
263	47	100.0	8	2	US-10-372-874-21	Sequence 21, Appl	336	47	100.0	12	1	US-08-709-177-53	Sequence 53, Appl
264	47	100.0	8	2	US-10-668-453-1	Sequence 1, Appl	337	47	100.0	12	2	US-08-792-832A-9	Sequence 9, Appl
265	47	100.0	8	2	US-10-308-373-5	Sequence 5, Appl	338	47	100.0	12	2	US-09-130-825-23	Sequence 23, Appl
266	47	100.0	8	2	US-10-195-707B-40	Sequence 40, Appl	339	47	100.0	12	2	US-09-455-061-23	Sequence 23, Appl
267	47	100.0	8	2	US-09-875-338-94	Sequence 94, Appl	340	47	100.0	12	2	US-09-622-839-14	Sequence 14, Appl
268	47	100.0	8	2	US-10-632-694A-9	Sequence 9, Appl	341	47	100.0	12	2	US-09-969-192-23	Sequence 23, Appl
269	47	100.0	8	2	US-08-743-868-3	Sequence 3, Appl	342	47	100.0	13	1	US-10-318-142-14	Sequence 14, Appl
270	47	100.0	8	3	US-10-157-447-5	Sequence 5, Appl	343	47	100.0	13	1	US-08-222-616-41	Sequence 41, Appl
271	47	100.0	8	3	US-09-844-508-14	Sequence 14, Appl	344	47	100.0	13	1	US-08-446-908-7	Sequence 7, Appl
272	47	100.0	8	3	US-10-019-735-17	Sequence 17, Appl	345	47	100.0	13	1	US-08-231-205A-7	Sequence 7, Appl
273	47	100.0	8	3	US-10-143-618-29	Sequence 29, Appl	346	47	100.0	13	1	US-08-690-011A-48	Sequence 48, Appl
274	47	100.0	8	3	US-10-835-096-16	Sequence 16, Appl	347	47	100.0	13	1	US-08-871-161-7	Sequence 7, Appl
275	47	100.0	8	3	US-10-241-476-26	Sequence 26, Appl	348	47	100.0	13	2	US-08-446-648-41	Sequence 41, Appl
276	47	100.0	8	3	US-10-006-069A-225	Sequence 225, App	349	47	100.0	13	2	US-09-299-495E-48	Sequence 48, Appl
277	47	100.0	8	3	US-09-876-790-11	Sequence 11, Appl	350	47	100.0	13	2	US-09-982-610-41	Sequence 41, Appl
278	47	100.0	8	3	US-09-837-992-45	Sequence 45, Appl	351	47	100.0	13	5	US-10-009-332-33	Sequence 33, Appl
279	47	100.0	8	3	US-10-133-797A-28	Sequence 28, Appl	352	47	100.0	13	5	PCT-US95-04228-41	Sequence 41, Appl
280	47	100.0	8	5	PCT-US93-1003A-1	Sequence 1, Appl	353	47	100.0	13	7	5395760-16	Patent No. 5395760
281	47	100.0	8	5	PCT-US94-0811A-15	Sequence 15, Appl	354	47	100.0	14	1	US-08-411-795B-403	Sequence 403, App
282	47	100.0	8	5	PCT-US94-1291A-15	Sequence 15, Appl	355	47	100.0	14	1	US-08-446-908-9	Sequence 9, Appl
283	47	100.0	8	5	PCT-US95-00362-3	Sequence 3, Appl	356	47	100.0	14	1	US-08-231-205A-9	Sequence 9, Appl
284	47	100.0	8	5	PCT-US95-06530-7	Sequence 7, Appl	357	47	100.0	14	1	US-08-469-319A-403	Sequence 403, App
285	47	100.0	8	5	PCT-US95-08534-3	Sequence 3, Appl	358	47	100.0	14	1	US-08-871-161-9	Sequence 9, Appl
286	47	100.0	8	5	PCT-US95-12960-2	Sequence 2, Appl	359	47	100.0	14	2	US-08-764-114-403	Sequence 403, App
287	47	100.0	8	5	PCT-US95-15781-6	Sequence 6, Appl	360	47	100.0	14	2	US-08-469-419-403	Sequence 403, App
288	47	100.0	8	7	PCT-US96-10895-7	Sequence 7, Appl	361	47	100.0	14	2	US-09-381-244B-5	Sequence 5, Appl
289	47	100.0	8	7	5194375-7	Patent No. 5194375	362	47	100.0	14	2	US-09-937-126-4	Sequence 4, Appl
290	47	100.0	8	7	5198342-3	Patent No. 5198342	363	47	100.0	15	2	US-09-896-915-2	Sequence 2, Appl
291	47	100.0	8	7	5395760-6	Patent No. 5395760	364	47	100.0	15	2	US-08-817-145-19	Sequence 19, Appl
292	47	100.0	9	1	US-08-605-002A-17	Sequence 17, Appl	365	47	100.0	16	2	US-09-252-656B-57	Sequence 57, Appl
293	47	100.0	9	1	US-08-950-449A-19	Sequence 19, Appl	366	47	100.0	16	2	US-09-285-912A-135	Sequence 135, App
294	47	100.0	9	2	US-08-968-747-4	Sequence 4, Appl	367	47	100.0	17	1	US-08-651-818A-22	Sequence 22, Appl
295	47	100.0	9	2	US-07-602-848B-9	Sequence 9, Appl	368	47	100.0	17	2	US-09-184-826-22	Sequence 22, Appl
296	47	100.0	9	2	US-09-645-456A-28	Sequence 28, Appl	369	47	100.0	17	2	US-09-832-464-22	Sequence 22, Appl
297	47	100.0	9	2	US-09-425-324A-28	Sequence 28, Appl	370	47	100.0	18	1	US-08-670-175-8	Sequence 8, Appl
298	47	100.0	9	2	US-09-645-791-28	Sequence 28, Appl	371	47	100.0	21	2	US-09-266-462-1	Sequence 1, Appl
299	47	100.0	9	2	US-09-700-820C-10	Sequence 10, Appl	372	47	100.0	21	2	US-09-266-462-3	Sequence 3, Appl
300	47	100.0	9	2	US-09-872-136B-11	Sequence 11, Appl	373	47	100.0	21	2	US-09-297-269-21	Sequence 21, Appl
301	47	100.0	9	2	US-10-039-659A-19	Sequence 19, Appl	374	47	100.0	21	2	US-09-809-517A-30	Sequence 30, Appl
302	47	100.0	9	2	US-09-826-312A-17	Sequence 17, Appl	375	47	100.0	22	1	US-08-701-124-29	Sequence 29, Appl
303	47	100.0	9	2	US-09-352-171-1	Sequence 1, Appl	376	47	100.0	22	2	US-09-130-225-29	Sequence 29, Appl
304	47	100.0	9	2	US-09-786-442B-13	Sequence 13, Appl	377	47	100.0	22	2	US-09-455-061-29	Sequence 29, Appl
305	47	100.0	9	2	US-09-896-915-6	Sequence 6, Appl	378	47	100.0	22	2	US-09-969-192-29	Sequence 29, Appl
306	47	100.0	9	2	US-09-896-915-39	Sequence 39, Appl	379	47	100.0	22	2	US-09-270-767-35444	Sequence 35444, A
307	47	100.0	9	2	US-09-622-500B-8	Sequence 8, Appl	380	47	100.0	22	2	US-09-270-767-50661	Sequence 50661, A
308	47	100.0	9	2	US-09-919-408A-11	Sequence 11, Appl	381	47	100.0	22	2	US-09-809-517A-33	Sequence 33, Appl
309	47	100.0	9	3	US-10-835-096-17	Sequence 17, Appl	382	47	100.0	22	2	US-09-667-365-1948	Sequence 1948, Ap
310	47	100.0	10	1	US-08-435-501-26	Sequence 26, Appl	383	47	100.0	23	2	US-09-370-767-34566	Sequence 34566, A
311	47	100.0	10	1	US-08-435-764-26	Sequence 26, Appl	384	47	100.0	23	2	US-09-270-767-49783	Sequence 49783, A
312	47	100.0	10	1	US-08-568-072-1	Sequence 1, Appl	385	47	100.0	24	2	US-09-266-462-4	Sequence 4, Appl
313	47	100.0	10	1	US-08-713-928B-14	Sequence 14, Appl	386	47	100.0	26	1	US-08-634-060-26	Sequence 26, Appl
314	47	100.0	10	2	US-08-559-397A-35	Sequence 35, Appl	387	47	100.0	29	5	PCT-US94-05150-37	Sequence 37, Appl
315	47	100.0	10	2	US-09-046-785-1	Sequence 1, Appl	388	47	100.0	30	1	US-08-634-060-39	Sequence 39, Appl
316	47	100.0	10	2	US-08-961-309-68	Sequence 68, Appl	389	47	100.0	34	2	US-09-896-915-8	Sequence 8, Appl
317	47	100.0	10	2	US-09-620-956-10	Sequence 10, Appl	390	47	100.0	35	2	US-09-460-145-9	Sequence 9, Appl
318	47	100.0	10	2	US-09-611-152-10	Sequence 10, Appl	391	47	100.0	35	2		

392	47	100.0	35	2	US-09-800-170-26	Sequence 26, Appl
393	47	100.0	35	2	US-09-895-547-9	Sequence 9, Appl
394	47	100.0	35	2	US-09-285-912A-66	Sequence 66, Appl
395	47	100.0	35	2	US-10-266-388-9	Sequence 9, Appl
396	47	100.0	40	2	US-09-669-516C-15	Sequence 15, Appl
397	47	100.0	42	2	US-09-053-866-5	Sequence 5, Appl
398	47	100.0	42	2	US-09-479-130-5	Sequence 5, Appl
399	47	100.0	42	2	US-09-472-130A-5	Sequence 5, Appl
400	47	100.0	43	2	US-09-962-756-1289	Sequence 1289, Ap
401	47	100.0	43	2	US-09-962-756-2191	Sequence 2191, Ap
402	47	100.0	48	2	US-09-962-756-2195	Sequence 2195, Ap
403	47	100.0	49	2	US-10-084-298-10	Sequence 10, Appl
404	47	100.0	53	1	US-08-651-818A-19	Sequence 19, Appl
405	47	100.0	53	2	US-09-184-825-19	Sequence 19, Appl
406	47	100.0	53	2	US-09-832-464-19	Sequence 23, Appl
407	47	100.0	54	1	US-08-651-818A-23	Sequence 23, Appl
408	47	100.0	54	2	US-09-184-825-23	Sequence 23, Appl
409	47	100.0	54	2	US-09-832-464-23	Sequence 23, Appl
410	47	100.0	57	2	US-09-962-756-2147	Sequence 2147, Ap
411	47	100.0	57	2	US-09-962-756-2179	Sequence 2179, Ap
412	47	100.0	61	2	US-09-962-756-2176	Sequence 2176, Ap
413	47	100.0	64	2	US-09-962-756-2148	Sequence 2148, Ap
414	47	100.0	64	2	US-09-962-756-2160	Sequence 2160, Ap
415	47	100.0	64	2	US-09-962-756-2180	Sequence 2180, Ap
416	47	100.0	65	2	US-09-962-756-2170	Sequence 2170, Ap
417	47	100.0	68	1	US-08-330-638D-2	Sequence 2, Appl
418	47	100.0	68	1	US-08-906-746A-2	Sequence 2, Appl
419	47	100.0	70	2	US-09-962-756-2112	Sequence 2112, Ap
420	47	100.0	70	2	US-09-962-756-2193	Sequence 2193, Ap
421	47	100.0	72	2	US-09-962-756-2114	Sequence 2114, Ap
422	47	100.0	72	2	US-09-962-756-2116	Sequence 2116, Ap
423	47	100.0	72	2	US-09-962-756-2192	Sequence 2192, Ap
424	47	100.0	72	2	US-09-962-756-2196	Sequence 2196, Ap
425	47	100.0	72	2	US-09-962-756-2197	Sequence 2197, Ap
426	47	100.0	74	2	US-09-962-756-2134	Sequence 2134, Ap
427	47	100.0	74	2	US-09-962-756-2189	Sequence 2189, Ap
428	47	100.0	76	2	US-09-962-756-2113	Sequence 2113, Ap
429	47	100.0	76	2	US-09-962-756-2182	Sequence 2182, Ap
430	47	100.0	76	2	US-09-962-756-2194	Sequence 2194, Ap
431	47	100.0	78	2	US-09-962-756-2115	Sequence 2115, Ap
432	47	100.0	78	2	US-09-962-756-2198	Sequence 2198, Ap
433	47	100.0	78	2	US-09-962-756-2201	Sequence 2201, Ap
434	47	100.0	80	2	US-09-962-756-2190	Sequence 2190, Ap
435	47	100.0	81	2	US-09-962-756-2200	Sequence 2200, Ap
436	47	100.0	84	2	US-09-399-495F-11	Sequence 11, Appl
437	47	100.0	84	2	US-09-826-312A-11	Sequence 14, Appl
438	47	100.0	84	2	US-10-108-767-14	Sequence 14, Appl
439	47	100.0	84	2	US-10-152-156-14	Sequence 14, Appl
440	47	100.0	84	3	US-10-835-096-14	Sequence 14, Appl
441	47	100.0	85	2	US-09-826-312A-15	Sequence 15, Appl
442	47	100.0	85	2	US-10-108-767-15	Sequence 15, Appl
443	47	100.0	85	2	US-10-152-156-15	Sequence 15, Appl
444	47	100.0	86	3	US-10-835-096-15	Sequence 15, Appl
445	47	100.0	86	3	US-09-826-312A-18	Sequence 18, Appl
446	47	100.0	86	3	US-09-962-756-2177	Sequence 2177, Ap
447	47	100.0	86	3	US-10-835-096-18	Sequence 18, Appl
448	47	100.0	88	1	US-08-690-011A-11	Sequence 11, Appl
449	47	100.0	90	2	US-09-962-756-2161	Sequence 2161, Ap
450	47	100.0	90	2	US-09-299-495F-9	Sequence 9, Appl
451	47	100.0	92	2	US-09-962-756-2171	Sequence 2171, Ap
452	47	100.0	92	2	US-09-962-756-2178	Sequence 2178, Ap
453	47	100.0	95	2	US-09-763-509-6	Sequence 6, Appl
454	47	100.0	96	2	US-09-962-756-2162	Sequence 2162, Ap
455	47	100.0	97	2	US-09-299-495F-19	Sequence 19, Appl
456	47	100.0	98	1	US-08-690-011A-19	Sequence 19, Appl
457	47	100.0	98	1	US-09-962-756-2172	Sequence 2172, Ap
458	47	100.0	105	1	US-08-383-348A-19	Sequence 19, Appl
459	47	100.0	105	1	US-08-383-804B-19	Sequence 19, Appl
460	47	100.0	105	1	US-08-383-748A-19	Sequence 19, Appl
461	47	100.0	105	1	US-08-814-309A-19	Sequence 19, Appl
462	47	100.0	105	1	US-08-690-011A-15	Sequence 15, Appl
463	47	100.0	105	2	US-09-299-495F-15	Sequence 15, Appl
464	47	100.0	108	2	US-09-473-551-15	Sequence 15, Appl

RESULT 1  
US-08-089-458B-7  
; Sequence 7, Application US/08089458B  
; Patent No. 5359039  
; GENERAL INFORMATION:  
; APPLICANT: Smith, Craig  
; APPLICANT: Goodwin, Raymond  
; TITLE OF INVENTION: Isolated Poxvirus A53R-Equivalent Tumor  
; TITLE OF INVENTION: Necrosis Factor Antagonists  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patricia Anne Perkins, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: U.S.A.  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.1  
; SOFTWARE: Microsoft Word, Version #5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/089,458B  
; FILING DATE: 07/09/93  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A.  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2608  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-089-458B-7

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. Se+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 2  
US-08-323-474-4  
Sequence 4, Application US/08323474  
Patent No. 5447860  
GENERAL INFORMATION:  
APPLICANT: Ziegler, Steven F.  
TITLE OF INVENTION: NOVEL TYROSINE KINASE  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/323,474  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/905,600  
FILING DATE: 26-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2609  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-323-474-4

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. Se+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 3

US-08-225-989-15  
Sequence 15, Application US/08225989  
Patent No. 5480981  
GENERAL INFORMATION:  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Smith, Craig A.  
APPLICANT: Armitage, Richard J.  
APPLICANT: Gruss, Hans-Jurgen  
TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/225,989  
FILING DATE: 12 APRIL 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/966,775  
FILING DATE: 27-OCT-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 907,224  
FILING DATE: 01-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,660  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 892,459  
FILING DATE: 02-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 889,717  
FILING DATE: 26-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2804-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
CLONE: FLAG peptide  
US-08-225-989-15

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. Se+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 4  
US-08-086-335C-12  
Sequence 12, Application US/08086335C

Patent No. 553863  
GENERAL INFORMATION:  
APPLICANT: Price, Virginia L.  
TITLE OF INVENTION: Expression System Comprising Mutant Yeast Strain and Expressi  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/086,335C  
FILING DATE: 01-JUL-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Anderson, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 1002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: FLAG peptide  
US-08-086-335C-12

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 5  
US-08-265-086-5  
Sequence 5, Application US/08265086  
Patent No. 5576191  
GENERAL INFORMATION:  
APPLICANT: Gayle, Margit  
APPLICANT: Slack, Jennifer  
APPLICANT: Gruss, Hans-Juergen  
APPLICANT: Sims, John E.  
APPLICANT: Dower, Steven K.  
TITLE OF INVENTION: No. 5576191el Cytokine That Binds ST2  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh

OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/265,086  
FILING DATE: June 17, 1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2825  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: FLAG peptide  
US-08-265-086-5

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 6  
US-08-236-918A-16  
Sequence 16, Application US/08236918A  
Patent No. 5674704  
GENERAL INFORMATION:  
APPLICANT: Alderson, Mark R.  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Smith, Craig A.  
TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kathryn A. Alderson, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple 7.5.3  
SOFTWARE: Microsoft Word, Version #6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/236,918A  
FILING DATE: 06-May-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/060,843  
FILING DATE: 07-May-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Anderson, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2801-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644

INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: FLAG peptide  
US-08-236-918A-16

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
DB 1 DYKDDDK 8

RESULT 7  
US-08-570-923-15  
Sequence 15, Application US/08570923  
Patent No. 5677430  
GENERAL INFORMATION:  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Smith, Craig A.  
APPLICANT: Armbrage, Richard J.  
APPLICANT: Grimes, Hans-Jurgen  
TITLE OF INVENTION: No. 5677430e1 Cytokine That Binds CD30  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/570,923  
FILING DATE: 12-DEC-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/225,989  
FILING DATE: 12 APRIL 1994  
APPLICATION NUMBER: US 07/966,775  
FILING DATE: 27-OCT-1992  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 907,224  
FILING DATE: 01-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,660  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 892,459  
FILING DATE: 02-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 889,717  
FILING DATE: 26-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2804-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430

TELEFAX: (206)233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
CLONE: FLAG peptide  
US-08-570-923-15

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
DB 1 DYKDDDK 8

RESULT 8  
US-08-446-908-6  
Sequence 6, Application US/08446908  
Patent No. 5705149  
GENERAL INFORMATION:  
APPLICANT: Namen, Anthony E.  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Lupton, Stephen D.  
APPLICANT: Mochizuki, Diane Y.  
TITLE OF INVENTION: Interleukin-7 and Antibodies Reactive  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446,908  
FILING DATE: 22-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/231,205  
FILING DATE: 21-APR-1994  
APPLICATION NUMBER: US 07/957,649  
FILING DATE: 06-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/511,438  
FILING DATE: 13-APR-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/255,209  
FILING DATE: 07-OCT-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/113,566  
FILING DATE: 26-OCT-1987  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2104-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 587-0644  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: FLAG peptide  
US-08-446-908-6

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
|||||||  
Db 1 DYKDDDDK 8

RESULT 9  
US-08-634-060-25  
Sequence 25, Application US/08634060  
Patent No. 5712136  
GENERAL INFORMATION:  
APPLICANT: Wickham, Thomas J.  
APPLICANT: Kovesdi, Imre  
APPLICANT: Roelink, Petrus W.  
TITLE OF INVENTION: ADENOVIRAL-MEDIATED CELL TARGETING COMMANDED BY  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leydig, Volt & Mayer, Ltd.  
STREET: Two Prudential Plaza, Suite 4900  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/634,060  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/303,162  
FILING DATE: 08-SEP-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kilyk, John Jr.  
REGISTRATION NUMBER: 30763  
REFERENCE/DOCKET NUMBER: 71602  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 616-5600  
TELEFAX: (312) 616-5700  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-634-060-25

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DYKDDDDK 8  
|||||||

Db 1 DYKDDDDK 8

RESULT 10  
US-08-231-205A-6  
Sequence 6, Application US/08231205A  
Patent No. 5714585  
GENERAL INFORMATION:  
APPLICANT: Namen, Anthony E.  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Lapton, Stephen D.  
APPLICANT: Mochizuki, Diane Y.  
TITLE OF INVENTION: Interleukin-7 and Antibodies Reactive  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/231,205A  
FILING DATE: 21-APR-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/957,649  
FILING DATE: 06-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/511,438  
FILING DATE: 13-APR-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/255,209  
FILING DATE: 07-OCT-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/113,566  
FILING DATE: 26-OCT-1987  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2104-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: FLAG peptide  
US-08-231-205A-6

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
|||||||  
Db 1 DYKDDDDK 8

RESULT 11

US-08-446-922-1  
; Sequence 1, Application US/08446922  
; Patent No. 5716805  
; GENERAL INFORMATION:  
; APPLICANT: Spriggs, Melanie  
; APPLICANT: Srinivasan, Subhashini  
; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.1  
; SOFTWARE: Microsoft Word for Apple, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446,922  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/107,353  
; FILING DATE: 08-13-93  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A.  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 1003-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHEetical: NO  
; ANTI-SENSE: NO  
US-08-446-922-1  
Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DYKDDDDK 8  
DB 1 DYKDDDDK 8  
RESULT 12  
US-08-430-633-3  
; Sequence 3, Application US/08430633  
; Patent No. 5726286  
; GENERAL INFORMATION:  
; APPLICANT: ALDERSON, MARK  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: COHEN, JEFFREY  
; APPLICANT: COMEAU, MICHAEL  
; APPLICANT: FARRAH, THERESA  
; APPLICANT: SPRIGGS, MELANIE  
; TITLE OF INVENTION: Isolated Epstein-Barr Virus BZLF2 Proteins  
; TITLE OF INVENTION: That Bind MHC Class II Beta Chains  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET

CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.1  
; SOFTWARE: Microsoft Word for Apple, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/430,633  
; FILING DATE: 28-APR-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/235,397  
; FILING DATE: 04/28/94  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A.  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2612  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; CLONE: FLAG\_peptide  
US-08-430-633-3

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
DB 1 DYKDDDDK 8

RESULT 13  
US-08-580-014-15  
; Sequence 15, Application US/08580014  
; Patent No. 5753203  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Ulrich  
; TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/580,014  
; FILING DATE: 20-DEC-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989  
; FILING DATE: 12 APRIL 1994  
; APPLICATION NUMBER: US 07/966,775

FILING DATE: 27-OCT-1992  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 907,224  
FILING DATE: 01-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,660  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 892,459  
FILING DATE: 02-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 889,717  
FILING DATE: 26-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2804-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
CLONE: FLAG peptide  
US-08-580-014-15

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 14  
US-08-670-354-7  
Sequence 7, Application US/08670354  
Patent No. 5763223  
GENERAL INFORMATION:  
APPLICANT: Steven R. Wiley and  
APPLICANT: Raymond G. Goodwin.  
TITLE OF INVENTION: Cytokine That Induces Apoptosis  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.5.2  
SOFTWARE: Microsoft Word, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/670,354  
FILING DATE: 25-JUN-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/496,632  
FILING DATE: 29-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/548,368

FILING DATE: 01-NOV-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Anderson, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2835-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: FLAG peptide  
US-08-670-354-7

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 15  
US-08-442-043A-15  
Sequence 15, Application US/08442043A  
Patent No. 5767064  
GENERAL INFORMATION:  
APPLICANT: Sims, John E.  
APPLICANT: Lupton, Stephen D.  
APPLICANT: Mosley, Bruce A.  
APPLICANT: Dower, Steven K.  
TITLE OF INVENTION: Type II Interleukin-1 Receptors  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,043A  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/534,193  
FILING DATE: 05-JUN-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/573,576  
FILING DATE: 24-AUG-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/627,071  
FILING DATE: 13-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/701,415  
FILING DATE: 16-MAY-1991  
PRIOR APPLICATION DATA:



APPLICATION NUMBER: US 08/091,519  
FILING DATE: 12-JULY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/242,211  
FILING DATE: 13-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2003-F  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-5570  
TELEFAX: 206-233-0644  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
CLONE: FLAG(r) peptide  
US-08-442-043A-15

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
DB 1 DYKDDDDK 8

RESULT 16  
US-08-604-333-5  
Sequence 5, Application US/08604333  
Patent No: 5776731  
GENERAL INFORMATION:  
APPLICANT: Parneet, Patricia et al.  
TITLE OF INVENTION: Receptor Designated 2F1  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/604,333  
FILING DATE: 21-FEB-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Anderson, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2619  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO

IMMEDIATE SOURCE:  
CLONE: FLAG peptide  
US-08-604-333-5

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
DB 1 DYKDDDDK 8

RESULT 17  
US-08-308-881-7  
Sequence 7, Application US/08308881  
Patent No: 5783672  
GENERAL INFORMATION:  
APPLICANT: Mosley, Bruce  
APPLICANT: Cosman, David J.  
TITLE OF INVENTION: Receptor for Oncostatin M  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/308,881  
FILING DATE: 12-SEP-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/249,553  
FILING DATE: 26-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2614-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: FLAG peptide  
US-08-308-881-7

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
DB 1 DYKDDDDK 8

RESULT 18  
US-08-660-626-1

```
; Sequence 1, Application US/08660626
; Patent No. 5789655
; GENERAL INFORMATION:
; APPLICANT: Stanley B. Prusiner
; APPLICANT: Glenn C. Telling
; APPLICANT: Fred E. Cohen
; APPLICANT: Michael R. Scott
; TITLE OF INVENTION: TRANSGENIC ANIMALS EXPRESSING
; TITLE OF INVENTION: EPIOTOPE-TAGGED PROTEINS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,626
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Valeta Gregg
; REGISTRATION NUMBER: 35,127
; REFERENCE/DOCKET NUMBER: 07532/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 322-5070
; TELEFAX: (415) 854-0875
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-660-626-1

Query Match      100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYKDDDDK 8
Db      1 DYKDDDDK 8

RESULT 19
US-08-526-014-1
; Sequence 1, Application US/08526014
; Patent No. 5801227
; GENERAL INFORMATION:
; APPLICANT: Fanslow, William C. III
; APPLICANT: Zappone, Judee
; APPLICANT: Alderson, Mark
; APPLICANT: Armitage, Richard J.
; TITLE OF INVENTION: ANTIBODIES TO CD40
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,014
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/130,541
; FILING DATE: October 1, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2816
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-526-014-1

Query Match      100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYKDDDDK 8
Db      1 DYKDDDDK 8

RESULT 20
US-08-684-687-6
; Sequence 6, Application US/08684687
; Patent No. 5830451
; GENERAL INFORMATION:
; APPLICANT: KIEFF, ELLIOTT D.
; APPLICANT: DEVERGNE, ODILE
; TITLE OF INVENTION: A NOVEL HAEMATOPOIETIC CYTOKINE AND USES
; THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/684,687
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,092
; FILING DATE: 11-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: B0801/7051
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-2441
; TELEFAX: 617-720-3500
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
```

LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: HOMO SAPIENS  
FEATURE:  
NAME/KEY: Binding-site  
LOCATION: 1..8  
OTHER INFORMATION: /label= FLAG\_EPTIPE  
US-08-684-687-6

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
DB 1 DYKDDDDK 8

RESULT 21  
US-08-701-124-2  
Sequence 2, Application US/08701124  
Patent No. 5846782

GENERAL INFORMATION:  
APPLICANT: Wickham, Thomas J.  
APPLICANT: Roelivink, Petrus W.  
TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF  
TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leydig, Voit & Mayer, Ltd.  
STREET: Two Prudential Plaza - 49th Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60601

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/701,124  
FILING DATE: 21-AUG-1996  
INFORMATION FOR SEQ. ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-701-124-2

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
DB 1 DYKDDDDK 8

RESULT 22  
US-08-649-341A-9  
Sequence 9, Application US/08649341A  
Patent No. 5847099

GENERAL INFORMATION:  
APPLICANT: Lin, Lih-Ling

APPLICANT: Chen, Jennifer H.  
TITLE OF INVENTION: NOVEL TNF RECEPTOR DEATH DOMAIN LIGAND  
TITLE OF INVENTION: PROTEINS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 CambridgePark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02140

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/649,341A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A,  
REGISTRATION NUMBER: 32,724  
REFERENCE/DOCKET NUMBER: G15232-FWC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8224  
TELEFAX: (617) 876-5851

INFORMATION FOR SEQ. ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-649-341A-9

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
DB 1 DYKDDDDK 8

RESULT 23  
US-08-494-440B-13  
Sequence 13, Application US/08494440B  
Patent No. 5849501

GENERAL INFORMATION:  
APPLICANT: Lin, Lih-Ling  
APPLICANT: Chen, Jennifer H.  
APPLICANT: Schievella, Andrea  
TITLE OF INVENTION: NOVEL TNF RECEPTOR DEATH DOMAIN LIGAND  
TITLE OF INVENTION: PROTEINS AND INHIBITORS OF LIGAND BINDING  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 CambridgePark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02140

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/494,440B  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A,

REGISTRATION NUMBER: 32, 724  
REFERENCE/DOCKET NUMBER: G15232A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8224  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-494-440B-13

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05; 0;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 24  
US-08-729-345-4  
Sequence 4, Application US/08729345  
Patent No. 5849999  
GENERAL INFORMATION:  
APPLICANT: Neve, Rachael L.  
APPLICANT: Berger-Sweeney, Joanne  
TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL  
TITLE OF INVENTION: EXPRESSING FLAG-APP-C100 FUSION PROTEIN  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/729,345  
FILING DATE: 16-OCT-1996  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 04843/027001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-729-345-4

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05; 0;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8

Db 1 DYKDDDDK 8

RESULT 25  
US-08-533-901B-15  
Sequence 15, Application US/08533901B  
Patent No. 5852173  
GENERAL INFORMATION:  
APPLICANT: Lin, Lin-Ling  
APPLICANT: Chen, Jennifer H.  
APPLICANT: Schievella, Andrea  
APPLICANT: Graham, James  
TITLE OF INVENTION: NOVEL TNF RECEPTOR DEATH DOMAIN LIGAND  
TITLE OF INVENTION: PROTEINS AND INHIBITORS OF LIGAND BINDING  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/533,901B  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724  
REFERENCE/DOCKET NUMBER: G15232  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8224  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-533-901B-15

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05; 0;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 26  
US-08-670-175-1  
Sequence 1, Application US/08670175  
Patent No. 5854081  
GENERAL INFORMATION:  
APPLICANT: LINDEN, JOEL  
APPLICANT: TAYLOR, HEIDI  
APPLICANT: ROBEVA, ANNA  
APPLICANT: WOODARD, ROBIN  
APPLICANT: JIN, XIOWEI  
TITLE OF INVENTION: STABLE EXPRESSION OF HUMAN ADENOSINE  
TITLE OF INVENTION: RECEPTORS, AND ASSAYS EMPLOYING THE SAME  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBION, SPIYAK, MCLELLAND, MAIER & NEUSTADT,  
ADDRESSEE: P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/670,175  
FILING DATE: 20-JUN-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 494-176-0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-670-175-1

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 27  
US-08-777-405A-15  
Sequence 15, Application US/08777405A  
Patent No. 5858753  
GENERAL INFORMATION:  
APPLICANT: Chantry, David  
APPLICANT: Hoekstra, Merl F.  
APPLICANT: Holtzman, Douglas A.  
TITLE OF INVENTION: No. 5858733el Lipid Kinase  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun  
STREET: 6300 Sears Tower/233 South Wacker Drive  
City: Chicago  
State: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/777,405A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5858753and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/33441  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
US-08-777-405A-15

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 28  
US-08-620-694A-3  
Sequence 3, Application US/08620694A  
Patent No. 5869286  
GENERAL INFORMATION:  
APPLICANT: Yao, Zhengbin  
APPLICANT: Spriegs, Melanie  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
City: Seattle  
State: WA  
COUNTRY: USA  
ZIP: 98101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/620,694A  
FILING DATE: 21 MARCH 1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/538,765  
FILING DATE: 7 AUGUST 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995

ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
CLONE: FLAG\_peptide  
US-08-620-694A-3

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
 |||||  
 Db 1 DYKDDDDK 8

## RESULT 29

US-08-720-258-7  
 ; Sequence 7, Application US/08720258  
 ; Patent No. 5871740  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Smith, Craig A.  
 ; TITLE OF INVENTION: Chemokine Inhibitor  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Immunex Corporation  
 ; STREET: 51 University Street  
 ; CITY: Seattle  
 ; STATE: Washington  
 ; COUNTRY: US  
 ; ZIP: 98101  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: Apple Power Macintosh  
 ; OPERATING SYSTEM: Apple System 7.5.3  
 ; SOFTWARE: Microsoft Word, Version 6.0.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/720,258  
 ; FILING DATE: 26-SEPT-1996  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/575,715  
 ; FILING DATE: 20-DEC-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/537,324  
 ; FILING DATE: 29-SEP-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Anderson, Kathryn A.  
 ; REGISTRATION NUMBER: 32,172  
 ; REFERENCE/DOCKET NUMBER: 2620-B  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206) 587-0430  
 ; TELEFAX: (206) 233-0644  
 ; TELEX: 756822  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 8 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; HYPOTHEICAL: NO  
 ; ANTI-SENSE: NO  
 ; IMMEDIATE SOURCE:  
 ; CLONE: FLAG peptide  
 ; US-08-720-258-7

Query Match 100.0%; Score 47; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5e+05; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0;

QY 1 DYKDDDDK 8  
 |||||  
 Db 1 DYKDDDDK 8

RESULT 30  
 US-08-977-871A-15  
 ; Sequence 15, Application US/08977871A  
 ; Patent No. 5882910  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chantley, David  
 ; APPLICANT: Hoekstra, Meri F.  
 ; APPLICANT: Holtzman, Douglas A

; TITLE OF INVENTION: No. 5882910e1 Lipid Kinase  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun  
 ; STREET: 6300 Sears Tower/233 South Wacker Drive  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60606

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/977,871A  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/777,405  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: No. 5882910and, Greta E.  
 ; REGISTRATION NUMBER: 35,302  
 ; REFERENCE/DOCKET NUMBER: 27866/33441  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (312) 474-6300  
 ; TELEFAX: (312) 474-0448  
 ; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 15:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 8 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: not relevant  
 ; TOPOLOGY: not relevant  
 ; MOLECULE TYPE: peptide  
 ; US-08-977-871A-15

Query Match 100.0%; Score 47; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5e+05; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0;

QY 1 DYKDDDDK 8  
 |||||  
 Db 1 DYKDDDDK 8

RESULT 31  
 US-08-839-032A-19  
 ; Sequence 19, Application US/08839032A  
 ; Patent No. 5891675  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lin, Lin-Ling  
 ; APPLICANT: Chen, Jennifer H.  
 ; APPLICANT: Schievella, Andrea  
 ; APPLICANT: Graham, James  
 ; TITLE OF INVENTION: NOVEL TNF RECEPTOR DEATH DOMAIN LIGAND PROTEINS  
 ; NUMBER OF SEQUENCES: 19  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genetics Institute, Inc.  
 ; STREET: 87 CambridgePark Drive  
 ; CITY: Cambridge  
 ; STATE: Massachusetts  
 ; COUNTRY: USA  
 ; ZIP: 02140

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/839,032A  
 ; FILING DATE:

```

; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15232DDIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-839-032A-19

Query Match      100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      1 DYKDDDDK 8
Db      1 DYKDDDDK 8

RESULT 32
US-09-058-263-7
; Sequence 7, Application US/09058263
; Patent No. 5891997
; GENERAL INFORMATION:
; APPLICANT: Mosley, Bruce
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: Receptor for Oncostatin M
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/058,263
; FILING DATE:
; PRIORITY INFORMATION:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/308,881
; FILING DATE: 12-SEP-1994
; APPLICATION NUMBER: US 08/249,553
; FILING DATE: 26-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2614-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
```

```

; CLONE: FLAG peptide
; US-09-058-263-7

Query Match      100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      1 DYKDDDDK 8
Db      1 DYKDDDDK 8

RESULT 33
US-08-870-518-27
; Sequence 27, Application US/08870518
; Patent No. 5925566
; GENERAL INFORMATION:
; APPLICANT: Davis, Roger J.
; APPLICANT: Galcheva-Gargova, Zoya
; TITLE OF INVENTION: NON-ACTIVATED RECEPTOR COMPLEX
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/870,518
; FILING DATE: 06-JUN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/019,219
; FILING DATE: 06-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faase, Peter J.
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 04020/102001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-870-518-27

Query Match      100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      1 DYKDDDDK 8
Db      1 DYKDDDDK 8

RESULT 34
US-08-936-854-3
; Sequence 3, Application US/08936854
; Patent No. 5925734
; GENERAL INFORMATION:
; APPLICANT: ALDERSON, MARK
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: COHEN, JEFFREY
```

```
APPLICANT: COMEAU, MICHAEL
APPLICANT: FARAH, THERESA
APPLICANT: SPRIGGS, MELANIE
TITLE OF INVENTION: Isolated Epstein-Barr Virus BZLF2 Proteins
TITLE OF INVENTION: That Bind MHC Class II Beta Chains
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSER: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,854
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/430,633
FILING DATE: 28-APR-1995
APPLICATION NUMBER: 08/235,397
FILING DATE: 04/26/94
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2612
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: FLAG_ peptide
US-08-936-854-3

Query Match      100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYKDDDDK 8
Db      1 DYKDDDDK 8

RESULT 35
US-09-059-099-7
; Sequence 7, Application US/09059099
; Patent No. 5925740
; GENERAL INFORMATION:
; APPLICANT: Mosley, Bruce
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: Receptor for Oncostatin M
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
```

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SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,099
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: FLAG peptide
US-09-059-099-7

Query Match      100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYKDDDDK 8
Db      1 DYKDDDDK 8

RESULT 36
US-08-713-928B-10
; Sequence 10, Application US/08713928B
; Patent No. 5929304
; GENERAL INFORMATION:
; APPLICANT: RADIN, DAVID N.
; APPLICANT: CRAMER, CAROLE L.
; APPLICANT: WEISSENBERG, DEBORAH L.
; TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
; TITLE OF INVENTION: PLANT-BASED EXPRESSION SYSTEMS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,928B
; FILING DATE: 13-SEP-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/003,737
; FILING DATE: 14-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
```



REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7956-0011-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-713-928B-10

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 37  
US-08-595-043A-1  
Sequence 1, Application US/08595043A  
Patent No. 5935824  
GENERAL INFORMATION:  
APPLICANT: SGARLATO, GREGORY D.  
TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM  
NUMBER OF SEQUENCES: 90  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/595,043A  
FILING DATE: 31-JAN-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: SGAR-00371  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-595-043A-1

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 38  
US-08-690-011A-50  
Sequence 50, Application US/08690011A  
Patent No. 5942433  
GENERAL INFORMATION:  
APPLICANT: VINSON, Charles R.  
APPLICANT: KRYLOV, Dmitry  
TITLE OF INVENTION: EXTENSION OF A PROTEIN-PROTEIN  
INTERACTION SURFACE TO INACTIVATE THE FUNCTION OF A  
CELLULAR PROTEIN  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 Park Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10154-0053  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/690,011A  
FILING DATE: 31-JUL-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/001,654  
FILING DATE: 31-JUL-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/018,496  
FILING DATE: 29-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Serunian, Leslie A.  
REGISTRATION NUMBER: 35,353  
REFERENCE/DOCKET NUMBER: 2026-41990S1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 751-6849  
TELEFAX: (212) 751-6849  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-690-011A-50

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 39  
US-08-839-031A-15  
Sequence 15, Application US/08839031A  
Patent No. 5948638  
GENERAL INFORMATION:  
APPLICANT: Lin, Lih-Ling  
APPLICANT: Chen, Jennifer H.  
APPLICANT: Schiavella, Andrea  
APPLICANT: Graham, James  
TITLE OF INVENTION: NOVEL TNF RECEPTOR DEATH DOMAIN LIGAND  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 CambridgePark Drive  
CITY: Cambridge

STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/839,031A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Sprunger, Suzanne A.,  
REGISTRATION NUMBER: 41,323  
REFERENCE/DOCKET NUMBER: G15232BDIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8284  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-839-031A-15

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDDK 8  
|||||||  
Db 1 DYKDDDDK 8

RESULT 40  
US-08-762-106-3  
Sequence 3, Application US/08762106  
Patent No. 5948677  
GENERAL INFORMATION:  
APPLICANT: Jarvik, Jonathan W.  
TITLE OF INVENTION: READING FRAME INDEPENDENT EPTOPE  
TITLE OF INVENTION: TAGGING  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Harris Brotman  
STREET: 202 Coast Blvd., Suite 111  
CITY: La Jolla  
STATE: California  
COUNTRY: US  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/762,106  
FILING DATE: 09-DEC-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Brotman, Harris F.  
REGISTRATION NUMBER: 35,461  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 654-2428  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal

US-08-762-106-3

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDDK 8  
|||||||  
Db 1 DYKDDDDK 8

RESULT 41  
US-09-016-366A-30  
Sequence 30, Application US/09016366A  
Patent No. 5955431  
GENERAL INFORMATION:  
APPLICANT: Stevens, Richard L.  
APPLICANT: Huang, Chifu  
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE  
TITLE OF INVENTION: INHIBITORS  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: MA  
COUNTRY: U.S.A.  
ZIP: 02210-2211  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/016,366A  
FILING DATE: January 30, 1998  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/037,090  
FILING DATE: 05-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Plumer, Elizabeth R.  
REGISTRATION NUMBER: 36,637  
REFERENCE/DOCKET NUMBER: B0801/7093  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-720-3500  
TELEFAX: 617-720-2441  
TELEX:  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-016-366A-30

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDDK 8  
|||||||  
Db 1 DYKDDDDK 8

RESULT 42  
US-08-700-846-8  
Sequence 8, Application US/08700846  
Patent No. 5962311  
GENERAL INFORMATION:  
APPLICANT: WICKHAM, THOMAS J.  
APPLICANT: ROELVINK, PETRUS W.

APPLICANT: KOVESDI, IMRE  
TITLE OF INVENTION: A SHORT-SHAFTED ADENOVIRAL FIBER AND ITS  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.  
STREET: TWO PRUDENTIAL PLAZA, SUITE 4900  
CITY: CHICAGO  
STATE: IL  
COUNTRY: USA  
ZIP: 60601-6780  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/700,846  
FILING DATE: 21-AUG-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: LARCHER, CAROL  
REGISTRATION NUMBER: 35243  
REFERENCE/DOCKET NUMBER: 74294  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 616-5600  
TELEFAX: (312) 616-5700  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-700-846-8

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
DB 1 DYKDDDDK 8

RESULT 43  
US-08-871-161-6  
Sequence 6, Application US/08871161  
Patent No. 5965122  
GENERAL INFORMATION:  
APPLICANT: Namen, Anthony E.  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Lupron, Stephen D.  
APPLICANT: Mochizuki, Diane Y.  
TITLE OF INVENTION: Interleukin-7 and Antibodies Reactive  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/871,161  
FILING DATE: 09-JUN-1997  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/446,908  
FILING DATE: 22-MAY-1995  
APPLICATION NUMBER: US 08/231,205  
FILING DATE: 21-APR-1994  
APPLICATION NUMBER: US 07/957,649  
FILING DATE: 06-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/511,438  
FILING DATE: 13-APR-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/255,209  
FILING DATE: 07-OCT-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/113,566  
FILING DATE: 26-OCT-1987  
ATTORNEY/AGENT INFORMATION:  
NAME: Seease, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2104-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: FLAG peptide  
US-08-871-161-6

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
DB 1 DYKDDDDK 8

RESULT 44  
US-08-832-935-1  
Sequence 1, Application US/08832935  
Patent No. 5965375  
GENERAL INFORMATION:  
APPLICANT: Valkirs, Gunars  
TITLE OF INVENTION: Diagnostic Tests and Kits for  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/832,935  
FILING DATE: 04-APR-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, Timothy L.  
REGISTRATION NUMBER: 35,367

```
REFERENCE/DOCKET NUMBER: 014907-001200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-832-935-1

Query Match      100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYKDDDDK 8
Db      1 DYKDDDDK 8

RESULT 45
US-08-482-728A-2
Sequence 2, Application US/08482728A
Patent No. 5968802
GENERAL INFORMATION:
APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Payan, Donald
TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobach, Test, Albritton
ADDRESSEE: & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,728A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-482-728A-2

Query Match      100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYKDDDDK 8
Db      1 DYKDDDDK 8
```

```
RESULT 46
US-08-876-882-5
Sequence 5, Application US/08876882
Patent No. 5981201
GENERAL INFORMATION:
APPLICANT: Avraham, Hava
APPLICANT: Groopman, Jerome E.
TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT
OF BREAST CANCER
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/876,882
FILING DATE: 16-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/035,228
FILING DATE: 08-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Doreen, Hogle M.
REGISTRATION NUMBER: 36,361
REFERENCE/DOCKET NUMBER: NEDH97-01pA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-876-882-5

Query Match      100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYKDDDDK 8
Db      1 DYKDDDDK 8

RESULT 47
US-09-225-951-15
Sequence 15, Application US/09225951
Patent No. 5985589
GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Hoekstra, Merl F.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: No. 5985589el Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
STREET: 6300 Sears Tower/233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
```

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/225,951  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: NO. 5985589and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/33441  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
US-09-225-951-15

Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
Db 1 DYKDDDK 8

RESULT 48  
US-09-058-264-7  
Sequence 7, Application US/09058264  
Patent No. 6010886  
GENERAL INFORMATION:  
APPLICANT: Mosley, Bruce  
APPLICANT: Cosman, David J.  
TITLE OF INVENTION: Receptor for Oncostatin M  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/058,264  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/308,881  
FILING DATE: 12-SEP-1994  
APPLICATION NUMBER: US 08/249,553  
FILING DATE: 26-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2614-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822

INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: FLAG peptide  
US-09-058-264-7

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
Db 1 DYKDDDK 8

RESULT 49  
US-08-991-426-8  
Sequence 8, Application US/08991426  
Patent No. 6013257  
GENERAL INFORMATION:  
APPLICANT: Pan, Yang  
TITLE OF INVENTION: NEUROTACTIN AND USES THEREFOR  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/991,426  
FILING DATE: 16-DEC-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/851,160  
FILING DATE: 05-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/643,798  
FILING DATE: 07-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Melkilejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 09404/043001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-991-426-8

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
Db 1 DYKDDDK 8

Db 1 DYKDDDK 8

RESULT 50  
US-08-996-139-7  
; Sequence 7, Application US/08996139  
; Patent No. 6017729  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Dirk M.  
; APPLICANT: Galibert, Laurent  
; APPLICANT: Maraskovsky, Eugene  
; TITLE OF INVENTION: Receptor Activator of NF-kappaB  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation, Law Department  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Power Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.5.5  
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/996,139  
; FILING DATE: 22 DECEMBER 1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 60/064,671  
; FILING DATE: 14 OCTOBER 1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/813,509  
; FILING DATE: 07 MARCH 1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/772,330  
; FILING DATE: 23 DECEMBER 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia Anne  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2851-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; CLONE: FLAG\_ peptide  
US-08-996-139-7

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 0;

Qy 1 DYKDDDK 8  
Db 1 DYKDDDK 8

RESULT 51  
US-08-792-832A-7  
; Sequence 7, Application US/08792832A  
; Patent No. 6017734  
; GENERAL INFORMATION:  
; APPLICANT: Summers Dr., Max D.  
; APPLICANT: Braunsagel Dr., Sharon C.  
; APPLICANT: Hong Dr., Tao

; TITLE OF INVENTION: UNIQUE NUCLEOTIDE AND AMINO ACID  
; TITLE OF INVENTION: SEQUENCE AND USES THEREOF  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/792,832A  
; FILING DATE: 30-JAN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/000,955  
; FILING DATE: 07-JUL-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/678,435  
; FILING DATE: 03-JUL-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hibler, David W.  
; REGISTRATION NUMBER: 41,071  
; REFERENCE/DOCKET NUMBER: TANK:190  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512/418-3000  
; TELEFAX: 512/474-7577  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-792-832A-7

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 0;

Qy 1 DYKDDDK 8  
Db 1 DYKDDDK 8

RESULT 52  
US-09-130-663-6  
; Sequence 6, Application US/09130663A  
; Patent No. 6020163  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
; FILE REFERENCE: 97-24  
; CURRENT APPLICATION NUMBER: US/09/130,663A  
; CURRENT FILING DATE: 1998-08-05  
; EARLIER APPLICATION NUMBER: 60/054,867  
; EARLIER FILING DATE: 1997-08-06  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FaastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Flag affinity peptide  
US-09-130-663-6

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 DYKDDDK 8  
Db 1 DYKDDDK 8

RESULT 53  
US-09-081-180-16  
Sequence 16, Application US/09081180  
Patent No. 6022847  
GENERAL INFORMATION:  
APPLICANT: Sheppard, Paul O.  
TITLE OF INVENTION: SECRETED SALIVARY ZSIG32  
TITLE OF INVENTION: POLYPEPTIDES  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Zymogenetics  
STREET: 1201 Eastlake Ave. E.  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/081,180  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/041,263  
FILING DATE: March 19, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Lingenfelter, Susan E  
REGISTRATION NUMBER: 41,156  
REFERENCE/DOCKET NUMBER: 97-17C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6675  
TELEFAX: 206-442-6678  
TELEX:  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-081-180-16

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8  
Db 1 DYKDDDK 8

RESULT 54  
US-09-040-786-16  
Sequence 16, Application US/09040786  
Patent No. 6025197  
GENERAL INFORMATION:  
APPLICANT: Sheppard, Paul O.  
TITLE OF INVENTION: SECRETED SALIVARY ZSIG32  
TITLE OF INVENTION: POLYPEPTIDES  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Zymogenetics  
STREET: 1201 Eastlake Ave. E.  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/040,786  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/041,263  
FILING DATE: March 19, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Lingenfelter, Susan E  
REGISTRATION NUMBER: 41,156  
REFERENCE/DOCKET NUMBER: 97-17  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6675  
TELEFAX: 206-442-6678  
TELEX:  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-040-786-16

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8  
Db 1 DYKDDDK 8

RESULT 55  
US-08-817-145-17  
Sequence 17, Application US/08817145  
Patent No. 6025329  
GENERAL INFORMATION:  
APPLICANT: UTSUMI, Jun  
APPLICANT: SUDO, Tetsuo  
APPLICANT: TANAKA, Yasuhiko  
APPLICANT: MATSUI, Mizuo  
TITLE OF INVENTION: THERAPEUTIC AGENT FOR OPHTHALMIC  
TITLE OF INVENTION: DISEASES  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Birch, Stewart, Kolaesch & Birch, LLP.  
STREET: P.O. Box 747  
CITY: Falls Church  
STATE: VA  
COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,145  
FILING DATE: 02-JUL-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:

NAME: MURPHY Jr., Gerald M.  
REGISTRATION NUMBER: 28,977  
REFERENCE/DOCKET NUMBER: 760-230P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-205-8000  
TELEFAX: 703-205-8050  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-817-145-17

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 56  
US-08-307-896-9  
Sequence 9, Application US/08307896C  
Patent No. 6034071  
GENERAL INFORMATION:  
APPLICANT: Iyengar, Srinivas Ravi  
TITLE OF INVENTION: MUTANT ACTIVATED GSALPHA AND ADENYLYL  
FILE OF INVENTION: CYCLASE 2 FOR USE AS THERAPEUTIC AGENTS  
CURRENT APPLICATION NUMBER: US/08/307,896C  
CURRENT FILING DATE: 1994-09-16  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 9  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Peptide sequence  
US-08-307-896-9

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 57  
US-08-785-247-9  
Sequence 9, Application US/08785247  
Patent No. 6040149  
GENERAL INFORMATION:  
APPLICANT: Kolesnick, Richard N.  
APPLICANT: Liu, Jun  
APPLICANT: Zhang, Yuhua  
TITLE OF INVENTION: ASSAY FOR IDENTIFYING AGENTS WHICH ACT ON THE  
TITLE OF INVENTION: CERAMIDE-ACTIVATED PROTEIN KINASE, KINASE  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/785,247  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 48582-A/JPW/CCA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-381-0526  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-785-247-9

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 58  
US-08-938-830-8  
Sequence 8, Application US/08938830  
Patent No. 6040437  
GENERAL INFORMATION:  
APPLICANT: Laskey, Laurence A.  
APPLICANT: Dowbenko, Donald J.  
TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage  
TITLE OF INVENTION: Furox-Associated Proteins (PSTPIPs)  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/938,830  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/798419  
FILING DATE: 07-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Dieger, Ginger R.  
REGISTRATION NUMBER: 33,055  
REFERENCE/DOCKET NUMBER: P1066P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-3216  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 8:



SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-938-830-8

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
DB 1 DYKDDDDK 8

RESULT 59  
US-08-828-741B-9  
Sequence 9, Application US/08828741B  
Patent No. 6043069

GENERAL INFORMATION:  
APPLICANT: Koentgen, Frank  
APPLICANT: Sues, Gabriele M.  
APPLICANT: Tarlinton, David M.  
APPLICANT: Treutlein, Herbert R.  
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSER: SCULLY, SCOTT, MURPHY & PRESSER  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: United States of America  
ZIP: 11530

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/828,741B  
FILING DATE: 26-MAR-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 10591  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-828-741B-9

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
DB 1 DYKDDDDK 8

RESULT 60  
US-08-819-177-14  
Sequence 14, Application US/08819177  
Patent No. 6043083

GENERAL INFORMATION:  
APPLICANT: Davis, Roger J.  
APPLICANT: Dickens, Martin  
TITLE OF INVENTION: INHIBITORS OF THE JNK SIGNAL  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/819,177  
FILING DATE: 28 April 1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:  
NAME: Fasse, J. Peter  
REGISTRATION NUMBER: 32,983  
REFERENCE/DOCKET NUMBER: 07917/037001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
OTHER INFORMATION: Flag epitope  
US-08-819-177-14

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
DB 1 DYKDDDDK 8

RESULT 61  
US-09-143-470-14  
Sequence 14, Application US/09143470  
Patent No. 6043086  
GENERAL INFORMATION:  
APPLICANT: Pan, Yang  
TITLE OF INVENTION: NEUROPROTECTIN AND USES THEREFOR  
FILE REFERENCE: 09404/049001  
CURRENT APPLICATION NUMBER: US/09/143,470  
CURRENT FILING DATE: 1998-08-28  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 14  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-143-470-14

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8

Db 1 DYKDDDK 8

RESULT 62  
US-08-950-720A-8  
; Sequence 8, Application US/08950720A  
; Patent No. 6046028  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; APPLICANT: Lofton-Day, Catherine E.  
; APPLICANT: Lok, Si  
; APPLICANT: Jaspers, Stephen R.  
; TITLE OF INVENTION: INSULIN HOMOLOG  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/950,720A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sawislak, Deborah A  
; REGISTRATION NUMBER: 37,438  
; REFERENCE/DOCKET NUMBER: 96-09  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6672  
; TELEFAX: 206-442-6678  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-950-720A-8

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. Se+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8  
Db 1 DYKDDDK 8

RESULT 63  
US-09-130-225-2  
; Sequence 2, Application US/09130225  
; Patent No. 6057155  
; GENERAL INFORMATION:  
; APPLICANT: Wickham, Thomas J.  
; APPLICANT: Roelivink, Petrus W.  
; APPLICANT: Kovesdi, Imre  
; TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF  
; TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS  
; NUMBER OF SEQUENCES: 80  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leydig, Volt & Mayer, Ltd.

STREET: Two Prudential Plaza - 49th Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/130,225  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 8-701124  
; FILING DATE: 21-AUG-1996  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-130-225-2

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. Se+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8  
Db 1 DYKDDDK 8

RESULT 64  
US-09-022-255-3  
; Sequence 3, Application US/09022255  
; Patent No. 6072033  
; GENERAL INFORMATION:  
; APPLICANT: Yao, Zhengbin  
; APPLICANT: Spriggs, Melanie  
; APPLICANT: Fanslow, William  
; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Power Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.5.5  
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/022,255  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/620,694  
; FILING DATE: 21 MARCH 1996  
; APPLICATION NUMBER: USSN 08/538,765  
; FILING DATE: 7 AUGUST 1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/410,535  
; FILING DATE: 23 MARCH 1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia Anne  
; REGISTRATION NUMBER: 34,695  
; REFERENCE/DOCKET NUMBER: 2617-B  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
CLONE: FLAG\_peptide  
US-09-022-255-3

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
DB 1 DYKDDDDK 8

RESULT 65  
US-09-022-696-3  
Sequence 3, Application US/09022696  
Patent No. 6072037  
GENERAL INFORMATION:  
APPLICANT: Yao, Zhenbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022, 696  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/620,694  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
CLONE: FLAG\_peptide  
US-09-022-696-3

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
DB 1 DYKDDDDK 8

RESULT 66  
US-08-883-036A-5  
Sequence 5, Application US/08883036A  
Patent No. 6072047  
GENERAL INFORMATION:  
APPLICANT: Rauch, Charles  
APPLICANT: Walczak, Henning  
TITLE OF INVENTION: Receptor That Binds TRAIL  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle,  
STATE: WA  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Macintosh 7.6  
SOFTWARE: Microsoft Word, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/883,036A  
FILING DATE: 26-JUN-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US --to be assigned--  
FILING DATE: 04-JUN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/829,536  
FILING DATE: 28-MAR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/815,255  
FILING DATE: 12-MAR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/799,861  
FILING DATE: 13-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Anderson, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2625-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: FLAG peptide  
US-08-883-036A-5

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8

Db 1 DYKDDDK 8

```
RESULT 67
US-09-030-613-35
; Sequence 35, Application US/09030613
; Patent No. 6083706
; GENERAL INFORMATION:
; APPLICANT: Florjencic, Robert Z.
; APPLICANT: Baird, J. Andrew
; TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,613
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6083706tensburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 760100.418C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-030-613-35

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. Se+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
Db 1 DYKDDDK 8

RESULT 68
US-09-073-569-5
; Sequence 5, Application US/090735569
; Patent No. 6084088
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Grossmann, Angelika
; TITLE OF INVENTION: NOVEL TUMOR ANTIGENS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
```

```
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,569
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-073-569-5
```

```
Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. Se+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
Db 1 DYKDDDK 8
```

```
RESULT 69
US-08-566-190-20
; Sequence 20, Application US/08566190
; Patent No. 6090784
; GENERAL INFORMATION:
; APPLICANT: Warren, Stephen L.
; TITLE OF INVENTION: RNA Polymerase II Peptides and Methods of Use
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/566,190
; FILING DATE: 1-DEC-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: YU116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-566-190-20
```

Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
 |||||  
 Db 1 DYKDDDK 8

## RESULT 70

US-09-110-618-5  
 ; Sequence 5, Application US/09110618  
 ; Patent No. 6090918  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Parnet, Patricia et al.  
 ; TITLE OF INVENTION: Receptor Designated 2P1  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation  
 ; STREET: 51 University Street  
 ; CITY: Seattle  
 ; STATE: WA  
 ; COUNTRY: USA  
 ; ZIP: 98101  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: Apple Macintosh  
 ; OPERATING SYSTEM: Apple 7.1  
 ; SOFTWARE: Microsoft Word, Version 5.1a  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/110,618  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/604,333  
 ; FILING DATE: 21-FEB-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Anderson, Kathryn A.  
 ; REGISTRATION NUMBER: 32,172  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206) 587-0430  
 ; TELEFAX: (206) 233-0644  
 ; TELEX: 756822  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 8 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; HYPOTHEICAL: NO  
 ; ANTI-SENSE: NO  
 ; IMMEDIATE SOURCE:  
 ; CLONE: FLAG peptide  
 ; US-09-110-618-5

Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
 |||||  
 Db 1 DYKDDDK 8

## RESULT 71

US-09-022-253-3  
 ; Sequence 3, Application US/09022253  
 ; Patent No. 6096305  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yao, Zhengbin  
 ; APPLICANT: Spriggs, Melanie

APPLICANT: Fanslow, William  
 ; TITLE OF INVENTION: No. 6096305e1 Receptor That Binds IL-17  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Immunex Corporation  
 ; STREET: 51 University Street  
 ; CITY: Seattle  
 ; STATE: WA  
 ; COUNTRY: USA  
 ; ZIP: 98101

COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: Apple Power Macintosh  
 ; OPERATING SYSTEM: Apple Operating System 7.5.5  
 ; SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/022,253  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/620,694  
 ; FILING DATE: 21-MARCH-1996  
 ; APPLICATION NUMBER: USSN 08/538,765  
 ; FILING DATE: 7 AUGUST 1995  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: USSN 08/410,535  
 ; FILING DATE: 23 MARCH 1995  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Perkins, Patricia Anne  
 ; REGISTRATION NUMBER: 34,695  
 ; REFERENCE/DOCKET NUMBER: 2617-B  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206) 587-0430  
 ; TELEFAX: (206)  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 8 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: No. 6096305 Relevant  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; IMMEDIATE SOURCE:  
 ; CLONE: FLAG\_peptide  
 ; US-09-022-253-3

Query Match 100.0%; Score 47; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
 |||||  
 Db 1 DYKDDDK 8

## RESULT 72

US-09-022-260-3  
 ; Sequence 3, Application US/09022260  
 ; Patent No. 6100235  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yao, Zhengbin  
 ; APPLICANT: Spriggs, Melanie  
 ; APPLICANT: Fanslow, William  
 ; TITLE OF INVENTION: No. 6100235e1 Receptor That Binds IL-17  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Immunex Corporation  
 ; STREET: 51 University Street  
 ; CITY: Seattle  
 ; STATE: WA  
 ; COUNTRY: USA  
 ; ZIP: 98101

```
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,260
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: FLAG_peptide
;
US-09-022-260-3
Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 73
US-09-020-222-8
; Sequence 8, Application US/090202222
; Patent No. 6111073
; GENERAL INFORMATION:
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage
; TITLE OF INVENTION: Furrow-Associated Proteins (PSTPIPS)
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,222
; FILING DATE: 06-Feb-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/798419
; FILING DATE: 02/07/1997
; ATTORNEY/AGENT INFORMATION:
```

```
NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1066r1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-09-020-222-8
Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 74
US-09-053-866-6
; Sequence 6, Application US/09053866
; Patent No. 6111075
; GENERAL INFORMATION:
; APPLICANT: Xu, Wenfeng
; APPLICANT: Presnell, Scott R.
; APPLICANT: Yee, David P.
; APPLICANT: Foster, Donald C.
; TITLE OF INVENTION: PROTEASE-ACTIVATED RECEPTOR
; TITLE OF INVENTION: PAR4 (ZCHEMR2)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/053,866
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Leith, Debra K
; REGISTRATION NUMBER: 32,619
; REFERENCE/DOCKET NUMBER: 98-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6674
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6111075e
;
US-09-053-866-6
Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 DYKDDDK 8  
| | | | |  
Db 1 DYKDDDK 8

## RESULT 75

US-08-816-346-50  
; Sequence 50, Application US/08816346  
; Patent No. 6127525  
; GENERAL INFORMATION:  
; APPLICANT: Crystal, Ronald G.  
; APPLICANT: Falck-Pedersen, Erik  
; APPLICANT: Gail, Jason  
; APPLICANT: Kovsed, Imre  
; APPLICANT: Wickham, Thomas J.  
; TITLE OF INVENTION: CHIMERIC ADENOVIIRAL COAT PROTEIN AND  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.  
; STREET: TWO PRUDENTIAL PLAZA - 4900  
; CITY: CHICAGO  
; STATE: ILLINOIS  
; COUNTRY: USA  
; ZIP: 60601-6780  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/816,346  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; REFERENCE/DOCKET NUMBER: 67167  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/616-5600  
; TELEFAX: 312/616-5700  
; TELEX: 25-3533  
; INFORMATION FOR SEQ ID NO: 50:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-816-346-50

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
| | | | |  
Db 1 DYKDDDK 8

RESULT 76  
US-09-071-710-40  
; Sequence 40, Application US/09071710  
; Patent No. 6130043  
; GENERAL INFORMATION:  
; APPLICANT: BILLING-MEDEL, PATRICIA  
; APPLICANT: COHEN, MAURICE  
; APPLICANT: COLPITS, TRACEY L.  
; APPLICANT: FRIEDMAN, PAULA N.  
; APPLICANT: GORDON, JULIAN  
; APPLICANT: GRANADOS, EDWARD N.  
; APPLICANT: HODGES, STEVEN C.  
; APPLICANT: KLAS, MICHAEL R.  
; APPLICANT: KRATOCHVIL, JON D.  
; APPLICANT: ROBERTS-RAVP, LISA

APPLICANT: RUSSELL, JOHN C.  
APPLICANT: STROUPE, STEPHEN D.  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
FOR DETECTING DISEASES OF THE PROSTATE  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/071,710  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/850,713  
FILING DATE: 02-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6083.US.P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6130043e  
US-09-071-710-40

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
| | | | |  
Db 1 DYKDDDK 8

RESULT 77  
US-08-888-429A-16  
; Sequence 16, Application US/08888429A  
; Patent No. 6136596  
; GENERAL INFORMATION:  
; APPLICANT: Davys, Roger J.  
; APPLICANT: Whitmarsh, Alan  
; APPLICANT: Tounier, Cathy  
; TITLE OF INVENTION: CYTOKINE-, STRESS-, AND ONCOPROTEIN-  
; TITLE OF INVENTION: ACTIVATED HUMAN PROTEIN KINASE KINASES  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/888,429A  
FILING DATE: 07-JUL-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/530,950  
FILING DATE: 19-SEP-1995  
APPLICATION NUMBER: 08/446,083  
FILING DATE: 19-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Fasse, Peter J.  
REGISTRATION NUMBER: 32,983  
REFERENCE/DOCKET NUMBER: 07917/053001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 299354  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-888-429A-16

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 78  
US-09-432-335-6  
Sequence 6, Application US/09432335  
Patent No. 6143720  
GENERAL INFORMATION:  
APPLICANT: Conklin, Darrell C.  
TITLE OF INVENTION: LIPOCALIN HOMOLOG  
FILE REFERENCE: 97-24  
CURRENT APPLICATION NUMBER: US/09/432,335  
CURRENT FILING DATE: 1999-11-02  
EARLIER APPLICATION NUMBER: 09/130,663  
EARLIER FILING DATE: 1998-08-06  
EARLIER APPLICATION NUMBER: 60/054,867  
EARLIER FILING DATE: 1997-08-06  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 6  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Flag affinity peptide  
US-09-432-335-6

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 79  
US-09-079-785-15  
Sequence 15, Application US/09079785  
Patent No. 6143869  
GENERAL INFORMATION:  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Smith, Craig A.

APPLICANT: Armilage, Richard J.  
APPLICANT: Gruss, Hans-Jürgen  
TITLE OF INVENTION: No. 6143869e1 Cytokine That Binds CD30  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,785  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/225,989  
FILING DATE: 12 APRIL 1994  
APPLICATION NUMBER: US 07/966,775  
FILING DATE: 27-OCT-1992  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 907,224  
FILING DATE: 01-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,660  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 892,459  
FILING DATE: 02-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 889,717  
FILING DATE: 26-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2804-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
CLONE: FLAG peptide  
US-09-079-785-15

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 80  
US-09-031-168-1  
Sequence 1, Application US/09031168  
Patent No. 6150583  
GENERAL INFORMATION:  
APPLICANT: Stanley B. Prusiner  
APPLICANT: Glenn C. Telling



APPLICANT: Fred E. Cohen  
APPLICANT: Michael R. Scott  
TITLE OF INVENTION: TRANSGENIC ANIMALS EXPRESSING  
TITLE OF INVENTION: EPITOPE-TAGGED PROTEINS  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 2200 Sand Hill Road, Suite 100  
City: Menlo Park  
STATE: California  
COUNTRY: USA  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/031,168  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/660,626  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Valeta Gregg  
REGISTRATION NUMBER: 35,127  
REFERENCE/DOCKET NUMBER: 07532/003001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 322-5070  
TELEFAX: (415) 854-0875  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-031-168-1

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 56+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
DB 1 DYKDDDDK 8

RESULT 81  
US-09-335-411-50  
Sequence 50, Application US/09335411  
Patent No. 6153435  
GENERAL INFORMATION:  
APPLICANT: Crystal, Ronald G.  
APPLICANT: Falck-Pedersen, Erik  
APPLICANT: Gall, Jason  
APPLICANT: Kovacs, Imre  
APPLICANT: Wickham, Thomas J.  
TITLE OF INVENTION: CHIMERIC ADENOVIRAL COAT PROTEIN AND  
TITLE OF INVENTION: METHODS OF USING SAME  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LEYDIG, VOIT & MAVER, LTD.  
STREET: TWO PRUDENTIAL PLAZA - 4900  
CITY: CHICAGO  
STATE: ILLINOIS  
COUNTRY: USA  
ZIP: 60601-6780  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/335,411  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/816,346  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
REFERENCE/DOCKET NUMBER: 67167  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/616-5600  
TELEFAX: 312/616-5700  
TELEX: 25-3533  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-335-411-50

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 56+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
DB 1 DYKDDDDK 8

RESULT 82  
US-08-883-086-5  
Sequence 5, Application US/08883086  
Patent No. 6171787  
GENERAL INFORMATION:  
APPLICANT: WILEY, STEVEN  
TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL  
TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
City: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/883,086  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Porembski, Priscilla E.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 6134.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847-937-0378  
TELEFAX: 847-938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6171787e

US-08-883-086-5

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8  
1 DYKDDDDK 8

RESULT 83

US-08-912-276-24  
; Sequence 24, Application US/08912276  
; Patent No. 6183952  
; GENERAL INFORMATION:  
; APPLICANT: Billing-Medel, Patricia A.  
; APPLICANT: Cohen, Maurice  
; APPLICANT: Colpitts, Tracey L.  
; APPLICANT: Friedman, Paula N.  
; APPLICANT: Gordon, Julian  
; APPLICANT: Granados, Edward N.  
; APPLICANT: Hodges, Steven C.  
; APPLICANT: Klass, Michael R.  
; APPLICANT: Kratochvil, Jon D.  
; APPLICANT: Roberts-Rapp, Lisa  
; APPLICANT: Russell, John C.  
; APPLICANT: Scroupe, Steven D.  
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/912,276  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Becker, Cheryl L.  
; REGISTRATION NUMBER: 35,441  
; REFERENCE/DOCKET NUMBER: 5972.US.P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 847/935-1729  
; TELEFAX: 847/938-2623  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-08-912-276-24

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8  
1 DYKDDDDK 8

Db

RESULT 84  
US-09-046-158A-20  
; Sequence 20, Application US/09046158A  
; Patent No. 6187552  
; GENERAL INFORMATION:  
; APPLICANT: Roberts, Steven L.  
; APPLICANT: Kayes, Paul S.  
; TITLE OF INVENTION: METHOD FOR IDENTIFYING INHIBITORS OF  
; TITLE OF INVENTION: JAK2/CYTOKINE RECEPTOR BINDING  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pharmacia & Upjohn Co., Intellectual Property  
; STREET: 301 Henrietta Street  
; CITY: Kalamazoo  
; STATE: MI  
; COUNTRY: USA  
; ZIP: 49001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/046,158A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Darnley Jr., James D.  
; REGISTRATION NUMBER: 33,673  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 616/833-2210  
; TELEFAX: 616/833-8897  
; TELEX: 224401  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-09-046-158A-20

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8  
1 DYKDDDDK 8

Db

RESULT 85

US-09-022-259-3  
; Sequence 3, Application US/09022259  
; Patent No. 6191104  
; GENERAL INFORMATION:  
; APPLICANT: Yao, Zhengbin  
; APPLICANT: Spriggs, Melanie  
; APPLICANT: Fanslow, William  
; TITLE OF INVENTION: No. 6191104e1 Receptor That Binds IL-17  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

Qy 1 DYKDDDDK 8  
1 DYKDDDDK 8

Db

```
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,259
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US98/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 587-0430
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: FLAG_peptide
US-09-022-259-3
```

```
Query Match      100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 DYKDDDDK 8
Db      1 DYKDDDDK 8
```

```
RESULT 86
US-09-022-257-3
Sequence 3, Application US/09022257
Patent No. 6197525
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Sprigge, Melanie
APPLICANT: Farnlow, William
TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,257
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
GENERAL INFORMATION:
```

```
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 587-0430
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: FLAG_peptide
US-09-022-257-3
```

```
Query Match      100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 DYKDDDDK 8
Db      1 DYKDDDDK 8
```

```
RESULT 87
US-09-153-804-16
Sequence 16, Application US/09153804
Patent No. 6207380
GENERAL INFORMATION:
APPLICANT: Patricia Billing-Medel
APPLICANT: Maurice Cohen
APPLICANT: Paula N. Friedman
APPLICANT: Julian Gordon
APPLICANT: Steven C. Hodges
APPLICANT: Michael R. Klass
APPLICANT: Jon D. Kratochvil
APPLICANT: Eric Russell
APPLICANT: Stephen D. Stroupe
TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of the Urinar
FILE REFERENCE: 6180.US.01
CURRENT APPLICATION NUMBER: US/09/153,804
CURRENT FILING DATE: 1998-09-15
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PASCSEQ for Windows Version 3.0
SEQ ID NO 16
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Affinity purification system recognition site
US-09-153-804-16
```

```
Query Match      100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 DYKDDDDK 8
Db      1 DYKDDDDK 8
```

```
RESULT 88
US-09-105-343A-5
Sequence 5, Application US/09105343A
Patent No. 6207642
GENERAL INFORMATION:
```

APPLICANT: WILEY, S.R.  
TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL  
TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-6050  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FASTSEQ for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/105,343A  
FILING DATE: 12-FEB-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US98/02859  
FILING DATE: 12-FEB-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: BECKER, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6048.US.P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847-935-1729  
TELEFAX: 847-938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6207642e  
US-09-105-343A-5

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 89  
US-08-693-211-1  
Sequence 1, Application US/08693211  
Patent No. 6218516  
GENERAL INFORMATION:  
APPLICANT: Wilks, Andrew  
APPLICANT: Stacker, Steven  
APPLICANT: Oelrichs, Robert  
TITLE OF INVENTION: Antibodies Specific For the Extracellular Domain of NYK/PLK-1  
TITLE OF INVENTION: And uses Thereof  
FILE REFERENCE: LUD 5347  
CURRENT APPLICATION NUMBER: US/08/693,211  
CURRENT FILING DATE: 1996-09-30  
PRIOR APPLICATION NUMBER: PCT/US95/01727  
PRIOR FILING DATE: 1995-02-09  
PRIOR APPLICATION NUMBER: PM3793  
PRIOR FILING DATE: 1994-02-10  
NUMBER OF SEQ ID NOS: 3  
SEQ ID NO 1  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Mus musculus  
US-08-693-211-1

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 90  
US-08-944-483-75  
Sequence 75, Application US/08944483  
Patent No. 6232456  
GENERAL INFORMATION:  
APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: KLAAS, MICHAEL R.  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: STEWART, KENT D.  
APPLICANT: STROUPE, STEVEN D.  
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS  
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/944,483  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6183.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 75:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-944-483-75

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 91  
US-09-227-717-5  
Sequence 5, Application US/09227717

Patent No. 6239268  
GENERAL INFORMATION:  
APPLICANT: Lovenberg, Timothy W.  
APPLICANT: Oltendorf, Tilmann  
APPLICANT: Liaw, Chen W.  
APPLICANT: Cleveenger, William R.  
TITLE OF INVENTION: INTERLEUKIN-1 TYPE 3 RECEPTORS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/227,717  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/526,704  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: McMaster, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 690068.402C1  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3123836  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-09-227-717-5

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 92  
US-08-995-659-7  
Sequence 7, Application US/08995659  
Patent No. 6242213  
GENERAL INFORMATION:  
APPLICANT: Anderson, Dirk M.  
APPLICANT: Galibert, Laurent  
APPLICANT: Maraskovsky, Eugene  
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation, Law Department  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Power Macintosh 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/995,659  
FILING DATE: 22 DECEMBER 1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 60/064,671  
FILING DATE: 14 OCTOBER 1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/813,509  
FILING DATE: 07 MARCH 1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/772,330  
FILING DATE: 23 DECEMBER 1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2852-A  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
CLONE: FLAG\_peptide  
US-08-995-659-7

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 93  
US-09-525-397-40  
Sequence 40, Application US/09525397  
Patent No. 6252047  
GENERAL INFORMATION:  
APPLICANT: BILLING-MEDEL, PATRICIA  
APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GORDON, JULIAN  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: HODGES, STEVEN C.  
APPLICANT: KLASS, MICHAEL R.  
APPLICANT: KRATOCHVIL, JON D.  
APPLICANT: ROBERTS-RAPP, LISA  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: STROUPE, STEPHEN D.  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
FOR DETECTING DISEASES OF THE PROSTATE  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette

```
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/525,397
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/071,710
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6083.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6252047e
US-09-525-397-40
```

```
Query Match      100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYKDDDDK 8
        |||||
Db       1 DYKDDDDK 8
```

```
RESULT 94
US-09-320-774-3
Sequence 3, Application US/09320774
Patent No. 6265545
GENERAL INFORMATION:
APPLICANT: Jarvik, Jonathan W.
TITLE OF INVENTION: READING FRAME INDEPENDENT EPTOPE
TITLE OR INVENTION: TAGGING
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESS: Harris Brotman
STREET: 202 Coast Blvd., Suite 111
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/320,774
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/762,106
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brotman, Harris F.
REGISTRATION NUMBER: 35,461
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 654-2428
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
```

```
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-320-774-3
```

```
Query Match      100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYKDDDDK 8
        |||||
Db       1 DYKDDDDK 8
```

```
RESULT 95
US-09-215-649A-7
Sequence 7, Application US/09215649A
Patent No. 6271349
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Marakovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: FLAG
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
```

```
US-09-215-649A-7
```

```
Query Match      100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYKDDDDK 8
        |||||
Db       1 DYKDDDDK 8
```

RESULT 96  
US-09-053-941-1  
; Sequence 1, Application US/09053941  
; Patent No. 6271354  
; GENERAL INFORMATION:  
; APPLICANT: SRINIVASAN, ALGARSAMY  
; APPLICANT: KOPROWSKI, HILARY  
; TITLE OF INVENTION: CHIMERIC VIRAL PROTEINS  
; FILE REFERENCE: CHIMERIC VIRAL Proteins  
; CURRENT APPLICATION NUMBER: US/09/053,941  
; CURRENT FILING DATE: 1998-04-02  
; EARLIER APPLICATION NUMBER: 60/043,380  
; EARLIER FILING DATE: 1999-04-03  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: FLAG epitope  
US-09-053-941-1

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 97  
US-09-320-424-7  
; Sequence 7, Application US/09320424  
; Patent No. 6284236  
; GENERAL INFORMATION:  
; APPLICANT: Wiley, Steven R.  
; APPLICANT: Goodwin, Raymond G.  
; TITLE OF INVENTION: Cytokine that Induces Apoptosis  
; FILE REFERENCE: 2835-E  
; CURRENT APPLICATION NUMBER: US/09/320,424  
; CURRENT FILING DATE: 1999-05-26  
; EARLIER APPLICATION NUMBER: 09/190,046  
; EARLIER FILING DATE: 1998-11-10  
; EARLIER APPLICATION NUMBER: 09/048,641  
; EARLIER FILING DATE: 1998-03-26  
; EARLIER APPLICATION NUMBER: 08/670,354  
; EARLIER FILING DATE: 1996-06-25  
; EARLIER APPLICATION NUMBER: 08/548,368  
; EARLIER FILING DATE: 1995-11-01  
; EARLIER APPLICATION NUMBER: 08/496,632  
; EARLIER FILING DATE: 1995-06-29  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: synthetic  
US-09-320-424-7

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 98

US-09-214-278-25  
; Sequence 25, Application US/09214278  
; Patent No. 6291210  
; GENERAL INFORMATION:  
; APPLICANT: Sakano, Seiji  
; APPLICANT: Itoh, Akira  
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE  
; FILE REFERENCE: KP-8576  
; CURRENT APPLICATION NUMBER: US/09/214,278  
; CURRENT FILING DATE: 1999-01-26  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 25  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic amino acid  
US-09-214-278-25

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 99  
US-09-140-084-9  
; Sequence 9, Application US/09140084A  
; Patent No. 630065  
; GENERAL INFORMATION:  
; APPLICANT: Kieke, et al.  
; TITLE OF INVENTION: Yeast Cell Surface Display of Proteins and Uses Thereof  
; FILE REFERENCE: D6061CIP2  
; CURRENT APPLICATION NUMBER: US/09/140,084A  
; CURRENT FILING DATE: 1998-08-26  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism:Epitope Tag  
US-09-140-084-9

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 100  
US-09-382-950-6  
; Sequence 6, Application US/09382950  
; Patent No. 630337  
; GENERAL INFORMATION:  
; APPLICANT: Rothschild, Kenneth  
; APPLICANT: Gite, Sadanand  
; APPLICANT: Olejnik, Jerzy  
; TITLE OF INVENTION: N-Terminal and C-Terminal Markers in Nascent Proteins  
; FILE REFERENCE: AMBER-03879  
; CURRENT APPLICATION NUMBER: US/09/382,950  
; CURRENT FILING DATE: 1999-08-25  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6

```
;
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial/Unknown
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (..T)
; OTHER INFORMATION: Synthetic
US-09-382-950-6
```

```
Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 DYKDDDDK 8
Db 1 DYKDDDDK 8
```

```
Search completed: June 29, 2006, 11:42:03
Job time : 56 secs
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OM protein - protein search, using SW model

Run on: June 29, 2006, 11:52:37 ; Search time 184 Seconds  
(without alignments)  
20.140 Million cell updates/sec

Title: US-10-671-054-2

Perfect score: 47

Sequence: 1 DYKDDDK 8

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

1: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US07\_PUBCOMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US08\_PUBCOMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US09\_PUBCOMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US10\_PUBCOMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US10\_PUBCOMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	8	2	US-08-971-317A-9
2	47	100.0	8	2	US-08-926-626-12
3	47	100.0	8	3	US-09-728-401A-14
4	47	100.0	8	3	US-09-042-643-3
5	47	100.0	8	3	US-09-754-105-3
6	47	100.0	8	3	US-09-050-516-48
7	47	100.0	8	3	US-09-276-600-10
8	47	100.0	8	3	US-09-771-956-12
9	47	100.0	8	3	US-09-065-383-32
10	47	100.0	8	3	US-09-785-934-3
11	47	100.0	8	3	US-09-835-147-10
12	47	100.0	8	3	US-09-760-008A-14
13	47	100.0	8	3	US-09-728-911-11
14	47	100.0	8	3	US-09-813-329-65
15	47	100.0	8	3	US-09-099-823-26
16	47	100.0	8	3	US-09-790-264-68
17	47	100.0	8	3	US-09-809-517A-8
18	47	100.0	8	3	US-09-234-717-24
19	47	100.0	8	3	US-09-850-178-18
20	47	100.0	8	3	US-09-193-538-22
21	47	100.0	8	3	US-09-250-883-22
22	47	100.0	8	3	US-09-735-368-4
23	47	100.0	8	3	US-09-096-259-32
24	47	100.0	8	3	US-09-215-652-47
25	47	100.0	8	3	US-09-970-308-1
26	47	100.0	8	3	US-09-309-668A-1
27	47	100.0	8	3	US-09-855-722-25

28	47	100.0	8	3	US-09-817-413-1	Sequence 1, Appli
29	47	100.0	8	3	US-09-193-663-9	Sequence 9, Appli
30	47	100.0	8	3	US-09-887-855-7	Sequence 7, Appli
31	47	100.0	8	3	US-09-904-245-3	Sequence 3, Appli
32	47	100.0	8	3	US-09-245-603A-15	Sequence 15, Appli
33	47	100.0	8	3	US-09-837-992-45	Sequence 45, Appli
34	47	100.0	8	3	US-09-923-995-6	Sequence 6, Appli
35	47	100.0	8	3	US-09-871-856-7	Sequence 7, Appli
36	47	100.0	8	3	US-09-841-994-0	Sequence 40, Appli
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38	47	100.0	8	3	US-09-065-902-15	Sequence 15, Appli
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41	47	100.0	8	3	US-09-193-881-28	Sequence 28, Appli
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46	47	100.0	8	3	US-09-859-604-7	Sequence 7, Appli
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55	47	100.0	8	3	US-09-995-193A-13	Sequence 13, Appli
56	47	100.0	8	3	US-09-900-530A-13	Sequence 13, Appli
57	47	100.0	8	3	US-09-923-246-37	Sequence 37, Appli
58	47	100.0	8	3	US-09-973-145-6	Sequence 6, Appli
59	47	100.0	8	3	US-09-825-661A-23	Sequence 23, Appli
60	47	100.0	8	3	US-09-049-695A-21	Sequence 21, Appli
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62	47	100.0	8	3	US-09-903-023-7	Sequence 7, Appli
63	47	100.0	8	3	US-09-852-391-3	Sequence 3, Appli
64	47	100.0	8	3	US-09-931-087A-19	Sequence 19, Appli
65	47	100.0	8	3	US-09-263-959-985	Sequence 985, App
66	47	100.0	8	3	US-09-969-192-2	Sequence 2, Appli
67	47	100.0	8	3	US-09-840-243B-20	Sequence 20, Appli
68	47	100.0	8	3	US-09-766-700A-8	Sequence 8, Appli
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71	47	100.0	8	3	US-09-858-332-12	Sequence 12, Appli
72	47	100.0	8	3	US-09-877-650-7	Sequence 7, Appli
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78	47	100.0	8	3	US-09-908-943A-186	Sequence 186, App
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84	47	100.0	8	3	US-09-846-033B-225	Sequence 225, App
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86	47	100.0	8	3	US-09-989-981A-12	Sequence 12, Appli
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90	47	100.0	8	3	US-09-880-748-3238	Sequence 3238, Ap
91	47	100.0	8	3	US-09-904-196B-14	Sequence 14, Appli
92	47	100.0	8	3	US-09-972-473-19	Sequence 19, Appli
93	47	100.0	8	3	US-09-922-226-39	Sequence 39, Appli
94	47	100.0	8	3	US-09-774-381-21	Sequence 21, Appli
95	47	100.0	8	3	US-09-876-790-11	Sequence 11, Appli
96	47	100.0	8	3	US-09-932-613-183	Sequence 183, App
97	47	100.0	8	3	US-09-782-587B-18	Sequence 18, Appli
98	47	100.0	8	3	US-09-892-949-35	Sequence 35, Appli
99	47	100.0	8	3	US-09-994-487-2	Sequence 2, Appli
100	47	100.0	8	3	US-09-803-472-5	Sequence 5, Appli

101	47	100.0	8	3	US-09-935-061-1	Sequence 1, Appl1	174	47	100.0	8	4	US-10-120-604-22	Sequence 22, Appl1
102	47	100.0	8	3	US-09-834-597-33	Sequence 33, Appl1	175	47	100.0	8	4	US-10-104-919-11	Sequence 11, Appl1
103	47	100.0	8	3	US-09-991-225-28	Sequence 28, Appl1	176	47	100.0	8	4	US-10-002-292A-10	Sequence 10, Appl1
104	47	100.0	8	3	US-09-925-055D-5	Sequence 5, Appl1	177	47	100.0	8	4	US-10-156-733-12	Sequence 12, Appl1
105	47	100.0	8	3	US-09-870-353A-31	Sequence 31, Appl1	178	47	100.0	8	4	US-10-263-677-21	Sequence 21, Appl1
106	47	100.0	8	3	US-09-870-933-7	Sequence 7, Appl1	179	47	100.0	8	4	US-10-067-649-28	Sequence 28, Appl1
107	47	100.0	8	3	US-09-746-375-15	Sequence 15, Appl1	180	47	100.0	8	4	US-10-127-816-42	Sequence 42, Appl1
108	47	100.0	8	3	US-09-861-012-15	Sequence 15, Appl1	181	47	100.0	8	4	US-10-269-353-68	Sequence 68, Appl1
109	47	100.0	8	3	US-09-932-322-183	Sequence 183, App	182	47	100.0	8	4	US-10-211-088-288	Sequence 288, App
110	47	100.0	8	3	US-09-962-736-1547	Sequence 1547, Ap	183	47	100.0	8	4	US-10-299-327-3	Sequence 3, Appl1
111	47	100.0	8	3	US-09-962-756-1779	Sequence 1779, Ap	184	47	100.0	8	4	US-10-128-599-74	Sequence 74, Appl1
112	47	100.0	8	3	US-09-080-140-30	Sequence 30, Appl1	185	47	100.0	8	4	US-10-313-135-7	Sequence 7, Appl1
113	47	100.0	8	3	US-09-897-787-8	Sequence 8, Appl1	186	47	100.0	8	4	US-10-133-797-28	Sequence 28, Appl1
114	47	100.0	8	3	US-09-972-473-19	Sequence 19, Appl1	187	47	100.0	8	4	US-10-005-956-553	Sequence 553, App
115	47	100.0	8	3	US-09-789-210-75	Sequence 75, Appl1	188	47	100.0	8	4	US-10-071-458-15	Sequence 15, Appl1
116	47	100.0	8	3	US-09-813-197-7	Sequence 7, Appl1	189	47	100.0	8	4	US-10-116-519-47	Sequence 47, Appl1
117	47	100.0	8	4	US-10-000-628-10	Sequence 10, Appl1	190	47	100.0	8	4	US-10-309-515-4	Sequence 4, Appl1
118	47	100.0	8	4	US-10-036-568-6	Sequence 6, Appl1	191	47	100.0	8	4	US-10-192-294-14	Sequence 14, Appl1
119	47	100.0	8	4	US-10-115-178-14	Sequence 14, Appl1	192	47	100.0	8	4	US-10-295-723-37	Sequence 37, Appl1
120	47	100.0	8	4	US-10-025-167-50	Sequence 50, Appl1	193	47	100.0	8	4	US-10-137-953-16	Sequence 16, Appl1
121	47	100.0	8	4	US-10-003-496-15	Sequence 15, Appl1	194	47	100.0	8	4	US-10-338-395-28	Sequence 28, Appl1
122	47	100.0	8	4	US-10-157-447-5	Sequence 5, Appl1	195	47	100.0	8	4	US-10-195-707B-40	Sequence 40, Appl1
123	47	100.0	8	4	US-10-035-451A-1	Sequence 1, Appl1	196	47	100.0	8	4	US-10-293-086-142	Sequence 142, App
124	47	100.0	8	4	US-10-158-895-5	Sequence 5, Appl1	197	47	100.0	8	4	US-10-173-461-26	Sequence 26, Appl1
125	47	100.0	8	4	US-10-029-009-1	Sequence 1, Appl1	198	47	100.0	8	4	US-10-032-214-236	Sequence 236, App
126	47	100.0	8	4	US-10-029-009-29	Sequence 29, Appl1	199	47	100.0	8	4	US-10-158-825-147	Sequence 147, App
127	47	100.0	8	4	US-10-082-659-15	Sequence 15, Appl1	200	47	100.0	8	4	US-10-187-049-6	Sequence 6, Appl1
128	47	100.0	8	4	US-10-086-135-6	Sequence 6, Appl1	201	47	100.0	8	4	US-10-284-400-18	Sequence 18, Appl1
129	47	100.0	8	4	US-10-808-357-8	Sequence 8, Appl1	202	47	100.0	8	4	US-10-028-083-12	Sequence 12, Appl1
130	47	100.0	8	4	US-10-116-273-40	Sequence 40, Appl1	203	47	100.0	8	4	US-10-028-374-16	Sequence 16, Appl1
131	47	100.0	8	4	US-10-076-248-1	Sequence 1, Appl1	204	47	100.0	8	4	US-10-200-244-25	Sequence 25, Appl1
132	47	100.0	8	4	US-10-216-408-26	Sequence 26, Appl1	205	47	100.0	8	4	US-10-153-234-261	Sequence 261, App
133	47	100.0	8	4	US-10-029-347-27	Sequence 27, Appl1	206	47	100.0	8	4	US-10-265-071-20	Sequence 20, Appl1
134	47	100.0	8	4	US-10-006-069A-225	Sequence 225, App	207	47	100.0	8	4	US-10-256-705-14	Sequence 14, Appl1
135	47	100.0	8	4	US-10-219-248-25	Sequence 25, Appl1	208	47	100.0	8	4	US-10-342-103-7	Sequence 7, Appl1
136	47	100.0	8	4	US-10-133-205-1	Sequence 1, Appl1	209	47	100.0	8	4	US-10-243-072-49	Sequence 49, Appl1
137	47	100.0	8	4	US-10-059-720-50	Sequence 50, Appl1	210	47	100.0	8	4	US-10-291-990-14	Sequence 14, Appl1
138	47	100.0	8	4	US-10-139-662-39	Sequence 39, Appl1	211	47	100.0	8	4	US-10-345-618-9	Sequence 9, Appl1
139	47	100.0	8	4	US-10-077-023-94	Sequence 94, Appl1	212	47	100.0	8	4	US-10-025-966A-70	Sequence 20, Appl1
140	47	100.0	8	4	US-10-075-846-36	Sequence 36, Appl1	213	47	100.0	8	4	US-10-128-587A-74	Sequence 74, Appl1
141	47	100.0	8	4	US-10-040-805-7	Sequence 7, Appl1	214	47	100.0	8	4	US-10-199-869-35	Sequence 35, Appl1
142	47	100.0	8	4	US-10-219-247-25	Sequence 25, Appl1	215	47	100.0	8	4	US-10-268-336-7	Sequence 7, Appl1
143	47	100.0	8	4	US-10-056-884-26	Sequence 26, Appl1	216	47	100.0	8	4	US-10-234-816-69	Sequence 69, Appl1
144	47	100.0	8	4	US-10-080-980-22	Sequence 22, Appl1	217	47	100.0	8	4	US-10-305-555-40	Sequence 40, Appl1
145	47	100.0	8	4	US-10-158-238-5	Sequence 5, Appl1	218	47	100.0	8	4	US-10-010-568-15	Sequence 15, Appl1
146	47	100.0	8	4	US-10-071-838-14	Sequence 14, Appl1	219	47	100.0	8	4	US-10-318-966-14	Sequence 14, Appl1
147	47	100.0	8	4	US-10-191-029-11	Sequence 11, Appl1	220	47	100.0	8	4	US-10-162-497-50	Sequence 50, Appl1
148	47	100.0	8	4	US-10-084-826-14	Sequence 14, Appl1	221	47	100.0	8	4	US-10-327-620-5	Sequence 5, Appl1
149	47	100.0	8	4	US-10-241-476-26	Sequence 26, Appl1	222	47	100.0	8	4	US-10-210-152-251	Sequence 251, App
150	47	100.0	8	4	US-10-270-877-32	Sequence 32, Appl1	223	47	100.0	8	4	US-10-384-743-5	Sequence 5, Appl1
151	47	100.0	8	4	US-10-230-875-5	Sequence 5, Appl1	224	47	100.0	8	4	US-10-372-874-21	Sequence 21, Appl1
152	47	100.0	8	4	US-10-185-425-12	Sequence 12, Appl1	225	47	100.0	8	4	US-10-372-874-21	Sequence 21, Appl1
153	47	100.0	8	4	US-10-270-837-32	Sequence 32, Appl1	226	47	100.0	8	4	US-10-005-966A-1	Sequence 1, Appl1
154	47	100.0	8	4	US-10-086-156-22	Sequence 22, Appl1	227	47	100.0	8	4	US-10-185-567-24	Sequence 24, Appl1
155	47	100.0	8	4	US-10-151-882-48	Sequence 48, Appl1	228	47	100.0	8	4	US-10-191-252-12	Sequence 12, Appl1
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157	47	100.0	8	4	US-10-139-683-39	Sequence 39, Appl1	230	47	100.0	8	4	US-10-190-414-21	Sequence 21, Appl1
158	47	100.0	8	4	US-10-092-771-34	Sequence 34, Appl1	231	47	100.0	8	4	US-10-143-618-29	Sequence 29, Appl1
159	47	100.0	8	4	US-10-222-334-73	Sequence 73, Appl1	232	47	100.0	8	4	US-10-166-098-17	Sequence 17, Appl1
160	47	100.0	8	4	US-10-112-788-13	Sequence 13, Appl1	233	47	100.0	8	4	US-10-126-764-4	Sequence 4, Appl1
161	47	100.0	8	4	US-10-090-365-11	Sequence 11, Appl1	234	47	100.0	8	4	US-10-084-706-54	Sequence 54, Appl1
162	47	100.0	8	4	US-10-040-862-10467	Sequence 10467, A	235	47	100.0	8	4	US-10-390-045-4	Sequence 4, Appl1
163	47	100.0	8	4	US-10-378-547-48	Sequence 48, Appl1	236	47	100.0	8	4	US-10-406-209-28	Sequence 28, Appl1
164	47	100.0	8	4	US-10-252-408-28	Sequence 28, Appl1	237	47	100.0	8	4	US-10-408-930-27	Sequence 27, Appl1
165	47	100.0	8	4	US-10-067-443-26	Sequence 26, Appl1	238	47	100.0	8	4	US-10-325-720-44	Sequence 44, Appl1
166	47	100.0	8	4	US-10-177-661-5	Sequence 5, Appl1	239	47	100.0	8	4	US-10-351-189-44	Sequence 44, Appl1
167	47	100.0	8	4	US-10-188-343-4	Sequence 4, Appl1	240	47	100.0	8	4	US-10-424-409-1	Sequence 1, Appl1
168	47	100.0	8	4	US-10-028-392-12	Sequence 12, Appl1	241	47	100.0	8	4	US-10-308-373-5	Sequence 5, Appl1
169	47	100.0	8	4	US-10-164-080-3	Sequence 3, Appl1	242	47	100.0	8	4	US-10-336-608-1	Sequence 1, Appl1
170	47	100.0	8	4	US-10-158-847-147	Sequence 147, App	243	47	100.0	8	4	US-10-414-186-49	Sequence 49, Appl1
171	47	100.0	8	4	US-10-104-943-34	Sequence 34, Appl1	244	47	100.0	8	4	US-10-405-878-7	Sequence 7, Appl1
172	47	100.0	8	4	US-10-174-368A-6	Sequence 6, Appl1	245	47	100.0	8	4	US-10-155-693-36	Sequence 36, Appl1
173	47	100.0	8	4	US-10-100-957A-36	Sequence 36, Appl1	246	47	100.0	8	4	US-10-325-717-77	Sequence 77, Appl1

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248	47	100.0	8	4	US-10-188-608-13	Sequence 13, Appl	321	47	100.0	8	4	US-10-019-065A-4	Sequence 4, Appl
249	47	100.0	8	4	US-10-183-770-16	Sequence 16, Appl	322	47	100.0	8	4	US-10-688-100-2	Sequence 2, Appl
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251	47	100.0	8	4	US-10-100-217-5	Sequence 5, Appl	324	47	100.0	8	4	US-10-431-096-122	Sequence 122, App
252	47	100.0	8	4	US-10-264-171-7	Sequence 7, Appl	325	47	100.0	8	4	US-10-399-518-135	Sequence 135, App
253	47	100.0	8	4	US-10-271-078-51	Sequence 51, Appl	326	47	100.0	8	4	US-10-399-518-142	Sequence 142, App
254	47	100.0	8	4	US-10-222-026A-39	Sequence 39, Appl	327	47	100.0	8	4	US-10-434-479-4	Sequence 4, Appl
255	47	100.0	8	4	US-10-203-531-9	Sequence 9, Appl	328	47	100.0	8	4	US-10-616-897-24	Sequence 24, Appl
256	47	100.0	8	4	US-10-264-127-7	Sequence 7, Appl	329	47	100.0	8	4	US-10-621-788A-37	Sequence 37, Appl
257	47	100.0	8	4	US-10-062-923-19	Sequence 19, Appl	330	47	100.0	8	4	US-10-343-663A-39	Sequence 39, Appl
258	47	100.0	8	4	US-10-193-477-117	Sequence 117, App	331	47	100.0	8	4	US-10-275-319A-8	Sequence 8, Appl
259	47	100.0	8	4	US-10-293-693-28	Sequence 28, Appl	332	47	100.0	8	4	US-10-659-684-37	Sequence 37, Appl
260	47	100.0	8	4	US-10-427-208-73	Sequence 73, Appl	333	47	100.0	8	4	US-10-763-992-34	Sequence 34, Appl
261	47	100.0	8	4	US-10-245-227B-9	Sequence 9, Appl	334	47	100.0	8	4	US-10-158-825-147	Sequence 147, App
262	47	100.0	8	4	US-10-350-516-30	Sequence 30, Appl	335	47	100.0	8	4	US-10-363-145A-13	Sequence 13, Appl
263	47	100.0	8	4	US-10-279-687-9	Sequence 9, Appl	336	47	100.0	8	4	US-10-742-161-3	Sequence 3, Appl
264	47	100.0	8	4	US-10-438-537-10	Sequence 10, Appl	337	47	100.0	8	4	US-10-276-272A-1	Sequence 1, Appl
265	47	100.0	8	4	US-10-351-157-36	Sequence 36, Appl	338	47	100.0	8	4	US-10-763-992-34	Sequence 34, Appl
266	47	100.0	8	4	US-10-372-003A-50	Sequence 50, Appl	339	47	100.0	8	4	US-10-456-153A-3	Sequence 3, Appl
267	47	100.0	8	4	US-10-275-025-8	Sequence 8, Appl	340	47	100.0	8	4	US-10-663-008A-37	Sequence 37, Appl
268	47	100.0	8	4	US-10-412-897-73	Sequence 73, Appl	341	47	100.0	8	4	US-10-612-410-16	Sequence 16, Appl
269	47	100.0	8	4	US-10-273-180-26	Sequence 26, Appl	342	47	100.0	8	4	US-10-467-243-3	Sequence 3, Appl
270	47	100.0	8	4	US-10-388-215-35	Sequence 35, Appl	343	47	100.0	8	4	US-10-451-947A-10	Sequence 10, Appl
271	47	100.0	8	4	US-10-293-418-3238	Sequence 3238, Ap	344	47	100.0	8	4	US-10-646-301A-37	Sequence 37, Appl
272	47	100.0	8	4	US-10-369-405-28	Sequence 28, Appl	345	47	100.0	8	4	US-10-745-034-29	Sequence 29, Appl
273	47	100.0	8	4	US-10-405-793-251	Sequence 251, App	346	47	100.0	8	4	US-10-769-131-12	Sequence 12, Appl
274	47	100.0	8	4	US-10-375-157-15	Sequence 15, Appl	347	47	100.0	8	4	US-10-772-331-35	Sequence 35, Appl
275	47	100.0	8	4	US-10-126-103-122	Sequence 122, App	348	47	100.0	8	4	US-10-656-441-2	Sequence 2, Appl
276	47	100.0	8	4	US-10-352-554-36	Sequence 36, Appl	349	47	100.0	8	4	US-10-684-332-55	Sequence 55, Appl
277	47	100.0	8	4	US-10-175-689-33	Sequence 33, Appl	350	47	100.0	8	4	US-10-738-454-9	Sequence 9, Appl
278	47	100.0	8	4	US-10-253-471-1547	Sequence 1547, Ap	351	47	100.0	8	4	US-10-154-670-3	Sequence 3, Appl
279	47	100.0	8	4	US-10-253-471-1779	Sequence 1779, Ap	352	47	100.0	8	4	US-10-806-294-15	Sequence 15, Appl
280	47	100.0	8	4	US-10-366-630-5	Sequence 5, Appl	353	47	100.0	8	4	US-10-615-659-61	Sequence 61, Appl
281	47	100.0	8	4	US-10-277-216-33	Sequence 33, Appl	354	47	100.0	8	4	US-10-692-071-1	Sequence 1, Appl
282	47	100.0	8	4	US-10-154-884B-11290	Sequence 11290, A	355	47	100.0	8	4	US-10-671-054-2	Sequence 2, Appl
283	47	100.0	8	4	US-10-200-242-25	Sequence 25, Appl	356	47	100.0	8	4	US-10-736-769-37	Sequence 37, Appl
284	47	100.0	8	4	US-10-602-350-5	Sequence 5, Appl	357	47	100.0	8	4	US-10-635-977-61	Sequence 61, Appl
285	47	100.0	8	4	US-10-204-581-11	Sequence 11, Appl	358	47	100.0	8	4	US-10-472-724-21	Sequence 21, Appl
286	47	100.0	8	4	US-10-609-296-54	Sequence 54, Appl	359	47	100.0	8	4	US-10-156-708-4	Sequence 4, Appl
287	47	100.0	8	4	US-10-339-712-7	Sequence 7, Appl	360	47	100.0	8	4	US-10-635-977-61	Sequence 61, Appl
288	47	100.0	8	4	US-10-339-712-63	Sequence 63, Appl	361	47	100.0	8	4	US-10-472-724-21	Sequence 21, Appl
289	47	100.0	8	4	US-10-390-585-66	Sequence 66, Appl	362	47	100.0	8	4	US-10-764-324-10467	Sequence 10467, A
290	47	100.0	8	4	US-10-436-715-464	Sequence 464, App	363	47	100.0	8	4	US-10-629-313-50	Sequence 50, Appl
291	47	100.0	8	4	US-10-356-289-3	Sequence 3, Appl	364	47	100.0	8	4	US-10-098-935-7	Sequence 7, Appl
292	47	100.0	8	4	US-10-126-022-33	Sequence 33, Appl	365	47	100.0	8	4	US-10-762-588-10	Sequence 10, Appl
293	47	100.0	8	4	US-10-320-104B-3	Sequence 3, Appl	366	47	100.0	8	4	US-10-343-389A-10	Sequence 10, Appl
294	47	100.0	8	4	US-10-395-418-15	Sequence 15, Appl	367	47	100.0	8	4	US-10-744-379-3	Sequence 3, Appl
295	47	100.0	8	4	US-10-275-589-13	Sequence 13, Appl	368	47	100.0	8	4	US-10-821-583-31	Sequence 31, Appl
296	47	100.0	8	4	US-10-253-493-1547	Sequence 1547, Ap	369	47	100.0	8	4	US-10-828-817-1	Sequence 1, Appl
297	47	100.0	8	4	US-10-253-493-1779	Sequence 1779, Ap	370	47	100.0	8	4	US-10-843-189-3	Sequence 3, Appl
298	47	100.0	8	4	US-10-449-831A-162	Sequence 162, App	371	47	100.0	8	4	US-10-715-998-49	Sequence 49, Appl
299	47	100.0	8	4	US-10-460-524-15	Sequence 15, Appl	372	47	100.0	8	4	US-10-612-742-33	Sequence 33, Appl
300	47	100.0	8	4	US-10-403-847-122	Sequence 122, App	373	47	100.0	8	4	US-10-699-088-93	Sequence 93, Appl
301	47	100.0	8	4	US-10-308-847-122	Sequence 122, App	374	47	100.0	8	4	US-10-474-600-1	Sequence 1, Appl
302	47	100.0	8	4	US-10-308-128-162	Sequence 162, App	375	47	100.0	8	4	US-10-842-906-3	Sequence 3, Appl
303	47	100.0	8	4	US-10-223-560-7	Sequence 7, Appl	376	47	100.0	8	4	US-10-627-592-39	Sequence 39, Appl
304	47	100.0	8	4	US-10-664-456-28	Sequence 28, Appl	377	47	100.0	8	4	US-10-768-976-22	Sequence 22, Appl
305	47	100.0	8	4	US-10-646-873-48	Sequence 48, Appl	378	47	100.0	8	4	US-10-103-294A-1	Sequence 1, Appl
306	47	100.0	8	4	US-10-649-873-26	Sequence 26, Appl	379	47	100.0	8	4	US-10-475-538A-48	Sequence 48, Appl
307	47	100.0	8	4	US-10-380-880-2	Sequence 2, Appl	380	47	100.0	8	5	US-10-627-582-48	Sequence 48, Appl
308	47	100.0	8	4	US-10-651-722-26	Sequence 26, Appl	381	47	100.0	8	5	US-10-761-905-24	Sequence 24, Appl
309	47	100.0	8	4	US-10-351-891-93	Sequence 93, Appl	382	47	100.0	8	5	US-10-817-607-96	Sequence 96, Appl
310	47	100.0	8	4	US-10-401-053A-8	Sequence 8, Appl	383	47	100.0	8	5	US-10-871-776-12	Sequence 12, Appl
311	47	100.0	8	4	US-10-652-244-7	Sequence 7, Appl	384	47	100.0	8	5	US-10-872-161-58	Sequence 58, Appl
312	47	100.0	8	4	US-10-296-718-3	Sequence 3, Appl	385	47	100.0	8	5	US-10-872-161-58	Sequence 58, Appl
313	47	100.0	8	4	US-10-257-864A-106	Sequence 106, App	386	47	100.0	8	5	US-10-872-161-58	Sequence 58, Appl
314	47	100.0	8	4	US-10-315-379-20	Sequence 20, Appl	387	47	100.0	8	5	US-10-872-161-58	Sequence 58, Appl
315	47	100.0	8	4	US-10-252-155-605	Sequence 605, App	388	47	100.0	8	5	US-10-872-161-58	Sequence 58, Appl
316	47	100.0	8	4	US-10-380-614-12	Sequence 12, Appl	389	47	100.0	8	5	US-10-699-113-2	Sequence 23, Appl
317	47	100.0	8	4	US-10-448-525-36	Sequence 36, Appl	390	47	100.0	8	5	US-10-677-593-15	Sequence 15, Appl
318	47	100.0	8	4	US-10-444-795B-38	Sequence 38, Appl	391	47	100.0	8	5	US-10-491-277-12	Sequence 12, Appl
319	47	100.0	8	4	US-10-668-453-1	Sequence 1, Appl	392	47	100.0	8	5	US-10-801-487-186	Sequence 186, App

393	47	100.0	8	5	US-10-705-745-14	Sequence 14, Appl
394	47	100.0	8	5	US-10-399-585-134	Sequence 134, App
395	47	100.0	8	5	US-10-399-585-140	Sequence 140, App
396	47	100.0	8	5	US-10-478-058A-20	Sequence 20, Appl
397	47	100.0	8	5	US-10-781-564-11	Sequence 11, Appl
398	47	100.0	8	5	US-10-888-918-11	Sequence 11, Appl
399	47	100.0	8	5	US-10-831-622-101	Sequence 101, App
400	47	100.0	8	5	US-10-745-447-29	Sequence 29, Appl
401	47	100.0	8	5	US-10-857-664-5	Sequence 5, Appl
402	47	100.0	8	5	US-10-801-938-186	Sequence 186, App
403	47	100.0	8	5	US-10-801-509-186	Sequence 186, App
404	47	100.0	8	5	US-10-801-486-186	Sequence 186, App
405	47	100.0	8	5	US-10-645-085A-106	Sequence 106, App
406	47	100.0	8	5	US-10-837-776-1	Sequence 1, Appl
407	47	100.0	8	5	US-10-787-442-37	Sequence 37, Appl
408	47	100.0	8	5	US-10-882-761-27	Sequence 27, Appl
409	47	100.0	8	5	US-10-812-232-10	Sequence 10, Appl
410	47	100.0	8	5	US-10-841-798-9	Sequence 9, Appl
411	47	100.0	8	5	US-10-802-133-7	Sequence 7, Appl
412	47	100.0	8	5	US-10-494-248-4	Sequence 4, Appl
413	47	100.0	8	5	US-10-888-867-11	Sequence 11, Appl
414	47	100.0	8	5	US-10-888-779-11	Sequence 11, Appl
415	47	100.0	8	5	US-10-888-780-11	Sequence 11, Appl
416	47	100.0	8	5	US-10-863-931-11	Sequence 11, Appl
417	47	100.0	8	5	US-10-863-729-12	Sequence 12, Appl
418	47	100.0	8	5	US-10-926-217-21	Sequence 21, Appl
419	47	100.0	8	5	US-10-851-637-83	Sequence 83, Appl
420	47	100.0	8	5	US-10-900-926-68	Sequence 68, Appl
421	47	100.0	8	5	US-10-925-448-19	Sequence 19, Appl
422	47	100.0	8	5	US-10-926-225-12	Sequence 12, Appl
423	47	100.0	8	5	US-10-858-367-18	Sequence 18, Appl
424	47	100.0	8	5	US-10-857-644-27	Sequence 27, Appl
425	47	100.0	8	5	US-10-719-523-7	Sequence 7, Appl
426	47	100.0	8	5	US-10-835-096-16	Sequence 16, Appl
427	47	100.0	8	5	US-10-874-923-66	Sequence 66, Appl
428	47	100.0	8	5	US-10-634-645-10	Sequence 10, Appl
429	47	100.0	8	5	US-10-841-250-101	Sequence 101, App
430	47	100.0	8	5	US-10-311-144-2	Sequence 2, Appl
431	47	100.0	8	5	US-10-769-088-15	Sequence 15, Appl
432	47	100.0	8	5	US-10-888-805-71	Sequence 71, Appl
433	47	100.0	8	5	US-10-699-114-93	Sequence 93, Appl
434	47	100.0	8	5	US-10-864-249-49	Sequence 49, Appl
435	47	100.0	8	5	US-10-926-386-73	Sequence 73, Appl
436	47	100.0	8	5	US-10-738-780-22	Sequence 22, Appl
437	47	100.0	8	5	US-10-865-663-2	Sequence 2, Appl
438	47	100.0	8	5	US-10-497-003A-17	Sequence 17, Appl
439	47	100.0	8	5	US-10-658-752-8	Sequence 8, Appl
440	47	100.0	8	5	US-10-765-063-3	Sequence 3, Appl
441	47	100.0	8	5	US-10-487-132-10	Sequence 10, Appl
442	47	100.0	8	5	US-10-968-432-11	Sequence 11, Appl
443	47	100.0	8	5	US-10-935-290-39	Sequence 39, Appl
444	47	100.0	8	5	US-10-819-054-19	Sequence 19, Appl
445	47	100.0	8	5	US-10-949-685-4	Sequence 4, Appl
446	47	100.0	8	5	US-10-258-182A-7	Sequence 7, Appl
447	47	100.0	8	5	US-10-801-493-186	Sequence 186, App
448	47	100.0	8	5	US-10-955-218-21	Sequence 21, Appl
449	47	100.0	8	5	US-10-917-844-91	Sequence 91, Appl
450	47	100.0	8	5	US-10-508-309-1	Sequence 1, Appl
451	47	100.0	8	5	US-10-988-091-32	Sequence 32, Appl
452	47	100.0	8	5	US-10-931-916-71	Sequence 71, Appl
453	47	100.0	8	5	US-10-980-669-9	Sequence 9, Appl
454	47	100.0	8	5	US-10-488-806-9	Sequence 9, Appl
455	47	100.0	8	5	US-10-918-685A-7	Sequence 7, Appl
456	47	100.0	8	5	US-10-922-339-39	Sequence 39, Appl
457	47	100.0	8	5	US-10-029-345A-75	Sequence 75, Appl
458	47	100.0	8	5	US-10-356-264A-22	Sequence 22, Appl
459	47	100.0	8	5	US-10-841-819B-22	Sequence 22, Appl
460	47	100.0	8	5	US-10-964-215-101	Sequence 101, App
461	47	100.0	8	5	US-10-957-433-4	Sequence 4, Appl
462	47	100.0	8	5	US-10-991-681-39	Sequence 39, Appl
463	47	100.0	8	5	US-10-479-901-296	Sequence 296, App
464	47	100.0	8	5	US-10-900-399-7	Sequence 7, Appl
465	47	100.0	8	5	US-10-764-212-80	Sequence 80, Appl

RESULT 1  
US-08-971-317A-9  
; Sequence 9, Application US/08971317A  
; Publication No. US20010010925A1  
; GENERAL INFORMATION:  
; APPLICANT: Wiley, Steven R.  
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USBS  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FASTSEQ for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/971,317A  
; FILING DATE: 17-NOV-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goller, Mimi C  
; REGISTRATION NUMBER: 39,046  
; REFERENCE/DOCKET NUMBER: 6255.US.01  
; TELECOMMUNICATION INFORMATION:

ALIGNMENTS

466	47	100.0	8	5	US-10-500-671A-18	Sequence 18, Appl
467	47	100.0	8	5	US-10-972-052-15	Sequence 15, Appl
468	47	100.0	8	5	US-10-507-421-28	Sequence 28, Appl
469	47	100.0	8	5	US-10-719-144-22	Sequence 22, Appl
470	47	100.0	8	5	US-10-790-273-3	Sequence 3, Appl
471	47	100.0	8	5	US-10-994-824-94	Sequence 94, Appl
472	47	100.0	8	5	US-10-994-987-21	Sequence 21, Appl
473	47	100.0	8	5	US-10-868-673-61	Sequence 61, Appl
474	47	100.0	8	5	US-10-981-998-11	Sequence 11, Appl
475	47	100.0	8	5	US-10-910-507-5	Sequence 5, Appl
476	47	100.0	8	5	US-10-982-555-35	Sequence 35, Appl
477	47	100.0	8	5	US-10-520-408-2	Sequence 2, Appl
478	47	100.0	8	5	US-10-482-803B-4	Sequence 4, Appl
479	47	100.0	8	5	US-10-997-078-81	Sequence 81, Appl
480	47	100.0	8	5	US-10-756-813-21	Sequence 21, Appl
481	47	100.0	8	5	US-10-800-248-56	Sequence 56, Appl
482	47	100.0	8	5	US-10-971-738-470	Sequence 470, App
483	47	100.0	8	5	US-10-484-271A-4	Sequence 4, Appl
484	47	100.0	8	5	US-10-990-276-7	Sequence 7, Appl
485	47	100.0	8	5	US-10-636-320-7	Sequence 7, Appl
486	47	100.0	8	5	US-10-966-483-52	Sequence 52, Appl
487	47	100.0	8	5	US-10-950-747-18	Sequence 18, Appl
488	47	100.0	8	5	US-10-983-120-20	Sequence 20, Appl
489	47	100.0	8	5	US-10-903-612B-121	Sequence 121, App
490	47	100.0	8	5	US-10-498-665-77	Sequence 77, Appl
491	47	100.0	8	5	US-10-993-568-6	Sequence 6, Appl
492	47	100.0	8	5	US-10-513-263-6	Sequence 6, Appl
493	47	100.0	8	5	US-10-381-094A-3	Sequence 3, Appl
494	47	100.0	8	5	US-10-237-813-43	Sequence 43, Appl
495	47	100.0	8	6	US-11-004-111-47	Sequence 47, Appl
496	47	100.0	8	6	US-11-004-461-14	Sequence 14, Appl
497	47	100.0	8	6	US-11-020-965-7	Sequence 7, Appl
498	47	100.0	8	6	US-11-045-944-11	Sequence 11, Appl
499	47	100.0	8	6	US-11-218-020-17	Sequence 17, Appl
500	47	100.0	8	6		

TELEPHONE: (847) 935-7550  
TELEFAX: (847) 938-2623  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. US20010010925A1e  
US-08-971-317A-9

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8  
Db 1 DYKDDDK 8

## RESULT 2

US-08-926-626-12  
Sequence 12, Application US/08926626  
Publication No. US20020035244A1

GENERAL INFORMATION:  
APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: KLASSEL, MICHAEL R.  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: STROUPE, STEVEN D.  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
TITLE OF INVENTION: FOR DETECTING DISEASE OF THE PROSTATE  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/926,626  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6158.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-926-626-12

Query Match 100.0%; Score 47; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8  
Db 1 DYKDDDK 8

## RESULT 3

US-09-728-401A-14  
Sequence 14, Application US/09728401A  
Publication No. US2001000075A1

GENERAL INFORMATION:  
APPLICANT: Pan, Yang  
TITLE OF INVENTION: NEURORACTIN AND USES THEREFOR  
FILE REFERENCE: MB1096-001CP2CN2M (formerly 07334-190003)  
CURRENT APPLICATION NUMBER: US/09/728,401A  
CURRENT FILING DATE: 2002-06-17  
PRIOR APPLICATION NUMBER: US 09/481,485  
PRIOR FILING DATE: 2000-01-11  
PRIOR APPLICATION NUMBER: US 08/991,426  
PRIOR FILING DATE: 1997-12-16  
PRIOR APPLICATION NUMBER: US 08/851,160  
PRIOR FILING DATE: 1997-05-05  
PRIOR APPLICATION NUMBER: US 08/643,798  
PRIOR FILING DATE: 1996-05-07  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 14  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-728-401A-14

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8  
Db 1 DYKDDDK 8

## RESULT 4

US-09-042-643-3  
Sequence 3, Application US/09042643  
Publication No. US20010008766A1

GENERAL INFORMATION:  
APPLICANT: DAUNERT, Sylvia  
APPLICANT: LEWIS, Jennifer C  
APPLICANT: HERNANDEZ, Emily  
TITLE OF INVENTION: QUANTITATIVE BINDING ASSAYS USING GREEN FLUORESCENT PROTEIN AS A  
FILE REFERENCE: 3798-0102P  
CURRENT APPLICATION NUMBER: US/09/042,643  
CURRENT FILING DATE: 1998-03-17  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Octapeptide fused to GFP  
US-09-042-643-3

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8  
Db 1 DYKDDDK 8

RESULT 5  
US-09-754-105-3  
Sequence 3, Application US/09754105  
Patent No. US20010009768A1  
GENERAL INFORMATION:  
APPLICANT: Cerretti, Douglas  
APPLICANT: Reddy, Pranhitha  
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING CYTOKINE DESIGNATED LERK-5  
FILE REFERENCE: 28332  
CURRENT APPLICATION NUMBER: US/09/754,105  
CURRENT FILING DATE: 2001-01-03  
PRIOR APPLICATION NUMBER: 09/329,531  
PRIOR FILING DATE: 1999-06-10  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 3  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Flag peptide  
NAME/KEY: Artificial  
LOCATION: (1)..(8)  
US-09-754-105-3

Query Match  
Best Local Similarity 100.0%; Score 47; DB 3; Length 8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 6  
US-09-050-516-48  
Sequence 48, Application US/09050516  
Patent No. US20010010904A1  
GENERAL INFORMATION:  
APPLICANT: BILLING-MEDEL, PATRICIA  
APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GORDON, JULIAN  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: HAYDEN, MARK  
APPLICANT: HODGES, STEVEN C.  
APPLICANT: KLAAS, MICHAEL R.  
APPLICANT: KRATOCHVIL, JON D.  
APPLICANT: ROBERTS-RAPP, LISA  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: STROUPE, STEPHEN D.  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL  
NUMBER OF SEQUENCES: 49  
NUMBER OF SEQUENCES: TRACT  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/050,516  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/828,855  
FILING DATE: 31-MAR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6065.US.P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-050-516-48

Query Match  
Best Local Similarity 100.0%; Score 47; DB 3; Length 8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 7  
US-09-276-600-10  
Sequence 10, Application US/09276600  
Patent No. US20010010908A1  
GENERAL INFORMATION:  
APPLICANT: Patricia Billing-Medel  
APPLICANT: Maurice Cohen  
APPLICANT: Tracey L. Colpitts  
APPLICANT: Julian Gordon  
APPLICANT: Edward N. Granados  
APPLICANT: John C. Russell  
APPLICANT: Stephen D. Stroupe  
TITLE OF INVENTION: Reagents and Methods Useful for  
TITLE OF INVENTION: Detecting Disease of the Prostate  
FILE REFERENCE: 6397.US.01  
CURRENT APPLICATION NUMBER: US/09/276,600  
CURRENT FILING DATE: 1999-03-25  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 10  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Affinity purification system recognition site  
US-09-276-600-10

Query Match  
Best Local Similarity 100.0%; Score 47; DB 3; Length 8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 8  
US-09-771-956-12  
Sequence 12, Application US/09771956  
Patent No. US20010031474A1  
GENERAL INFORMATION:  
APPLICANT: Bennett, Michele  
APPLICANT: Brobeck, Robbin  
APPLICANT: Krause, James  
TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors  
FILE REFERENCE: N2000.001

CURRENT APPLICATION NUMBER: US/09/771,956  
CURRENT FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 12  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: FLAG EPITOPE  
US-09-771-956-12

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
DB 1 DYKDDDK 8

## RESULT 9

US-09-065-383-32  
Sequence 32, Application US/09065383  
Publication No. US20010055758A1  
GENERAL INFORMATION:  
APPLICANT: BILLING-MEDEL, PATRICIA  
APPLICANT: COHEN, MAURICE  
APPLICANT: COLBITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GORDON, JULIAN  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: HODGES, STEVEN C.  
APPLICANT: KLAS, MICHAEL R.  
APPLICANT: KRATOCHVIL, JON D.  
APPLICANT: ROBERTS-RAPP, LISA  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: STROUPE, STEPHEN D.  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/065,383  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/842,385  
FILING DATE: 23-APR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6084.US.PI  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-065-383-32

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
DB 1 DYKDDDK 8

## RESULT 10

US-09-785-934-3  
Sequence 3, Application US/09785934  
Patent No. US2002002132A1  
GENERAL INFORMATION:  
APPLICANT: Plueneke, John  
TITLE OF INVENTION: USE OF INTERLEUKIN-4 ANTAGONISTS AND COMPOSITIONS  
TITLE OF INVENTION: THEREOF  
FILE REFERENCE: 3005  
CURRENT APPLICATION NUMBER: US/09/785,934  
CURRENT FILING DATE: 2001-02-15  
PRIOR APPLICATION NUMBER: 09/579,808  
PRIOR FILING DATE: 2000-05-26  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: FLAG Peptide  
US-09-785-934-3

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
DB 1 DYKDDDK 8

## RESULT 11

US-09-835-147-10  
Sequence 10, Application US/09835147  
Patent No. US2002002277A1  
GENERAL INFORMATION:  
APPLICANT: Maliszewski, Charles R.  
APPLICANT: Gayle III, Richard B.  
APPLICANT: Price, Virginia L.  
APPLICANT: Gimpel, Steven D.  
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment  
FILE REFERENCE: 2879-US  
CURRENT APPLICATION NUMBER: US/09/835,147  
CURRENT FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: US 60/104,585  
PRIOR FILING DATE: 1998-10-16  
PRIOR APPLICATION NUMBER: US 60/107,466  
PRIOR FILING DATE: 1998-11-06  
PRIOR APPLICATION NUMBER: US 60/149,010  
PRIOR FILING DATE: 1999-08-13  
PRIOR APPLICATION NUMBER: PCT/US99/22955  
PRIOR FILING DATE: 1999-10-13  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
US-09-835-147-10

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
|||||  
Db 1 DYKDDDDK 8

RESULT 12  
US-09-760-008A-14  
Sequence 14, Application US/09760008A  
Patent No. US20020004483A1  
GENERAL INFORMATION:  
APPLICANT: NISSEN, TORBEN LAUESGAARD  
APPLICANT: ANDERSEN, KIM VILBOUR  
APPLICANT: HANSEN, CHRISTIAN KARSTEN  
APPLICANT: MIKKELSEN, JAN MOLLER  
TITLE OF INVENTION: G-CSF CONJUGATES  
FILE REFERENCE: 31-000700US  
CURRENT APPLICATION NUMBER: US/09/760,008A  
CURRENT FILING DATE: 2001-05-11  
PRIOR APPLICATION NUMBER: 60/176,376  
PRIOR FILING DATE: 2000-01-14  
PRIOR APPLICATION NUMBER: 60/189,506  
PRIOR FILING DATE: 2000-03-15  
PRIOR APPLICATION NUMBER: 60/215,644  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: DK PA 2000 00024  
PRIOR FILING DATE: 2000-01-10  
PRIOR APPLICATION NUMBER: DK PA 2000 00341  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: DK PA 2000 00943  
PRIOR FILING DATE: 2000-06-16  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 14  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-760-008A-14

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
|||||  
Db 1 DYKDDDDK 8

RESULT 13  
US-09-728-911-11  
Sequence 11, Application US/09728911  
Patent No. US20020012669A1  
GENERAL INFORMATION:  
APPLICANT: Presnell, Scott R.  
APPLICANT: Xu, Wenfeng  
APPLICANT: Kindsvogel, Wayne  
APPLICANT: Chen, Zhi  
TITLE OF INVENTION: Human Cytokine Receptor  
FILE REFERENCE: 99-93  
CURRENT APPLICATION NUMBER: US/09/728,911  
CURRENT FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: US 60/169,049  
PRIOR FILING DATE: 1999-12-03

PRIOR APPLICATION NUMBER: US 60/232,219  
PRIOR FILING DATE: 2000-09-13  
PRIOR APPLICATION NUMBER: US 60/244,610  
PRIOR FILING DATE: 2000-10-31  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 11  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: FLAG Tag amino acid sequence  
US-09-728-911-11

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
|||||  
Db 1 DYKDDDDK 8

RESULT 14  
US-09-813-329-65  
Sequence 65, Application US/09813329  
Patent No. US20020012968A1  
GENERAL INFORMATION:  
APPLICANT: Bristol-Myers Squibb Company  
TITLE OF INVENTION: No. US20020012968A1e1 Drosophila Tumor Necrosis Factor Class Molc  
FILE REFERENCE: D0016.np  
CURRENT APPLICATION NUMBER: US/09/813,329  
CURRENT FILING DATE: 2001-03-20  
PRIOR APPLICATION NUMBER: 60/190,816  
PRIOR FILING DATE: 2000-03-21  
NUMBER OF SEQ ID NOS: 65  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 65  
LENGTH: 8  
TYPE: PRT  
ORGANISM: bacteriophage T7  
US-09-813-329-65

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
|||||  
Db 1 DYKDDDDK 8

RESULT 15  
US-09-823-26  
Sequence 26, Application US/0909823  
Patent No. US20020018990A1  
GENERAL INFORMATION:  
APPLICANT: BILLING-MEDEL, PATRICIA  
APPLICANT: COHEN, MAURICE  
APPLICANT: COLLITS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GORDON, JULIAN  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: HODGES, STEVEN C.  
APPLICANT: KLAAS, MICHAEL R.  
APPLICANT: KRATOCHVIL, JON D.  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: SCHEFFEL, CHRISTI  
APPLICANT: STROUBE, STEPHEN D.  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR DETECTING DISEASES OF THE BREAST



```

;
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099,823
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/879,354
; FILING DATE: 20-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. US20020018990A1e
; US-09-099-823-26

Query Match      100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYKDDDDK 8
DB      1 DYKDDDDK 8

RESULT 16
US-09-790-264-68
; Sequence 68, Application US/09790264
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Goodearl, Andrew D.J.
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: 07334-322001
; CURRENT APPLICATION NUMBER: US/09/790,264
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 09/065,661
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/298,511
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 09/065,363
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/337,930
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: US 09/102,705
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: US 09/363,630
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 09/124,538
```

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;
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: flag epitope
; US-09-790-264-68

Query Match      100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYKDDDDK 8
DB      1 DYKDDDDK 8

RESULT 17
US-09-809-517A-8
; Sequence 8, Application US/09809517A
; Patent No. US2002003473A1
; GENERAL INFORMATION:
; APPLICANT: Lohning, Corinna
; TITLE OF INVENTION: Particles via disulfide bonds
; FILE REFERENCE: WO98/011
; CURRENT APPLICATION NUMBER: US/09/809,517A
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: EP 99114072.4
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: EP 00103551.8
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic module
; US-09-809-517A-8

Query Match      100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYKDDDDK 8
DB      1 DYKDDDDK 8

RESULT 18
US-09-234-717-24
; Sequence 24, Application US/09234717A
; Patent No. US20020034740A1
; GENERAL INFORMATION:
; APPLICANT: Patricia Billing-Medel
; APPLICANT: Maurice Cohen
; APPLICANT: Tracey L. Coldilts
; APPLICANT: Paula N. Friedman
; APPLICANT: Julian Gordon
; APPLICANT: Edward N. Granados
; APPLICANT: Steven C. Hodges
; APPLICANT: Michael R. Klass
; APPLICANT: Jon D. Kratochvil
; APPLICANT: John C. Russell
; APPLICANT: Stephen D. Stroupe
; TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of
; FILE REFERENCE: 6450.US.01
```

```

; CURRENT APPLICATION NUMBER: US/09/234,717A
; CURRENT FILING DATE: 1999-01-21
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Affinity purification system recognition site
US-09-234-717-24

Query Match
Best Local Similarity 100.0%; Score 47; DB 3; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 19
US-09-850-178-18
; Sequence 18, Application US/09850178
; Patent No. US20020034749A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Billing-Medel, Patricia A.
; APPLICANT: Cohen, Maurice
; APPLICANT: Colpitts, Tracey L.
; APPLICANT: Friedman, Paula N.
; APPLICANT: Russell, John C.
; APPLICANT: Granados, Edward N.
; APPLICANT: Hodges, Steven C.
; APPLICANT: Klase, Michael R.
; APPLICANT: Kratochvil, Jon D.
; APPLICANT: Roberts-Rapp, Lisa
; APPLICANT: Stroupe, Stephen D.
; APPLICANT: Gordon, Julian
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR
; TITLE OF INVENTION: DETECTING DISEASES OF THE BREAST
; FILE REFERENCE: 6251.US.P1
; CURRENT APPLICATION NUMBER: US/09/850,178
; CURRENT FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: US 08/972,376
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Affinity purification system recognition site
US-09-850-178-18

Query Match
Best Local Similarity 100.0%; Score 47; DB 3; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 20
US-09-193-538-22
; Sequence 22, Application US/09193538A
; Patent No. US20020037503A1
; GENERAL INFORMATION:
; APPLICANT: Patricia Billing-Medel
; APPLICANT: Maurice Cohen
; APPLICANT: Tracey L. Colpitts
```

```

; APPLICANT: Paula N. Friedman
; APPLICANT: Julian Gordon
; APPLICANT: Edward N. Granados
; APPLICANT: Steven C. Hodges
; APPLICANT: Michael R. Klase
; APPLICANT: Jon D. Kratochvil
; APPLICANT: Lisa Roberts-Rapp
; APPLICANT: John C. Russell
; APPLICANT: Stephen D. Stroupe
; TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of the
; TITLE OF INVENTION: Breast
; FILE REFERENCE: 6193.US.P1
; CURRENT APPLICATION NUMBER: US/09/193,538A
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: US 08/971,772
; EARLIER FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Affinity purification system recognition site
US-09-193-538-22

Query Match
Best Local Similarity 100.0%; Score 47; DB 3; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 21
US-09-250-883-22
; Sequence 22, Application US/09250883
; Patent No. US20020042049A1
; GENERAL INFORMATION:
; APPLICANT: Russell, John
; APPLICANT: Colpitts, Tracey
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASE OF THE BREAST
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/250,883
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/889,316
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6131.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 22:
```

SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-250-883-22

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
1 DYKDDDK 8

RESULT 22  
US-09-735-368-4  
Sequence 4, Application US/09735368  
Patent No. US20020042094A1  
GENERAL INFORMATION:  
APPLICANT: Venezia, Domenick R.  
APPLICANT: Taft, David W.  
APPLICANT: Whitmore, Theodore E.  
TITLE OF INVENTION: RING FINGER PROTEIN ZAPOP2  
FILE REFERENCE: 98-11  
CURRENT APPLICATION NUMBER: US/09/735,368  
CURRENT FILING DATE: 2000-12-12  
PRIOR APPLICATION NUMBER: US 60/171,258  
PRIOR FILING DATE: 1999-12-15  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 4  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Flag peptide sequence  
US-09-735-368-4

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
1 DYKDDDK 8

RESULT 23  
US-09-096-259-32  
Sequence 32, Application US/09096259  
Patent No. US20020045164A1  
GENERAL INFORMATION:  
APPLICANT: BILLING-MEDEL, PATRICIA  
APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GORDON, JULIAN  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: HODGES, STEVEN C.  
APPLICANT: KLAS, MICHAEL R.  
APPLICANT: KRATOCHVIL, JON D.  
APPLICANT: ROBERTS-RAPP, LISA  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: STROUPE, STEPHEN D.  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park

STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/096,259  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/049,183  
FILING DATE: 11-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6113, US, 01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-096-259-32

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
1 DYKDDDK 8

RESULT 24  
US-09-215-652-47  
Sequence 47, Application US/09215652  
Patent No. US20020045165A1  
GENERAL INFORMATION:  
APPLICANT: Patricia Billing-Medel  
APPLICANT: Maurice Cohen  
APPLICANT: Tracey L. Colpits  
APPLICANT: Paula N. Friedman  
APPLICANT: Julian Gordon  
APPLICANT: Edward N. Granados  
APPLICANT: Steven C. Hodges  
APPLICANT: Michael R. Kلاس  
APPLICANT: Jon D. Kratochvil  
APPLICANT: Lisa Roberts-Rapp  
APPLICANT: John C. Russell  
APPLICANT: Stephen D. Stroupe  
TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of the  
TITLE OF INVENTION: Breast  
FILE REFERENCE: 6192, US, P1  
CURRENT APPLICATION NUMBER: US/09/215,652  
CURRENT FILING DATE: 1998-12-16  
EARLIER APPLICATION NUMBER: US 08/998,496  
EARLIER FILING DATE: 1997-12-26  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 47  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Affinity purification system recognition site  
US-09-215-652-47

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8  
|||||  
Db 1 DYKDDDDK 8

## RESULT 25

US-09-970-308-1  
; Sequence 1, Application US/0970308  
; Patent No. US20020045193A1  
; GENERAL INFORMATION:  
; APPLICANT: BRIZZARD, BILLY L.  
; APPLICANT: HERMAN, RON  
; TITLE OF INVENTION: PURIFICATION OF RECOMBINANT PROTEINS FUSED TO MULTIPLE  
; TITLE OF INVENTION: EPITOPES  
; FILE REFERENCE: SGM 6933.2  
; CURRENT APPLICATION NUMBER: US/09/970,308  
; CURRENT FILING DATE: 2001-10-03  
; PRIOR APPLICATION NUMBER: 09/415,000  
; PRIOR FILING DATE: 1999-10-08  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:synthesized  
US-09-970-308-1

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8  
|||||  
Db 1 DYKDDDDK 8

## RESULT 26

US-09-309-668A-1  
; Sequence 1, Application US/09309668A  
; Patent No. US20020045271A1  
; GENERAL INFORMATION:  
; APPLICANT: Hussain, M. Mahmood  
; APPLICANT: Bakillah, Ahmed  
; TITLE OF INVENTION: Compounds and Methods for Identifying Compounds that  
; TITLE OF INVENTION: Interact with Mitochondrial Triglyceride Transfer Protein  
; TITLE OF INVENTION: Binding Sites on Apolipoprotein B and Modulate Lipid  
; TITLE OF INVENTION: Biosynthesis  
; FILE REFERENCE: MCP-0006  
; CURRENT APPLICATION NUMBER: US/09/309,668A  
; CURRENT FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/088,767  
; PRIOR FILING DATE: 1998-06-10  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
US-09-309-668A-1

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8  
|||||  
Db 1 DYKDDDDK 8

## RESULT 27

US-09-855-722-25  
; Sequence 25, Application US/09855722  
; Patent No. US20020049306A1  
; GENERAL INFORMATION:  
; APPLICANT: Sakano, Sei-ji  
; APPLICANT: Itoh, Akira  
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE  
; FILE REFERENCE: KP-8576  
; CURRENT APPLICATION NUMBER: US/09/855,722  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: 09/214,278  
; PRIOR FILING DATE: 1999-01-26  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 25  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic amino acid  
US-09-855-722-25

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8  
|||||  
Db 1 DYKDDDDK 8

## RESULT 28

US-09-817-413-1  
; Sequence 1, Application US/09817413  
; Publication No. US20020052478A1  
; GENERAL INFORMATION:  
; APPLICANT: SRINIVASAN, ALGARSAMY  
; APPLICANT: KOPROWSKI, HILARY  
; TITLE OF INVENTION: CHIMERIC VIRAL PROTEINS  
; FILE REFERENCE: Chimeric Viral Proteins  
; CURRENT APPLICATION NUMBER: US/09/817,413  
; CURRENT FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: 60/043,380  
; PRIOR FILING DATE: 1999-04-03  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: FLAG epitope  
US-09-817-413-1

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8  
|||||  
Db 1 DYKDDDDK 8

## RESULT 29

US-09-193-663-9  
; Sequence 9, Application US/09193663

Patent No. US20020055624A1  
; GENERAL INFORMATION:  
; APPLICANT: Wiley, Steven R.  
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF  
; FILE REFERENCE: 6255 US.02  
; CURRENT APPLICATION NUMBER: US/09/193,663  
; EARLIER FILING DATE: 1998-11-17  
; EARLIER APPLICATION NUMBER: 60/065,916  
; EARLIER FILING DATE: 1997-11-17  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-193-663-9

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 30  
US-09-887-855-7  
; Sequence 7, Application US/09887855  
; Patent No. US20020058310A1  
; GENERAL INFORMATION:  
; APPLICANT: Immunex Corporation  
; APPLICANT: Anderson, Dirk M.  
; TITLE OF INVENTION: LECTIN SS3939 DNA AND POLYPEPTIDES  
; FILE REFERENCE: 2883-US  
; CURRENT APPLICATION NUMBER: US/09/887,855  
; CURRENT FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: antigenic peptide used in fusion proteins  
US-09-887-855-7

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 31  
US-09-904-245-3  
; Sequence 3, Application US/09904245  
; Patent No. US20020076409A1  
; GENERAL INFORMATION:  
; APPLICANT: March, Carl  
; APPLICANT: Pluemeke, John  
; APPLICANT: O'Neal, Larry  
; TITLE OF INVENTION: METHOD FOR TREATING CANCER  
; FILE REFERENCE: 2943-A  
; CURRENT APPLICATION NUMBER: US/09/904,245  
; CURRENT FILING DATE: 2001-07-11  
; PRIOR APPLICATION NUMBER: 60/217,888  
; PRIOR FILING DATE: 2000-07-12

; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: FLAG peptide  
US-09-904-245-3

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 32  
US-09-245-603A-15  
; Sequence 15, Application US/09245603A  
; Patent No. US20020081280A1  
; GENERAL INFORMATION:  
; APPLICANT: Curiel, David T.  
; APPLICANT: Krasnykh, Victor N.  
; APPLICANT: Dmitriev, Igor  
; TITLE OF INVENTION: Adenovirus Vector Containing A Heterologous Peptide  
; TITLE OF INVENTION: Epitope in the HI Loop of the Fiber Knob  
; FILE REFERENCE: D6080  
; CURRENT APPLICATION NUMBER: US/09/245,603A  
; CURRENT FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: US 60/099,801  
; PRIOR FILING DATE: 1998-09-10  
; NUMBER OF SEQ ID NOS: 17  
; SEQ ID NO 15  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Amino acid sequence of the FLAG octapeptide.  
US-09-245-603A-15

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 33  
US-09-837-992-45  
; Sequence 45, Application US/09837992  
; Patent No. US20020081687A1  
; GENERAL INFORMATION:  
; APPLICANT: Tian, Hui  
; APPLICANT: Schultz, Joshua  
; APPLICANT: Shan, Bei  
; APPLICANT: Tularik Inc.  
; TITLE OF INVENTION: Siderostolemia Susceptibility Gene (SSG): Compositions  
; FILE REFERENCE: 018781-006020US  
; CURRENT APPLICATION NUMBER: US/09/837,992  
; CURRENT FILING DATE: 2001-04-18  
; PRIOR APPLICATION NUMBER: US 60/198,465  
; PRIOR FILING DATE: 2000-04-18  
; PRIOR APPLICATION NUMBER: US 60/204,234  
; PRIOR FILING DATE: 2000-05-15  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 45

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; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:anti-DYKDDDDK
; US-09-837-992-45

Query Match
Best Local Similarity 100.0%; Score 47; DB 3; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 34
US-09-923-995-6
; Sequence 6, Application US/09923995
; Patent No. US20020081700A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: SNAKE VENOM POLYPEPTIDE ZSNK1
; FILE REFERENCE: 00-47
; CURRENT APPLICATION NUMBER: US/09/923,995
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 60/223,164
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FLAG peptide tag
; US-09-923-995-6

Query Match
Best Local Similarity 100.0%; Score 47; DB 3; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 35
US-09-871-856-7
; Sequence 7, Application US/09871856
; Patent No. US20020081720A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Power Macintosh
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/871,856
; FILING DATE: 31-May-2001
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; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: No.
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: FLAG-peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
; US-09-871-856-7

Query Match
Best Local Similarity 100.0%; Score 47; DB 3; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 36
US-09-841-894-40
; Sequence 40, Application US/09841894
; Publication No. US20020086301A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; COHEN, MAURICE
; COLPITTS, TRACEY L.
; FRIEDMAN, PAULA N.
; GORDON, JULIAN
; GRANADOS, EDWARD N.
; HODGES, STEVEN C.
; KLAS, MICHAEL R.
; KRATOCHVIL, JON D.
; ROBERTS-RAP, LISA
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/841,894
; FILING DATE: 25-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/071,710
; FILING DATE: <Unknown>
```

ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6083.US.PI  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: None  
SEQUENCE DESCRIPTION: SEQ ID NO: 40:  
US-09-841-894-40

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
DB 1 DYKDDDDK 8

RESULT 37  
US-09-991-681-32  
Sequence 32, Application US/09991681  
Publication No. US20020086316A1  
GENERAL INFORMATION:  
APPLICANT: BILLING-MEDEL, PATRICIA  
COHEN, MAURICE  
COLBITTS, TRACEY L.  
FRIEDMAN, PAULA N.  
GORDON, JULIAN  
GRANADOS, EDWARD N.  
HODGES, STEVEN C.  
KLASS, MICHAEL R.  
KRATOCHVIL, JON D.  
ROBERTS-RAIP, LISA  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
FOR DETECTING DISEASES OF THE PROSTATE  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/991,681  
FILING DATE: 26-Nov-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/065,383  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6084.US.PI  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 32:  
US-09-991-681-32

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
DB 1 DYKDDDDK 8

RESULT 38  
US-09-065-902-15  
Sequence 15, Application US/09065902  
Publication No. US20020086444A1  
GENERAL INFORMATION:  
APPLICANT: Tanzi, Rudolph E.  
Kim, Tae-Wan  
TITLE OF INVENTION: A Purified 20 KDa Presentin 2  
C-terminal Fragment and Methods of Screening for Compounds  
that Inhibit Proteolysis of Presentin 2  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, NW, Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/065,902  
FILING DATE: 24-Apr-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/044,262  
FILING DATE: 24-Apr-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0609.4270001/JAG/S-S  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2540  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-09-065-902-15

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
DB 1 DYKDDDDK 8

```

/ STREET: 51 University Street
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98101
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: Apple Power Macintosh
/ OPERATING SYSTEM: Apple Operating System 7.5.5
/ SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/871,291
/ FILING DATE: 30-May-2001
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/996,139
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: US98 08/813,509
/ FILING DATE: 07 MARCH 1997
/ APPLICATION NUMBER: US98 08/772,330
/ FILING DATE: 23 DECEMBER 1996
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Perkins, Patricia Anne
/ REGISTRATION NUMBER: 34,693
/ REFERENCE/DOCKET NUMBER: 2851-A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 587-0430
/ TELEFAX: (206) 233-0644
/
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 8 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ IMMEDIATE SOURCE:
/ CLONE: FLAG: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 7:
/
/ US-09-871-291-7
/
/ Query Match 100.0%; Score 47; DB 3; Length 8;
/ Best Local Similarity 100.0%; Pred. No. 1.9e+06;
/ Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 1 DYKDDDDK 8
/ |||||
/ Db 1 DYKDDDDK 8
/
/ RESULT 41
/ US-09-193-881-28
/ Sequence 28, Application US/09193881A
/ Publication No. US20020086979A1
/
/ GENERAL INFORMATION:
/ APPLICANT: Patricia Billing-Medel
/ APPLICANT: Maurice Cohen
/ APPLICANT: Tracey L. Colpitts
/ APPLICANT: Paula N. Friedman
/ APPLICANT: Edward N. Granados
/ APPLICANT: Michael R. Klass
/ APPLICANT: John C. Russell
/ APPLICANT: Stephen D. Stroupe
/ TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of the
/ TITLE OF INVENTION: Breast
/ FILE REFERENCE: 6248 US. P1
/ CURRENT APPLICATION NUMBER: US/09/193,881A
/ CURRENT FILING DATE: 1998-11-18
/ NUMBER OF SEQ ID NOS: 29
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 28
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/

```



```
; FEATURE:
; OTHER INFORMATION: Affinity purification system recognition site
US-09-193-881-28

Query Match
Best Local Similarity 100.0%; Score 47; DB 3; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 42
US-09-875-338-94
; Sequence 94, Application US/09875338
; Patent No. US20020095024A1
; GENERAL INFORMATION:
; APPLICANT: MIKESILL, GLEN E.
; APPLICANT: CHANG, HAN
; APPLICANT: FINGER, JOSHUA N.
; APPLICANT: YANG, GUOCHEN
; APPLICANT: LU, PIN
; APPLICANT: ZHOU, XIA-DI
; APPLICANT: PEACH, ROBERT
; TITLE OF INVENTION: B7-RELATED NUCLEIC ACIDS AND POLYPEPTIDES USEFUL FOR
; FILE REFERENCE: 3053-4071US2
; CURRENT APPLICATION NUMBER: US/09/875,338
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/272,107
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/209,811
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 94
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Epitope tag
US-09-875-338-94

Query Match
Best Local Similarity 100.0%; Score 47; DB 3; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 43
US-09-903-248-7
; Sequence 7, Application US/09903248
; Patent No. US20020102263A1
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R.
; APPLICANT: de la Monte, Suzanne M.
; APPLICANT: Ince, Nedim
; APPLICANT: Carlson, Rolf I.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
; FILE REFERENCE: 21486-032 DIV5
; CURRENT APPLICATION NUMBER: US/09/903,248
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/436,184
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: FLAG epitope
US-09-903-248-7

Query Match
Best Local Similarity 100.0%; Score 47; DB 3; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 44
US-09-798-584-17
; Sequence 17, Application US/09798584
; Patent No. US20020102676A1
; GENERAL INFORMATION:
; APPLICANT: Mu, David
; APPLICANT: Powers, Scott
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: KCNB: A NO. US20020102676A1el Potassium Channel Protein
; FILE REFERENCE: 018781-004010US
; CURRENT APPLICATION NUMBER: US/09/798,584
; PRIOR FILING DATE: 2001-03-03
; PRIOR APPLICATION NUMBER: US 60/186,951
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 17
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: anti-DYKDDDDK
US-09-798-584-17

Query Match
Best Local Similarity 100.0%; Score 47; DB 3; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 45
US-09-978-339-3
; Sequence 3, Application US/0978339
; Patent No. US20020103358A1
; GENERAL INFORMATION:
; APPLICANT: Cerretti, Douglas P.
; APPLICANT: Reddy, Pranhitha
; TITLE OF INVENTION: No. US20020103358A1el Cytokine Designated Lerk-5
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/978,339
; FILING DATE: 15-Oct-2001
; CLASSIFICATION: <Unknown>
```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/271,948
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2823
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: FLAG peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-978-339-3

Query Match          100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 46
US-09-859-604-7
; Sequence 7, Application US/09859604
; Patent No. US20020110559A1
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R.
; APPLICANT: de la Monte, Suzanne M
; APPLICANT: Deutch, Alan H
; APPLICANT: Chaudhri, Hossein A
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
; FILE REFERENCE: 21486-032 CIP
; CURRENT APPLICATION NUMBER: US/09/859,604
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 09/436,184
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: FLAG epitope
US-09-859-604-7

Query Match          100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 47
US-09-903-063-7
; Sequence 7, Application US/09903063
; Patent No. US20020114810A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Wands, Jack R.
; APPLICANT: de la Monte, Suzanne M.
; APPLICANT: Ince, Nedim
; APPLICANT: Carlson, Rolf I.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
; FILE REFERENCE: 21486-032 DIV3
; CURRENT APPLICATION NUMBER: US/09/903,063
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 09/436,184
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: FLAG epitope
US-09-903-063-7

Query Match          100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 48
US-09-903-216-7
; Sequence 7, Application US/09903216
; Patent No. US20020114811A1
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R.
; APPLICANT: de la Monte, Suzanne M.
; APPLICANT: Ince, Nedim
; APPLICANT: Carlson, Rolf I.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
; FILE REFERENCE: 21486-032 DIV2
; CURRENT APPLICATION NUMBER: US/09/903,216
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/436,184
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: FLAG epitope
US-09-903-216-7

Query Match          100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 49
US-09-844-508-14
; Sequence 14, Application US/09844508
; Patent No. US20020115215A1
; GENERAL INFORMATION:
; APPLICANT: WOLFFE, Alan P.
; APPLICANT: COLLINGWOOD, Trevor
; TITLE OF INVENTION: TARGETED MODIFICATION OF CHROMATIN STRUCTURE
; FILE REFERENCE: 8325-0014 / S14-US1
; CURRENT APPLICATION NUMBER: US/09/844,508
```

```
/ CURRENT FILING DATE: 2001-04-27
/ PRIOR APPLICATION NUMBER: 60/200,590
/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: 60/228,523
/ PRIOR FILING DATE: 2000-08-28
/ NUMBER OF SEQ ID NOS: 49
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 14
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:
/ OTHER INFORMATION: double-stranded oligonucleotide encoding a FLAG
US-09-844-508-14
```

```
Query Match      100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 DYKDDDDK 8
Db      1 DYKDDDDK 8
```

```
RESULT 50
US-09-888-358-17
/ Sequence 17, Application US/09888358
/ Patent No. US20020119137A1
/ GENERAL INFORMATION:
/ APPLICANT: LEWIN, DAVID
/ APPLICANT: ADAMS, SEAN H.
/ APPLICANT: YU, KING XIAN
/ TITLE OF INVENTION: CGI-69 COMPOSITIONS AND METHODS OF USE
/ FILE REFERENCE: 10716/66
/ CURRENT APPLICATION NUMBER: US/09/888,358
/ CURRENT FILING DATE: 2001-06-22
/ PRIOR APPLICATION NUMBER: 60/213,307
/ PRIOR FILING DATE: 2000-06-22
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 17
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: FLAG tag
US-09-888-358-17
```

```
Query Match      100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 DYKDDDDK 8
Db      1 DYKDDDDK 8
```

```
RESULT 51
US-09-903-199-7
/ Sequence 7, Application US/09903199
/ Patent No. US20020122802A1
/ GENERAL INFORMATION:
/ APPLICANT: Wands, Jack R.
/ APPLICANT: de la Monte, Suzanne M.
/ APPLICANT: Ince, Nedim
/ APPLICANT: Carlson, Rolf I.
/ TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
/ FILE REFERENCE: 21486-032 DIV4
/ CURRENT APPLICATION NUMBER: US/09/903,199
/ CURRENT FILING DATE: 2001-07-11
/ PRIOR APPLICATION NUMBER: 09/436,184
```

```
/ PRIOR FILING DATE: 1999-11-08
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 7
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: FLAG epitope
US-09-903-199-7
```

```
Query Match      100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 DYKDDDDK 8
Db      1 DYKDDDDK 8
```

```
RESULT 52
US-09-745-605-43
/ Sequence 43, Application US/09745605
/ Patent No. US20020123617A1
/ GENERAL INFORMATION:
/ APPLICANT: Starling, Gary C.
/ APPLICANT: Finger, Joshua N.
/ TITLE OF INVENTION: NOVEL IMMUNOGLOBIN SUPERFAMILY MEMBERS APEX-1, APEX-2,
/ FILE REFERENCE: DB13NP
/ CURRENT APPLICATION NUMBER: US/09/745,605
/ CURRENT FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/172,025
/ PRIOR FILING DATE: 1999-12-23
/ NUMBER OF SEQ ID NOS: 44
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 43
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: FLAG tag
US-09-745-605-43
```

```
Query Match      100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 DYKDDDDK 8
Db      1 DYKDDDDK 8
```

```
RESULT 53
US-09-780-933-20
/ Sequence 20, Application US/09780933
/ Patent No. US20020127652A1
/ GENERAL INFORMATION:
/ APPLICANT: SCHAMBEY, HANS T.
/ APPLICANT: ANDERSEN, KIM V.
/ APPLICANT: VAN DEN HAZEL, BART
/ APPLICANT: CHRISTIANSEN, JESPER
/ APPLICANT: JEPSEN, CLAUD B.
/ TITLE OF INVENTION: FOLLICLE STIMULATING HORMONES
/ FILE REFERENCE: 31-001000US
/ CURRENT APPLICATION NUMBER: US/09/780,933
/ CURRENT FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: PA 2000 00220
/ PRIOR FILING DATE: 2000-02-11
/ PRIOR APPLICATION NUMBER: 60/184,035
/ PRIOR FILING DATE: 2000-02-22
/ PRIOR APPLICATION NUMBER: PA 2000 01092
```

;; PRIOR FILING DATE: 2000-07-14  
;; PRIOR APPLICATION NUMBER: 60/225,558  
;; PRIOR FILING DATE: 2000-08-16  
;; NUMBER OF SEQ ID NOS: 30  
;; SOFTWARE: Patent In Ver. 2.1  
;; SEQ ID NO 20  
;; LENGTH: 8  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-780-933-20

Query Match                    100.0%;    Score 47;    DB 3;    Length 8;  
Best Local Similarity    100.0%;    Pred. No. 1.9e+06;  
Matches    8;    Conservative    0;    Mismatches    0;    Indels    0;    Gaps    0;

Qy                    1 DYKDDDDK 8  
                      |||||  
Db                    1 DYKDDDDK 8

RESULT 54  
US-09-873-106B-14  
; Sequence 14, Application US/09873106B  
; Patent No. US20020127657A1  
; GENERAL INFORMATION:  
; APPLICANT: Reinherz, Ellis L.  
; APPLICANT: Freund, Christian  
; APPLICANT: Li, Jing  
; APPLICANT: Nishizawa, Kazuhisa  
; APPLICANT: Wagner, Gerhard  
; TITLE OF INVENTION: Cloning and Characterization of a CD2  
; FILE REFERENCE: 1062.1021-004  
; CURRENT APPLICATION NUMBER: US/09/873,106B  
; PRIOR FILING DATE: 2001-06-01  
; PRIOR APPLICATION NUMBER: US 60/111,007  
; PRIOR FILING DATE: 1998-12-04  
; PRIOR FILING DATE: 1999-01-13  
; PRIOR FILING DATE: 1999-01-13  
; PRIOR APPLICATION NUMBER: PCT/US99/26993  
; PRIOR FILING DATE: 1999-11-15  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Flag Epitope  
US-09-873-106B-14

Query Match                    100.0%;    Score 47;    DB 3;    Length 8;  
Best Local Similarity    100.0%;    Pred. No. 1.9e+06;  
Matches    8;    Conservative    0;    Mismatches    0;    Indels    0;    Gaps    0;

Qy                    1 DYKDDDDK 8  
                      |||||  
Db                    1 DYKDDDDK 8

RESULT 55  
US-09-995-593A-13  
; Sequence 13, Application US/09995593A  
; Patent No. US20020128197A1  
; GENERAL INFORMATION:  
; APPLICANT: SAKANO, SEIJI  
; APPLICANT: ITOH, AKIRA  
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE  
; FILE REFERENCE: KP8447DIV  
; CURRENT APPLICATION NUMBER: US/09/995,593A

;; CURRENT FILING DATE: 2002-02-28  
;; PRIOR APPLICATION NUMBER: 09/068,740  
;; PRIOR FILING DATE: 1998-06-18  
;; PRIOR APPLICATION NUMBER: JP 7-299611  
;; PRIOR FILING DATE: 1995-11-17  
;; PRIOR APPLICATION NUMBER: JP 7-311811  
;; PRIOR FILING DATE: 1995-11-30  
;; PRIOR APPLICATION NUMBER: PCT/JP96/03356  
;; PRIOR FILING DATE: 1996-11-15  
;; NUMBER OF SEQ ID NOS: 48  
;; SOFTWARE: Patent In Ver. 2.1  
;; SEQ ID NO 13  
;; LENGTH: 8  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-995-593A-13

Query Match                    100.0%;    Score 47;    DB 3;    Length 8;  
Best Local Similarity    100.0%;    Pred. No. 1.9e+06;  
Matches    8;    Conservative    0;    Mismatches    0;    Indels    0;    Gaps    0;

Qy                    1 DYKDDDDK 8  
                      |||||  
Db                    1 DYKDDDDK 8

RESULT 56  
US-09-900-530A-13  
; Sequence 13, Application US/09900530A  
; Patent No. US20020128438A1  
; GENERAL INFORMATION:  
; APPLICANT: Seol, Dae-Wu  
; APPLICANT: Billiar, Timothy R.  
; TITLE OF INVENTION: DNA Cassette for the Production of  
; TITLE OF INVENTION: Secretable Recombinant Trimeric Trail Proteins, Tetracycline  
; TITLE OF INVENTION: /Doxycycline-Inducible Adeno-Associated Virus Vector, Their  
; TITLE OF INVENTION: Combination and Use in Gene Therapy  
; FILE REFERENCE: 5006-1-002  
; CURRENT APPLICATION NUMBER: US/09/900,530A  
; PRIOR FILING DATE: 2002-03-19  
; PRIOR APPLICATION NUMBER: KR 2000-38441  
; PRIOR FILING DATE: 2000-07-06  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: FLAG-tag  
US-09-900-530A-13

Query Match                    100.0%;    Score 47;    DB 3;    Length 8;  
Best Local Similarity    100.0%;    Pred. No. 1.9e+06;  
Matches    8;    Conservative    0;    Mismatches    0;    Indels    0;    Gaps    0;

Qy                    1 DYKDDDDK 8  
                      |||||  
Db                    1 DYKDDDDK 8

RESULT 57  
US-09-923-246-37  
; Sequence 37, Application US/09923246  
; Patent No. US20020128446A1  
; GENERAL INFORMATION:  
; APPLICANT: No. US20020128446A1ak, Julia E.  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Foster, Donald C.

APPLICANT: Holly, Richard D.  
APPLICANT: Gross, Jane A.  
APPLICANT: Johnston, Janet V.  
APPLICANT: Nelson, Andrew J.  
APPLICANT: Dillon, Stacey R.  
APPLICANT: Hammond, Angela K.  
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND  
FILE REFERENCE: 99-16  
CURRENT APPLICATION NUMBER: US/09/923,246  
CURRENT FILING DATE: 2001-08-03  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217  
PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01  
NUMBER OF SEQ ID NOS: 115  
SOFTWARE: Fasteq for Windows Version 3.0  
SEQ ID NO 37  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: C-terminal FLAG amino acid sequence  
US-09-923-246-37

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 58  
US-09-973-145-6  
Sequence 6, Application US/09973145  
Patent No. US20020132248A1  
GENERAL INFORMATION:  
APPLICANT: Rochechild, Kenneth J.  
APPLICANT: Gite, Sadanand  
APPLICANT: Olejnik, Jerzy  
TITLE OF INVENTION: N-Terminal and C-Terminal Markers in Nascent Proteins  
FILE REFERENCE: AMBER-06819  
CURRENT APPLICATION NUMBER: US/09/973,145  
CURRENT FILING DATE: 2001-10-09  
PRIOR APPLICATION NUMBER: 09/382,950  
PRIOR FILING DATE: 1999-08-25  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
FEATURE:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: Synthetic  
US-09-973-145-6

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 59  
US-09-825-561A-23

Sequence 23, Application US/09825561A  
Patent No. US20020137677A1  
GENERAL INFORMATION:  
APPLICANT: Sprecher, Cindy A.  
APPLICANT: No. US20020137677A1ak, Julia E.  
APPLICANT: West, James W.  
APPLICANT: Presnell, Scott R.  
APPLICANT: Holly, Richard D.  
APPLICANT: Nelson, Andrew J.  
TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS  
FILE REFERENCE: 00-22  
CURRENT APPLICATION NUMBER: US/09/825,561A  
CURRENT FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: US 60/194,731  
PRIOR FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: US 60/222,121  
PRIOR FILING DATE: 2000-07-28  
NUMBER OF SEQ ID NOS: 86  
SOFTWARE: Fasteq for Windows Version 3.0  
SEQ ID NO 23  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: FLAG tag amino acid sequence  
US-09-825-561A-23

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 60  
US-09-049-695A-21  
Sequence 21, Application US/09049695A  
Patent No. US20020137904A1  
GENERAL INFORMATION:  
APPLICANT: BILLING-MEDEL, PATRICIA A.  
APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: HAYDEN, MARK  
APPLICANT: KLASS, MICHAEL R.  
APPLICANT: ROBERTS-RAPP, LISA  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: STROUPE, STEPHEN D.  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
FOR DETECTING DISEASES OF THE GASTROINTESTINAL  
TITLE OF INVENTION: TRACT  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: Fasteq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/049,695A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/828,845  
FILING DATE: 31-MAR-1997

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6066.US.PI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-049-695A-21

Query Match          100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYKDDDDK 8
DB      1 DYKDDDDK 8

RESULT 61
US-09-092-297-21
; Sequence 21, Application US/09092297
; Patent No. US20020142371A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRAMADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLAS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAFF, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; APPLICANT: YU, HONG
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE URINARY TRACT
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/092,297
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/869,579
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6107.US.PI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:

```

```

; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-092-297-21

Query Match          100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYKDDDDK 8
DB      1 DYKDDDDK 8

RESULT 62
US-09-903-023-7
; Sequence 7, Application US/09903023
; Patent No. US20020146421A1
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R.
; APPLICANT: de la Monte, Suzanne M.
; APPLICANT: Ince, Nedim
; APPLICANT: Carlson, Rolf I.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
; FILE REFERENCE: 21486-032 DIV1
; CURRENT APPLICATION NUMBER: US/09/903,023
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 09/436,184
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: FLAG epitope
;
US-09-903-023-7

Query Match          100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYKDDDDK 8
DB      1 DYKDDDDK 8

RESULT 63
US-09-852-391-3
; Sequence 3, Application US/09852391
; Patent No. US2002014619A1
; GENERAL INFORMATION:
; APPLICANT: Sims, John
; APPLICANT: Lyman, Stewart
; APPLICANT: Armstrong, Allison
; APPLICANT: McKenna, Hilary
; TITLE OF INVENTION: Human TSLP DNA and Polypeptides
; FILE REFERENCE: 03260.0087-00304/2881-WO
; CURRENT APPLICATION NUMBER: US/09/852,391
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 60/108,452
; PRIOR FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:

```

OTHER INFORMATION: Description of Artificial Sequence: antigenic  
OTHER INFORMATION: peptide used in fusion proteins  
US-09-852-391-3

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 64  
US-09-931-087A-19  
Sequence 19, Application US/09931087A  
Patent No. US20020147322A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
TITLE OF INVENTION: NSP Molecules  
FILE REFERENCE: P123R1E  
CURRENT APPLICATION NUMBER: US/09/931,087A  
CURRENT FILING DATE: 2001-08-15  
PRIOR APPLICATION NUMBER: 09/367,206  
PRIOR FILING DATE: 1999-08-09  
PRIOR APPLICATION NUMBER: US 60/082,767  
PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: US 60/113,296  
PRIOR FILING DATE: 1998-12-22  
NUMBER OF SEQ ID NOS: 35  
SEQ ID NO 19  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-931-087A-19

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 65  
US-09-263-959-985  
Sequence 985, Application US/09263959  
Patent No. US20020150891A1  
GENERAL INFORMATION:  
APPLICANT: Hood, Leroy E.  
APPLICANT: Rowen, Lee  
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
NUMBER OF SEQUENCES: 1279  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/263,959  
FILING DATE: 05-MAR-1999  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: McMaesters, David D.

REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 920010.426C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 985:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-09-263-959-985

QY 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 66  
US-09-969-192-2  
Sequence 2, Application US/09969192  
Patent No. US20020151027A1  
GENERAL INFORMATION:  
APPLICANT: WICKHAM, THOMAS J.  
ROELVINK, PETRUS W.  
KOVESDI, IMRE  
TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF  
CONSTRAINED PEPTIDE MOTIFS  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Leydig, Voigt & Mayer, Ltd.  
STREET: Two Prudential Plaza - 49th Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60601

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/969,192  
FILING DATE: 01-Oct-2001  
PRIOR APPLICATION NUMBER: US 9-455061  
FILING DATE: 06-DEC-1999  
APPLICATION NUMBER: US 9-130225  
FILING DATE: 06-AUG-1998  
APPLICATION NUMBER: US 8-701124  
FILING DATE: 21-AUG-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Hefner, M. Daniel  
REGISTRATION NUMBER: 41,826  
REFERENCE/DOCKET NUMBER: 213564  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-969-192-2

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8

Db 1 DYKDDDDK 8

RESULT 67  
US-09-840-243B-20  
; Sequence 20, Application US/09840243B  
; Patent No. US20020156258A1  
; GENERAL INFORMATION:  
; APPLICANT: MASTERNAK, Krzysztof  
; APPLICANT: REITH, Walter  
; APPLICANT: MACH, Bernard  
; TITLE OF INVENTION: New Transcription Factor of MHC Class II Genes, Substances  
; TITLE OF INVENTION: Capable of Inhibiting This New Transcription Factor and  
; FILE REFERENCE: 010830-117  
; CURRENT APPLICATION NUMBER: US/09/840,243B  
; PRIOR FILING DATE: 2001-04-24  
; PRIOR APPLICATION NUMBER: EP 98120085.0  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: FLAG epitope  
US-09-840-243B-20

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 68  
US-09-766-700A-8  
; Sequence 8, Application US/09766700A  
; Patent No. US2002015989A1  
; GENERAL INFORMATION:  
; APPLICANT: Bein, Kietai  
; APPLICANT: Simons, Michael  
; TITLE OF INVENTION: Peptide Inhibitor of MMP Activity and Angiogenesis  
; FILE REFERENCE: BIT-003  
; CURRENT APPLICATION NUMBER: US/09/766,700A  
; PRIOR FILING DATE: 2001-01-22  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Flag tag  
US-09-766-700A-8

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 69  
US-09-843-245-12  
; Sequence 12, Application US/09843245  
; Patent No. US20020164672A1

; GENERAL INFORMATION:  
; APPLICANT: McPherson, Peter S.  
; APPLICANT: Ramjoun, Antoine Rachid  
; TITLE OF INVENTION: REGULATION OF JNK ACTIVITY BY MODULATION OF THE  
; TITLE OF INVENTION: INTERACTION BETWEEN THE ENDOCYTIC PROTEIN ENDOPHILIN  
; TITLE OF INVENTION: AND THE GERMINAL CENTER KINASE-LIKE KINASE  
; FILE REFERENCE: 9555.116US01  
; CURRENT APPLICATION NUMBER: US/09/843,245  
; PRIOR FILING DATE: 2001-04-25  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: FLAG Epitope  
US-09-843-245-12

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 70  
US-09-989-350-19  
; Sequence 19, Application US/09989350  
; Patent No. US20020164716A1  
; GENERAL INFORMATION:  
; APPLICANT: Lin, Lih-Ling  
; APPLICANT: Chen, Jennifer H.  
; APPLICANT: Schiavella, Andrea  
; APPLICANT: Graham, James  
; TITLE OF INVENTION: No. US20020164716A1 TNF receptor death domain ligand proteins a  
; TITLE OF INVENTION: Inhibitors of ligand binding (as amended)  
; FILE REFERENCE: GFN-5232CP4DV3  
; CURRENT APPLICATION NUMBER: US/09/989,350  
; PRIOR FILING DATE: 2001-11-20  
; PRIOR APPLICATION NUMBER: 09/185,258  
; PRIOR FILING DATE: 1998-11-02  
; PRIOR APPLICATION NUMBER: 08/839,032  
; PRIOR FILING DATE: 1997-04-23  
; PRIOR APPLICATION NUMBER: 08/698,551  
; PRIOR FILING DATE: 1996-08-15  
; PRIOR APPLICATION NUMBER: 08/602,228  
; PRIOR FILING DATE: 1996-02-15  
; PRIOR APPLICATION NUMBER: 08/533,901  
; PRIOR FILING DATE: 1995-09-26  
; PRIOR APPLICATION NUMBER: 08/494,440  
; PRIOR FILING DATE: 1995-06-19  
; PRIOR APPLICATION NUMBER: 08/327,514  
; PRIOR FILING DATE: 1994-10-19  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Flag-tag  
US-09-989-350-19

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8



RESULT 71  
US-09-858-332-12  
; Sequence 12, Application US/09858332  
; Patent No. US20020164718A1  
; GENERAL INFORMATION:  
; APPLICANT: Tchaga, Grigory S.  
; TITLE OF INVENTION: Metal Ion Affinity Tags and Methods for  
; TITLE OF INVENTION: Using the Same  
; FILE REFERENCE: CLON056CIP  
; CURRENT APPLICATION NUMBER: US/09/858,332  
; CURRENT FILING DATE: 2002-07-02  
; PRIOR APPLICATION NUMBER: 09/404,017  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: 60/101,867  
; PRIOR FILING DATE: 1998-09-25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
US-09-858-332-12  
; OTHER INFORMATION: synthetic peptide

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

## RESULT 72

US-09-877-650-7  
; Sequence 7, Application US/09877650  
; Patent No. US20020169117A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Dirk M.  
; Galibert, Laurent  
; Maraskovsky, Eugene  
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation, Law Department  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Power Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.5.5  
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1  
; CURRENT APPLICATION NUMBER: US/09/877,650  
; FILING DATE: 08-Jun-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/995,659  
; FILING DATE: 1997-12-22  
; APPLICATION NUMBER: USSN 08/813,509  
; FILING DATE: 07 MARCH 1997  
; APPLICATION NUMBER: USSN 08/772,330  
; FILING DATE: 23 DECEMBER 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia Anne  
; REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2852-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
CLONE: FLAG peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-877-650-7

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

## RESULT 73

US-09-981-636-1  
; Sequence 1, Application US/09981636  
; Publication No. US20020182643A1  
; GENERAL INFORMATION:  
; APPLICANT: MARKS, JAMES  
; APPLICANT: NIELSEN, ULRIK  
; APPLICANT: KIRPOTIN, DMITRI  
; TITLE OF INVENTION: METHODS OF HIGH-THROUGHPUT SCREENING FOR INTERNALIZING ANTIBODIES  
; FILE REFERENCE: 407T-897710US  
; CURRENT APPLICATION NUMBER: US/09/981,636  
; CURRENT FILING DATE: 2002-06-25  
; PRIOR APPLICATION NUMBER: US 60/241,279  
; PRIOR FILING DATE: 2000-10-18  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: epitope tag  
US-09-981-636-1

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

## RESULT 74

US-09-092-296-19  
; Sequence 19, Application US/09092296  
; Publication No. US20020188114A1  
; GENERAL INFORMATION:  
; APPLICANT: BILLING-MEDEL, PATRICIA  
; APPLICANT: COHEN, MAURICE  
; APPLICANT: COLPITTS, TRACEY L.  
; APPLICANT: FRIEDMAN, PAULA N.  
; APPLICANT: KLAAS, MICHAEL R.  
; APPLICANT: RUSSELL, JOHN C.  
; APPLICANT: STROUBE, STEPHEN D.  
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG  
; NUMBER OF SEQUENCES: 20

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Abbott Laboratories  
;; STREET: 100 Abbott Park Road  
;; CITY: Abbott Park  
;; STATE: IL  
;; COUNTRY: USA  
;; ZIP: 60064-3500  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: DOS  
;; SOFTWARE: FASTSEQ for Windows Version 2.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/092,296  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 60/048,910  
;; FILING DATE: 05-JUN-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Becker, Cheryl L.  
;; REGISTRATION NUMBER: 35,441  
;; REFERENCE/DOCKET NUMBER: 6104.US.01  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 847/935-1729  
;; TELEFAX: 847/938-2623  
;;  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 19:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 8 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;;  
US-09-092-236-19  
Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DYKDDDDK 8  
|||  
Db 1 DYKDDDDK 8  
  
RESULT 75  
US-09-104-408-36  
; Sequence 36, Application US/09104408  
; Publication No. US20020188115A1  
; GENERAL INFORMATION:  
; APPLICANT: Billing-Medel, Patricia A. et al.  
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/104,408  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 6122.US.01  
; FILING DATE: 25-JUN-1997  
; ATTORNEY/AGENT INFORMATION:

;; NAME: Becker, Cheryl L  
;; REGISTRATION NUMBER: 35,441  
;; REFERENCE/DOCKET NUMBER:  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 847/935-1729  
;; TELEFAX: 847/938-2623  
;;  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 36:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 8 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;;  
US-09-104-408-36  
Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DYKDDDDK 8  
|||  
Db 1 DYKDDDDK 8  
  
RESULT 76  
US-09-861-097-15  
; Sequence 15, Application US/09861097  
; Publication No. US20020192218A1  
; GENERAL INFORMATION:  
; APPLICANT: KARIN, MICHAEL  
; DAVIS, ROGER  
; MASAHITO, HIBI  
; ANNING, LIN  
; DERRARD, BENOIT  
; TITLE OF INVENTION: ONCOPROTEIN PROTEIN KINASE  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FISH & RICHARDSON P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/861,097  
; FILING DATE: 18-May-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/220,602  
; FILING DATE: 25-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hallie, Ph.D., Lisa A.,  
; REGISTRATION NUMBER: 38,347  
; REFERENCE/DOCKET NUMBER: 07257/015001 (PD3205)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 678-5070  
; TELEFAX: (619) 678-5099  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..8  
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-09-861-097-15

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDK 8  
Db 1 DYKDDDK 8

RESULT 77

US-09-814-604-5  
; Sequence 5, Application US/09814604  
; Publication No. US2003003517A1  
; GENERAL INFORMATION:  
; APPLICANT: Klein, Elliott S.  
; APPLICANT: Chandraratna Roshantha A.  
; TITLE OF INVENTION: Methods of Detecting Disassociated Nuclear  
; TITLE OF INVENTION: Hormone Receptor Ligands  
; FILE REFERENCE: P-AR 4528  
; CURRENT APPLICATION NUMBER: US/09/814,604  
; CURRENT FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide  
US-09-814-604-5

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDK 8  
Db 1 DYKDDDK 8

RESULT 78

US-09-908-943A-186  
; Sequence 186, Application US/09908943A  
; Publication No. US20030017991A1  
; GENERAL INFORMATION:  
; APPLICANT: Yan, Riqiang  
; APPLICANT: Tomasselli, Alfredo G.  
; APPLICANT: Gurney, Mark E.  
; APPLICANT: Emmons, Thomas L.  
; APPLICANT: Bienkowski, Mike J.  
; APPLICANT: Heiniksen, Robert L.  
; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY  
; FILE REFERENCE: 29915/00281A.US1  
; CURRENT APPLICATION NUMBER: US/09/908,943A  
; CURRENT FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: 60/219,795  
; PRIOR FILING DATE: 2000-07-19  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 186  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide sequence  
US-09-908-943A-186

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDK 8  
Db 1 DYKDDDK 8

RESULT 79

US-09-997-623-47  
; Sequence 47, Application US/09997623  
; Publication No. US20030018175A1  
; GENERAL INFORMATION:  
; APPLICANT: Maxygen Aps; Maxygen Holdings  
; TITLE OF INVENTION: Protein C or activated protein C-like molecules  
; FILE REFERENCE: 0219us410 - protein C  
; CURRENT APPLICATION NUMBER: US/09/997,623  
; CURRENT FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: US 09/978,917  
; PRIOR FILING DATE: 2001-10-17  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 47  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: peptide tag  
US-09-997-623-47

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDK 8  
Db 1 DYKDDDK 8

RESULT 80

US-09-995-898A-12  
; Sequence 12, Application US/09995898A  
; Publication No. US20030027253A1  
; GENERAL INFORMATION:  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Xu, Wenfeng  
; APPLICANT: No. US20030027253A1ak, Julia E.  
; APPLICANT: Whitmore, Theodore E.  
; APPLICANT: Grant, Francis J.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19  
; FILE REFERENCE: 00-108  
; CURRENT APPLICATION NUMBER: US/09/995,898A  
; CURRENT FILING DATE: 2001-11-28  
; PRIOR APPLICATION NUMBER: US 60/253,561  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US 60/267,211  
; PRIOR FILING DATE: 2001-02-07  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 12  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: FLAG peptide tag  
US-09-995-898A-12

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDK 8  
Db 1 DYKDDDK 8

```
RESULT 81
US-09-978-917A-47
; Sequence 47, Application US/09978917A
; Publication No. US20030027299A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Aps; Maxygen Holdings
; TITLE OF INVENTION: Protein C or activated protein C-like molecules
; FILE REFERENCE: 0219us310 - Protein C
; CURRENT APPLICATION NUMBER: US/09/978,917A
; CURRENT FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide tag
US-09-978-917A-47

Query Match          100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 82
US-09-436-184-7
; Sequence 7, Application US/09436184
; Publication No. US20030031670A1
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R.
; APPLICANT: de la Monte, Suzanne M.
; APPLICANT: Ince, Nedim
; APPLICANT: Carlson, Rolf I.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
; FILE REFERENCE: R.I. Hosp. - Malignant Neoplasms
; CURRENT APPLICATION NUMBER: US/09/436,184
; CURRENT FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: FLAG epitope
US-09-436-184-7

Query Match          100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 83
US-09-950-634-23
; Sequence 23, Application US/09950634
; Publication No. US20030032775A1
; GENERAL INFORMATION:
; APPLICANT: Molnar-Kimber, Katherine L.
; APPLICANT: Falli, Amedeo F.
; APPLICANT: Caggiano, Thomas J.
; APPLICANT: Nakanishi, Koji
; APPLICANT: Chen, Yangju
; TITLE OF INVENTION: EFFECTOR PROTEINS OF RAPAMYCIN
```

```
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: Finnegan, Henderson, Farabow, Garrett &
Dunnet, L.L.P.
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/950,634
FILING DATE: 13-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/471,112
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/384,524
FILING DATE: 13-FEB-1995
APPLICATION NUMBER: US 08/312,023
FILING DATE: 26-SEP-1995
APPLICATION NUMBER: US 08/207,975
FILING DATE: 08-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Siekman, Michael T.
REGISTRATION NUMBER: 36,276
REFERENCE/DOCKET NUMBER: 01142, 0058-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-950-634-23

Query Match          100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 84
US-09-846-033B-225
; Sequence 225, Application US/09846033B
; Publication No. US20030044404A1
; GENERAL INFORMATION:
; APPLICANT: Rebar, Edward
; APPLICANT: Jamieson, Andrew
; APPLICANT: Liu, Qiang
; APPLICANT: Liu, Pei-Qi
; APPLICANT: Wolfe, Alan
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Angiogenesis with Zinc
; FILE REFERENCE: 019496-005820US
; CURRENT APPLICATION NUMBER: US/09/846,033B
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 09/733,604
; PRIOR FILING DATE: 2000-12-07
```

PRIOR APPLICATION NUMBER: US 09/736,083  
PRIOR FILING DATE: 2000-12-12  
NUMBER OF SEQ ID NOS: 252  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 225  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: FLAG peptide  
US-09-846-033B-225

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8  
Db 1 DYKDDDK 8

## RESULT 85

US-09-861-098-15  
Sequence 15, Application US/09861098  
Publication No. US20030044788A1

GENERAL INFORMATION:  
APPLICANT: KARIN, MICHAEL

DAVIS, ROGER  
MASAHITO, HIBI  
ANNING, LIN

DERJARD, BENOIT  
TITLE OF INVENTION: ONCOPROTEIN PROTEIN KINASE

NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:

ADDRESSER: FISH & RICHARDSON P.C.  
STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla  
STATE: California

COUNTRY: USA  
ZIP: 92037

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/861,098  
FILING DATE: 18-May-2001

CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/220,602  
FILING DATE: 25-MAR-1994

ATTORNEY/AGENT INFORMATION:  
NAME: Hallie, Ph.D., Lisa A.,

REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07257/015001 (PD3205)

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 678-5070

TELEFAX: (619) 678-5099  
INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids

TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: peptide

FEATURE:  
NAME/KEY: Peptide

LOCATION: 1..8  
SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-09-861-098-15

Query Match 100.0%; Score 47; DB 3; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8  
Db 1 DYKDDDK 8

## RESULT 86

US-09-989-981A-12

Sequence 12, Application US/09989981A  
Publication No. US20030049730A1

GENERAL INFORMATION:  
APPLICANT: Hobbs, Helen H.

APPLICANT: Shan, Bel  
APPLICANT: Barnes, Robert

APPLICANT: Tian, Hui  
APPLICANT: Talarik Inc.

APPLICANT: Board of Regents, The University of Texas System  
TITLE OF INVENTION: ABCG5 and ABCG8: Compositions and Methods of Use

FILE REFERENCE: 018781-007320US  
CURRENT APPLICATION NUMBER: US/09/989,981A

CURRENT FILING DATE: 2002-07-23  
PRIOR APPLICATION NUMBER: US 60/252,235

PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/253,645

PRIOR FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO 12

LENGTH: 8  
TYPE: PRT

ORGANISM: Artificial Sequence  
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: anti-DYKDDDK  
US-09-989-981A-12

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8  
Db 1 DYKDDDK 8

## RESULT 87

US-09-993-180-33

Sequence 33, Application US/09993180  
Publication No. US2003005445A1

GENERAL INFORMATION:  
APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN SERPIN SECRETED FROM LYMPH

FILE REFERENCE: D0051.NP  
CURRENT APPLICATION NUMBER: US/09/993,180

CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: US 60/248,434

PRIOR FILING DATE: 2000-11-14  
PRIOR APPLICATION NUMBER: US 60/257,610

PRIOR FILING DATE: 2000-12-21  
PRIOR APPLICATION NUMBER: US 60/282,745

PRIOR FILING DATE: 2001-04-10  
NUMBER OF SEQ ID NOS: 46

SOFTWARE: Patent in version 3.0  
SEQ ID NO 33

LENGTH: 8  
TYPE: PRT

ORGANISM: Bacteriophage T7  
US-09-993-180-33

Query Match 100.0%; Score 47; DB 3; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
|||||  
Db 1 DYKDDDDK 8

## RESULT 88

US-09-759-595-7  
; Sequence 7, Application US/09/759595  
; Publication No. US20030059916A1  
; GENERAL INFORMATION:  
; APPLICANT: Wesche, Holger  
; APPLICANT: Li, Shyun  
; APPLICANT: Tularik Inc.  
; TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use  
; FILE REFERENCE: 018781-003910US  
; CURRENT APPLICATION NUMBER: US/09/759,595  
; PRIOR FILING DATE: 2001-01-13  
; PRIOR APPLICATION NUMBER: US 60/176,395  
; PRIOR FILING DATE: 2000-01-13  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:epitope tag  
US-09-759-595-7

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
|||||  
Db 1 DYKDDDDK 8

## RESULT 89

US-09-999-220B-9  
; Sequence 9, Application US/09999220B  
; Publication No. US20030059923A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUB  
; FILE REFERENCE: D0050NP  
; CURRENT APPLICATION NUMBER: US/09/999,220B  
; PRIOR FILING DATE: 2002-06-04  
; PRIOR APPLICATION NUMBER: US 60/245,383  
; PRIOR FILING DATE: 2000-11-02  
; PRIOR APPLICATION NUMBER: US 60/257,780  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: US 60/269,854  
; PRIOR FILING DATE: 2001-02-20  
; NUMBER OF SEQ ID NOS: 143  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: bacteriophage T7  
US-09-999-220B-9

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
|||||  
Db 1 DYKDDDDK 8

## RESULT 90

US-09-880-748-3238  
; Sequence 3238, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PFS23  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3238  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; NAME/KEY: site  
; LOCATION: (1)..(8)  
; OTHER INFORMATION: Flag Tag  
US-09-880-748-3238

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
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Db 1 DYKDDDDK 8

## RESULT 91

US-09-904-196B-14  
; Sequence 14, Application US/09904196B  
; Publication No. US20030064922A1  
; GENERAL INFORMATION:  
; APPLICANT: NISSEN, TORBEN LAUESGAARD  
; APPLICANT: ANDERSEN, KIM VILBOUR  
; APPLICANT: HANSEN, CHRISTIAN KARSTEN  
; APPLICANT: MIKKELSEN, JAN MOLLER  
; TITLE OF INVENTION: G-CSF CONJUGATES  
; FILE REFERENCE: 31-000700US  
; CURRENT APPLICATION NUMBER: US/09/904,196B  
; PRIOR FILING DATE: 2001-07-11  
; PRIOR APPLICATION NUMBER: US/09/760,008  
; PRIOR FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: 60/176,376  
; PRIOR FILING DATE: 2000-01-14  
; PRIOR APPLICATION NUMBER: 60/189,506  
; PRIOR FILING DATE: 2000-03-15  
; PRIOR APPLICATION NUMBER: 60/215,644  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: DK PA 2000 00024  
; PRIOR FILING DATE: 2000-01-10  
; PRIOR APPLICATION NUMBER: DK PA 2000 00341  
; PRIOR FILING DATE: 2000-03-02  
; PRIOR APPLICATION NUMBER: DK PA 2000 00943  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14

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; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-904-196B-14
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Query Match      100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 DYKDDDDK 8
Db      1 DYKDDDDK 8
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RESULT 92
US-09-972-473-19
; Sequence 19, Application US/09972473
; Publication No. US20030068312A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: NOVEL HUMAN DICKKOPF-RELATED PROTEIN AND NUCLEIC ACID
; FILE REFERENCE: NMI-108CP2
; CURRENT APPLICATION NUMBER: US/09/972,473
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 09/263,022
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: 08/843,704
; PRIOR FILING DATE: 1997-04-16
; PRIOR APPLICATION NUMBER: 08/842,898
; PRIOR FILING DATE: 1997-04-17
; PRIOR APPLICATION NUMBER: 60/071,589
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: 09/009,802
; PRIOR FILING DATE: 1998-01-20
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 8
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-972-473-19
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Query Match      100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 DYKDDDDK 8
Db      1 DYKDDDDK 8
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RESULT 93
US-09-922-226-39
; Sequence 39, Application US/09922226
; Publication No. US20030077664A1
; GENERAL INFORMATION:
; APPLICANT: Zhao, Yi
; APPLICANT: Thacher, Scott M.
; APPLICANT: Xiao, Jia-Hao
; APPLICANT: Kusari, Jyotirmoy
; APPLICANT: Chanaratana, Roshantha A.
; TITLE OF INVENTION: Methods of Screening For Compounds That
; FILE REFERENCE: P-AR 4681
; CURRENT APPLICATION NUMBER: US/09/922,226
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: US 60/284,797
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 191
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-922-226-39
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Query Match      100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 DYKDDDDK 8
Db      1 DYKDDDDK 8
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RESULT 94
US-09-774-381-21
; Sequence 21, Application US/09774381
; Publication No. US20030082677A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Pan, Yang
; APPLICANT: Geating, David P.
; TITLE OF INVENTION: NOVEL EDIIF, MTR-1, LSP-1, TAP-1, AND PA-I MOLECULES
; FILE REFERENCE: NMI-107CP2
; CURRENT APPLICATION NUMBER: US/09/774,381
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 08/941,354
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/010,674
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/061,149
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 09/014,347
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 60/061,159
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 09/474,151
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 09/004,206
; PRIOR FILING DATE: 1998-01-08
; PRIOR APPLICATION NUMBER: 60/061,143
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 09/483,414
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/213,571
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/994,890
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: flag epitope
US-09-774-381-21
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Query Match      100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 DYKDDDDK 8
Db      1 DYKDDDDK 8
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RESULT 97  
US-09-782-587B-18  
; Sequence 18, Application US/09782587B

Query Match	100.0%;	Score 47;	DB 3;	length 8;
Best Local Similarity	100.0%;	Pred. No. 1.9e+06;		
Matches	8;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0

QY	1	DYKDDDDK	8
Db	1	DYKDDDDK	8



## RESULT 99

US-09-994-487-2  
; Sequence 2, Application US/09994487  
; Publication No. US20030099954A1  
; GENERAL INFORMATION:  
; APPLICANT: Miltenyi, Stefan  
; APPLICANT: Kohler, Matthias  
; TITLE OF INVENTION: Apparatus and method for modification of  
; TITLE OF INVENTION: magnetically immobilized biomolecules  
; FILE REFERENCE: MLT004  
; CURRENT APPLICATION NUMBER: US/09/994,487  
; CURRENT FILING DATE: 2001-11-26  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide  
US-09-994-487-2

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
|||  
Db 1 DYKDDDDK 8

## RESULT 100

US-09-803-472-5  
; Sequence 5, Application US/09803472  
; Publication No. US20030118990A1  
; GENERAL INFORMATION:  
; APPLICANT: Brooks, Alan R.  
; APPLICANT: Deng, Gary G.  
; APPLICANT: Rubanyi, Gabor M.  
; APPLICANT: Schering Aktiengesellschaft  
; TITLE OF INVENTION: No. US20030118990A1 Estrogen-Regulated G Protein Gamma Subunit;  
; FILE REFERENCE: 015303-000510US  
; CURRENT APPLICATION NUMBER: US/09/803,472  
; CURRENT FILING DATE: 2001-03-10  
; PRIOR APPLICATION NUMBER: US 60/188,460  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: General  
US-09-803-472-5

Query Match 100.0%; Score 47; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
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Db 1 DYKDDDDK 8

Search completed: June 29, 2006, 11:55:57  
Job time : 193 secs

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OM protein - protein search, using sw model

Run on: June 29, 2006, 11:52:56 ; Search time 19 Seconds  
(without alignments)  
9.945 Million cell updates/sec

Title: US-10-671-054-2

Perfect score: 47  
Sequence: 1 DYKDDDK 8

Scoring table: BLOSUM62  
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Searched: 103426 seqs, 23619683 residues

Total number of hits satisfying chosen parameters: 103426

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 500 summaries

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Published Applications AA New:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	47	100.0	8	1 US-09-728-720A-13	Sequence 13, Appl
2	47	100.0	8	6 US-10-623-808-16	Sequence 16, Appl
3	47	100.0	8	6 US-10-660-893A-3	Sequence 3, Appl
4	47	100.0	8	7 US-11-299-013-1	Sequence 1, Appl
5	47	100.0	8	7 US-11-252-276-36	Sequence 36, Appl
6	47	100.0	8	7 US-11-261-630-5	Sequence 5, Appl
7	47	100.0	8	7 US-11-134-228A-5	Sequence 5, Appl
8	47	100.0	8	7 US-11-313-356-28	Sequence 28, Appl
9	47	100.0	8	7 US-11-328-747-16	Sequence 16, Appl
10	47	100.0	8	7 US-11-264-463-2	Sequence 2, Appl
11	47	100.0	8	7 US-11-128-422-16	Sequence 16, Appl
12	47	100.0	8	7 US-11-270-796-29	Sequence 29, Appl
13	47	100.0	9	7 US-11-328-747-17	Sequence 17, Appl
14	47	100.0	9	7 US-11-264-463-3	Sequence 3, Appl
15	47	100.0	19	7 US-11-251-734-0	Sequence 20, Appl
16	47	100.0	20	6 US-10-821-930-26	Sequence 26, Appl
17	47	100.0	23	7 US-11-251-734-18	Sequence 18, Appl
18	47	100.0	23	7 US-11-251-734-19	Sequence 19, Appl
19	47	100.0	84	7 US-11-328-747-14	Sequence 14, Appl
20	47	100.0	84	7 US-11-090-563-14	Sequence 14, Appl
21	47	100.0	85	7 US-11-328-747-15	Sequence 15, Appl
22	47	100.0	85	7 US-11-090-563-15	Sequence 15, Appl
23	47	100.0	86	7 US-11-328-747-18	Sequence 18, Appl
24	47	100.0	99	6 US-10-971-483-12	Sequence 12, Appl
25	47	100.0	340	7 US-11-180-855-3	Sequence 3, Appl

26	47	100.0	531	7	US-11-180-855-2	Sequence 2, Appl
27	47	100.0	671	7	US-11-267-837A-6	Sequence 6, Appl
28	43	91.5	8	7	US-11-134-228A-6	Sequence 6, Appl
29	42	89.4	7	6	US-10-484-105-4	Sequence 4, Appl
30	42	89.4	35	7	US-11-299-013-17	Sequence 17, Appl
31	42	89.4	91	6	US-10-953-349-29832	Sequence 29831, A
32	39	83.0	92	6	US-10-953-349-29831	Sequence 29831, A
33	39	83.0	428	6	US-10-953-349-33141	Sequence 33141, A
34	39	83.0	429	6	US-10-953-349-33140	Sequence 33140, A
35	39	83.0	463	6	US-10-953-349-33139	Sequence 33139, A
36	38	80.9	275	6	US-10-953-349-6317	Sequence 6317, Ap
37	38	80.9	294	6	US-10-953-349-6316	Sequence 6316, Ap
38	38	80.9	315	6	US-10-953-349-6315	Sequence 6315, Ap
39	37	78.7	164	6	US-10-449-902-29313	Sequence 29313, A
40	37	78.7	389	6	US-10-953-349-21221	Sequence 21221, A
41	37	78.7	433	6	US-10-953-349-21220	Sequence 21220, A
42	37	78.7	567	7	US-10-449-902-45116	Sequence 45116, A
43	36	76.6	194	6	US-10-449-902-29232	Sequence 29232, A
44	36	76.6	194	6	US-10-449-902-49424	Sequence 49424, A
45	36	76.6	411	6	US-10-449-902-54492	Sequence 54492, A
46	36	76.6	533	6	US-10-449-902-40889	Sequence 40889, A
47	36	76.6	8	7	US-11-267-837A-9	Sequence 9, Appl
48	35	74.5	204	6	US-10-449-902-34551	Sequence 34551, A
49	35	74.5	342	6	US-10-449-902-31822	Sequence 31822, A
50	35	74.5	342	6	US-10-449-902-40463	Sequence 40463, A
51	35	74.5	351	6	US-10-449-902-44996	Sequence 44996, A
52	35	74.5	351	6	US-10-449-902-46241	Sequence 46241, A
53	35	74.5	734	6	US-10-449-902-46241	Sequence 46241, A
54	34	72.3	133	6	US-10-953-349-18302	Sequence 18302, A
55	34	72.3	133	6	US-10-953-349-39990	Sequence 39990, A
56	34	72.3	150	6	US-10-953-349-6258	Sequence 6258, Ap
57	34	72.3	163	6	US-10-953-349-6257	Sequence 6257, Ap
58	34	72.3	219	6	US-10-449-902-31740	Sequence 31740, A
59	34	72.3	219	6	US-10-449-902-40441	Sequence 40441, A
60	34	72.3	222	6	US-10-953-349-6256	Sequence 6256, Ap
61	34	72.3	229	6	US-10-953-349-2040	Sequence 2040, Ap
62	34	72.3	294	6	US-10-449-902-41697	Sequence 41697, A
63	34	72.3	301	6	US-10-953-349-36044	Sequence 36044, A
64	34	72.3	338	6	US-10-953-349-2039	Sequence 2039, Ap
65	34	72.3	340	6	US-10-953-349-2038	Sequence 2038, Ap
66	34	72.3	362	6	US-10-953-349-51131	Sequence 51131, Ap
67	34	72.3	373	6	US-10-449-902-52372	Sequence 52372, A
68	34	72.3	410	6	US-10-449-902-43294	Sequence 43294, A
69	34	72.3	437	6	US-10-449-902-42067	Sequence 42067, A
70	34	72.3	497	6	US-10-449-902-50266	Sequence 50266, A
71	34	72.3	520	6	US-10-449-902-44569	Sequence 44569, A
72	34	72.3	521	6	US-10-449-902-45621	Sequence 45621, A
73	34	72.3	684	6	US-10-449-902-45113	Sequence 45113, A
74	34	72.3	75	6	US-10-953-349-21280	Sequence 21280, A
75	33	70.2	145	6	US-10-449-902-30504	Sequence 30504, A
76	33	70.2	171	6	US-10-449-902-34122	Sequence 34122, A
77	33	70.2	203	6	US-10-953-349-37604	Sequence 37604, A
78	33	70.2	221	6	US-10-449-902-50940	Sequence 50940, A
79	33	70.2	431	6	US-10-449-902-30872	Sequence 30872, A
80	33	70.2	508	6	US-10-449-902-37911	Sequence 37911, A
81	33	70.2	553	6	US-10-471-571A-3230	Sequence 3230, Ap
82	33	70.2	770	6	US-10-449-902-40911	Sequence 40911, A
83	33	70.2	876	6	US-10-449-902-11438	Sequence 31438, A
84	33	70.2	936	6	US-10-449-902-56037	Sequence 56037, A
85	33	70.2	1179	6	US-10-449-902-52762	Sequence 52762, A
86	33	70.2	1180	6	US-10-449-902-53947	Sequence 53947, A
87	33	70.2	1230	7	US-11-289-902-378	Sequence 378, App
88	32	68.1	39	7	US-11-074-497-41	Sequence 41, Appl
89	32	68.1	74	6	US-10-449-902-33449	Sequence 43449, A
90	32	68.1	80	6	US-10-449-902-33753	Sequence 33753, A
91	32	68.1	146	6	US-10-449-902-36276	Sequence 36276, A
92	32	68.1	203	6	US-10-953-349-62282	Sequence 62282, Ap
93	32	68.1	205	6	US-10-449-902-29282	Sequence 29282, A
94	32	68.1	221	6	US-10-516-753-74	Sequence 74, Appl
95	32	68.1	231	6	US-10-953-349-6226	Sequence 6226, Ap
96	32	68.1	234	6	US-10-953-349-16219	Sequence 16219, A
97	32	68.1	240	6	US-10-953-349-16218	Sequence 16218, A
98	32	68.1	252	6	US-10-953-349-31660	Sequence 31660, A

99	32	68.1	255	6	US-10-953-349-20549	Sequence 20549, A	172	31	66.0	546	6	US-10-953-349-952	Sequence 952, App
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101	32	68.1	266	6	US-10-449-902-44903	Sequence 44903, A	174	31	66.0	614	6	US-10-449-902-55812	Sequence 55812, A
102	32	68.1	267	6	US-10-449-902-40045	Sequence 40045, A	175	31	66.0	733	6	US-10-449-902-41111	Sequence 41111, A
103	32	68.1	269	6	US-10-953-349-20548	Sequence 20548, A	176	31	66.0	751	6	US-10-539-630-1	Sequence 1, Appl1
104	32	68.1	277	6	US-10-449-902-33165	Sequence 33165, A	177	31	66.0	866	6	US-10-449-902-36491	Sequence 36491, A
105	32	68.1	277	6	US-10-449-902-43906	Sequence 43906, A	178	31	66.0	1015	6	US-10-953-349-2317	Sequence 2317, Ap
106	32	68.1	277	6	US-10-449-902-51355	Sequence 51355, A	179	31	66.0	1074	6	US-10-953-349-2316	Sequence 2316, Ap
107	32	68.1	298	6	US-10-953-349-7011	Sequence 7011, Ap	180	31	66.0	1100	6	US-10-953-349-2315	Sequence 2315, Ap
108	32	68.1	310	6	US-10-449-902-28498	Sequence 28498, A	181	31	66.0	1273	6	US-10-449-902-32945	Sequence 32945, A
109	32	68.1	310	6	US-10-449-902-51718	Sequence 51718, A	182	30.5	64.9	378	6	US-10-953-349-19598	Sequence 19598, A
110	32	68.1	332	6	US-10-449-902-29386	Sequence 29386, A	183	30.5	64.9	392	6	US-10-953-349-19597	Sequence 19597, A
111	32	68.1	334	6	US-10-953-349-20199	Sequence 20199, A	184	30.5	64.9	415	6	US-10-953-349-19596	Sequence 19596, A
112	32	68.1	350	6	US-10-953-349-7010	Sequence 7010, Ap	185	30	63.8	116	6	US-10-953-349-6027	Sequence 6027, Ap
113	32	68.1	350	6	US-10-449-902-55155	Sequence 55155, A	186	30	63.8	116	6	US-10-953-349-6027	Sequence 6027, Ap
114	32	68.1	354	6	US-10-953-349-20198	Sequence 20199, A	187	30	63.8	131	6	US-10-953-349-38860	Sequence 38860, A
115	32	68.1	368	6	US-10-449-902-55863	Sequence 55863, A	188	30	63.8	137	6	US-10-953-349-18211	Sequence 18211, A
116	32	68.1	369	6	US-10-449-902-29848	Sequence 29848, A	189	30	63.8	145	6	US-10-953-349-18241	Sequence 18241, Ap
117	32	68.1	371	6	US-10-449-902-33123	Sequence 33123, A	190	30	63.8	145	6	US-10-953-349-6871	Sequence 6871, Ap
118	32	68.1	375	6	US-10-449-902-45980	Sequence 45980, A	191	30	63.8	158	6	US-10-953-349-18105	Sequence 18105, A
119	32	68.1	381	6	US-10-449-902-50140	Sequence 50140, A	192	30	63.8	158	6	US-10-953-349-6870	Sequence 6870, Ap
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121	32	68.1	390	6	US-10-953-349-22063	Sequence 22063, A	194	30	63.8	186	6	US-10-953-349-2917	Sequence 2917, Ap
122	32	68.1	422	6	US-10-449-902-37495	Sequence 37495, A	195	30	63.8	187	6	US-10-449-902-56082	Sequence 56082, A
123	32	68.1	447	6	US-10-449-902-53423	Sequence 53423, A	196	30	63.8	208	6	US-10-953-349-6026	Sequence 6026, Ap
124	32	68.1	490	6	US-10-449-902-40643	Sequence 40643, A	197	30	63.8	209	6	US-10-449-902-37987	Sequence 37987, A
125	32	68.1	525	6	US-10-953-349-8358	Sequence 8358, Ap	198	30	63.8	211	6	US-10-535-267-25	Sequence 25, Appl1
126	32	68.1	534	6	US-10-449-902-47590	Sequence 47590, A	199	30	63.8	213	6	US-10-953-349-27842	Sequence 27842, A
127	32	68.1	597	6	US-10-953-349-8357	Sequence 8357, Ap	200	30	63.8	214	6	US-10-449-902-35673	Sequence 35673, A
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129	32	68.1	630	6	US-10-953-349-10969	Sequence 10969, A	202	30	63.8	215	7	US-11-254-679-2	Sequence 2, Appl1
130	32	68.1	646	6	US-10-953-349-10968	Sequence 10968, A	203	30	63.8	217	6	US-10-449-902-30495	Sequence 30495, A
131	32	68.1	658	6	US-10-449-902-40962	Sequence 40962, A	204	30	63.8	219	6	US-10-449-902-47993	Sequence 47993, A
132	32	68.1	660	6	US-10-953-349-10967	Sequence 10967, A	205	30	63.8	226	6	US-10-953-349-38859	Sequence 38859, A
133	32	68.1	711	6	US-10-449-902-48927	Sequence 48927, A	206	30	63.8	229	6	US-10-449-902-50980	Sequence 50980, A
134	32	68.1	877	6	US-10-449-902-55247	Sequence 55247, A	207	30	63.8	226	6	US-10-953-349-10756	Sequence 10756, A
135	32	68.1	922	7	US-11-273-537-14	Sequence 14, Appl1	208	30	63.8	226	6	US-10-953-349-10756	Sequence 10756, A
136	32	68.1	928	6	US-10-449-902-41155	Sequence 41155, A	209	30	63.8	228	6	US-10-449-902-38879	Sequence 38879, A
137	32	68.1	1001	6	US-10-449-902-41217	Sequence 41217, A	210	30	63.8	240	6	US-10-953-349-38858	Sequence 38858, A
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141	31	66.0	222	6	US-10-449-902-50962	Sequence 50962, A	214	30	63.8	246	6	US-10-953-349-10755	Sequence 10755, A
142	31	66.0	237	6	US-10-471-571A-162	Sequence 162, App	215	30	63.8	247	6	US-10-449-902-38361	Sequence 38361, A
143	31	66.0	247	6	US-10-449-902-56243	Sequence 56243, A	216	30	63.8	249	6	US-10-449-902-46432	Sequence 46432, A
144	31	66.0	248	6	US-10-449-902-33569	Sequence 33569, A	217	30	63.8	250	6	US-10-953-349-2915	Sequence 2915, Ap
145	31	66.0	264	6	US-10-449-902-38887	Sequence 38887, A	218	30	63.8	255	6	US-10-449-902-33302	Sequence 33302, A
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153	31	66.0	374	6	US-10-449-902-46833	Sequence 46833, A	226	30	63.8	328	6	US-10-449-902-38174	Sequence 38174, A
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165	31	66.0	458	6	US-10-953-349-8079	Sequence 8079, Ap	238	30	63.8	394	6	US-10-449-902-39594	Sequence 39594, A
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247	30	63.8	427	6	US-10-449-902-54385	Sequence 54385, A	320	29	61.7	65	7	US-11-325-265-7	Sequence 7, Appl
248	30	63.8	441	6	US-10-449-902-54653	Sequence 54653, A	321	29	61.7	66	7	US-11-324-947-26	Sequence 26, Appl
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287	30	63.8	777	6	US-10-449-902-53211	Sequence 53211, A	360	29	61.7	226	6	US-10-449-902-11658	Sequence 30420, A
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303	30	63.8	1181	7	US-11-241-596-257	Sequence 257, App	376	29	61.7	249	7	US-11-289-102-376	Sequence 376, App
304	30	63.8	1181	7	US-11-241-596-258	Sequence 258, App	377	29	61.7	252	6	US-10-449-902-48996	Sequence 48996, A
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306	30	63.8	1291	7	US-11-289-102-389	Sequence 389, App	379	29	61.7	252	7	US-11-345-110-8	Sequence 8, Appl
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316	29	61.7	9	7	US-11-240-651-10	Sequence 10, Appl	389	29	61.7	282	6	US-10-449-902-41677	Sequence 41677, A
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394	29	61.7	288	6	US-10-449-902-33889	Sequence 33889, A
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414	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
415	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
416	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
417	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
418	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
419	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
420	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
421	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
422	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
423	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
424	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
425	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
426	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
427	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
428	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
429	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
430	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
431	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
432	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
433	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
434	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
435	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
436	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
437	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
438	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
439	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
440	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
441	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
442	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
443	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
444	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
445	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
446	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
447	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
448	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
449	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
450	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
451	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
452	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
453	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
454	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
455	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
456	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
457	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
458	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
459	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
460	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
461	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
462	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A
463	29	61.7	288	6	US-10-953-349-7583	Sequence 7583, A

464	29	61.7	447	7	US-11-263-326-120	Sequence 120, App
465	29	61.7	447	7	US-10-953-349-22056	Sequence 22056, A
466	29	61.7	447	7	US-10-449-902-34736	Sequence 34736, A
467	29	61.7	447	7	US-10-706-435A-26	Sequence 26, App1
468	29	61.7	447	7	US-10-706-435A-4	Sequence 4, App1
469	29	61.7	447	7	US-10-527-411-70	Sequence 70, App1
470	29	61.7	447	7	US-10-527-411-114	Sequence 114, App
471	29	61.7	447	7	US-10-449-902-49209	Sequence 49209, A
472	29	61.7	447	7	US-10-449-902-34283	Sequence 34283, A
473	29	61.7	447	7	US-10-449-902-34283	Sequence 34283, A
474	29	61.7	447	7	US-10-449-902-34283	Sequence 34283, A
475	29	61.7	447	7	US-10-449-902-34283	Sequence 34283, A
476	29	61.7	447	7	US-10-449-902-34283	Sequence 34283, A
477	29	61.7	447	7	US-10-449-902-34283	Sequence 34283, A
478	29	61.7	447	7	US-10-449-902-34283	Sequence 34283, A
479	29	61.7	447	7	US-10-449-902-34283	Sequence 34283, A
480	29	61.7	447	7	US-10-449-902-34283	Sequence 34283, A
481	29	61.7	447	7	US-10-449-902-34283	Sequence 34283, A
482	29	61.7	447	7	US-10-449-902-34283	Sequence 34283, A
483	29	61.7	447	7	US-10-449-902-34283	Sequence 34283, A
484	29	61.7	447	7	US-10-449-902-34283	Sequence 34283, A
485	29	61.7	447	7	US-10-449-902-34283	Sequence 34283, A
486	29	61.7	447	7	US-10-449-902-34283	Sequence 34283, A
487	29	61.7	447	7	US-10-449-902-34283	Sequence 34283, A
488	29	61.7	447	7	US-10-449-902-34283	Sequence 34283, A
489	29	61.7	447	7	US-10-449-902-34283	Sequence 34283, A
490	29	61.7	447	7	US-10-449-902-34283	Sequence 34283, A
491	29	61.7	447	7	US-10-449-902-34283	Sequence 34283, A
492	29	61.7	447	7	US-10-449-902-34283	Sequence 34283, A
493	29	61.7	447	7	US-10-449-902-34283	Sequence 34283, A
494	29	61.7	447	7	US-10-449-902-34283	Sequence 34283, A
495	29	61.7	447	7	US-10-449-902-34283	Sequence 34283, A
496	29	61.7	447	7	US-10-449-902-34283	Sequence 34283, A
497	29	61.7	447	7	US-10-449-902-34283	Sequence 34283, A
498	29	61.7	447	7	US-10-449-902-34283	Sequence 34283, A
499	29	61.7	447	7	US-10-449-902-34283	Sequence 34283, A
500	29	61.7	447	7	US-11-293-697-4703	Sequence 4703, App

## ALIGNMENTS

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RESULT 1
US-09-728-720A-13
; Sequence 13, Application US/09728720A
; Publication No. US20060104980A1
; GENERAL INFORMATION:
; APPLICANT: Fourn, Steven K.H.
; APPLICANT: Hadlock, Kenneth G.
; TITLE OF INVENTION: Prevention and Treatment of HCV Infection Employing
; TITLE OF INVENTION: Antibodies that Inhibit the Interaction of HCV Virions
; TITLE OF INVENTION: with Their Receptor.
; FILE REFERENCE: 2002850-0009
; CURRENT APPLICATION NUMBER: US/09/728,720A
; CURRENT FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Flag Epitope
US-09-728-720A-13
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Query Match 100.0%; Score 47; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.6e+04;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DYKDDDK 8  
1 DYKDDDK 8

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RESULT 2
US-10-623-808-16
; Sequence 16, Application US/10623808
; Publication No. US20060110802A1
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark R.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple 7.5.3
; SOFTWARE: Microsoft Word, Version #6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/623,808
; FILING DATE: 22-JUL-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,918
; FILING DATE: 06-May-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/060,843
; FILING DATE: 07-May-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2801-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: FLAG peptide
US-10-623-808-16

Query Match      100.0%; Score 47; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.6e+04;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 DYKDDDDK 8
      |||||
Db      1 DYKDDDDK 8

RESULT 3
US-10-660-893A-3
; Sequence 3, Application US/10660893A
; Publication No. US20060134629A1
; GENERAL INFORMATION:
; APPLICANT: Link, Charles
; TITLE OF INVENTION: Methods and Compositions for Elucidating Protein Expression
; TITLE OF INVENTION: Profiles in Cells
; FILE REFERENCE: 05237.0003.CPUS00
```

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; CURRENT APPLICATION NUMBER: US/10/660,893A
; CURRENT FILING DATE: 2003-09-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthesized in laboratory
US-10-660-893A-3

Query Match      100.0%; Score 47; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.6e+04;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 DYKDDDDK 8
      |||||
Db      1 DYKDDDDK 8

RESULT 4
US-11-299-013-1
; Sequence 1, Application US/11299013
; Publication No. US20060088878A1
; GENERAL INFORMATION:
; APPLICANT: BRIZARD, BILLY L
; APPLICANT: HERNAN, RON
; TITLE OF INVENTION: PURIFICATION OF RECOMBINANT PROTEINS FUSED TO MULTIPLE EPITOPES
; FILE REFERENCE: SG6933.7
; CURRENT APPLICATION NUMBER: US/11/299,013
; CURRENT FILING DATE: 2005-12-09
; PRIOR APPLICATION NUMBER: US 09/415,000
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/970,308
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthesized sequence
US-11-299-013-1

Query Match      100.0%; Score 47; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.6e+04;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 DYKDDDDK 8
      |||||
Db      1 DYKDDDDK 8

RESULT 5
US-11-252-276-36
; Sequence 36, Application US/11252276
; Publication No. US20060094868A1
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
; APPLICANT: Bright, Gary
; APPLICANT: Olson, Keith
; APPLICANT: Burroughs-Tencza, Sarah
; TITLE OF INVENTION: A System for Cell Based Screening
; FILE REFERENCE: 97-022-K2-CO
; CURRENT APPLICATION NUMBER: US/11/252,276
; CURRENT FILING DATE: 2005-10-17
; PRIOR APPLICATION NUMBER: 09/713,572
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: 09/430,656
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 09/398,965
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/ PRIOR FILING DATE: 1999-09-17
/ PRIOR APPLICATION NUMBER: 09/031,271
/ PRIOR FILING DATE: 1998-02-27
/ PRIOR APPLICATION NUMBER: 08/810,983
/ PRIOR FILING DATE: 1997-02-27
/ PRIOR APPLICATION NUMBER: 60/136,078
/ PRIOR FILING DATE: 1999-05-26
/ PRIOR APPLICATION NUMBER: 60/106,308
/ PRIOR FILING DATE: 1998-10-30
/ NUMBER OF SEQ ID NOS: 168
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 36
/ LENGTH: 8
/ TYPE: PRM
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: FLAG epitope
US-11-252-276-36
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Query Match          100.0%; Score 47; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.6e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 DYKDDDDK 8
        |||||
Db       1 DYKDDDDK 8
```

```
RESULT 6
US-11-261-630-5
/ Sequence 5, Application US/11261630
/ Publication No. US20060094062A1
/ GENERAL INFORMATION:
/ APPLICANT: Wu, Herten
/ TITLE OF INVENTION: ULTRA HIGH THROUGHPUT CAPTURE LIFT SCREENING METHODS
/ FILE REFERENCE: A6703US
/ CURRENT APPLICATION NUMBER: US/11/261,630
/ CURRENT FILING DATE: 2005-10-31
/ PRIOR APPLICATION NUMBER: 60/623,240
/ PRIOR FILING DATE: 2004-11-01
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 5
/ LENGTH: 8
/ TYPE: PRM
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: epitope tag
US-11-261-630-5
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```
Query Match          100.0%; Score 47; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.6e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 DYKDDDDK 8
        |||||
Db       1 DYKDDDDK 8
```

```
RESULT 7
US-11-134-228A-5
/ Sequence 5, Application US/11134228A
/ Publication No. US20060105320A1
/ GENERAL INFORMATION:
/ APPLICANT: Lindquist et al.
/ TITLE OF INVENTION: ELECTRICAL CONDUCTORS AND DEVICES FROM PRION-LIKE PROTEINS
/ FILE REFERENCE: 30554/40155A
/ CURRENT APPLICATION NUMBER: US/11/134,228A
/ CURRENT FILING DATE: 2005-05-20
/ PRIOR APPLICATION NUMBER: 60/573,277
/ PRIOR FILING DATE: 2004-05-20
/ NUMBER OF SEQ ID NOS: 73
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/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 5
/ LENGTH: 8
/ TYPE: PRM
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: FLAG peptide
US-11-134-228A-5
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```
Query Match          100.0%; Score 47; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.6e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 DYKDDDDK 8
        |||||
Db       1 DYKDDDDK 8
```

```
RESULT 8
US-11-313-356-28
/ Sequence 28, Application US/11313356
/ Publication No. US20060105379A1
/ GENERAL INFORMATION:
/ APPLICANT: Wu, Shujian
/ APPLICANT: Chen, Jian
/ APPLICANT: Feder, John
/ APPLICANT: Lee, Liana
/ APPLICANT: Krystek, Stanley
/ TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALLOPROTEASE HIGHLY EXPRESSED
/ FILE REFERENCE: D0141DIV
/ CURRENT APPLICATION NUMBER: US/11/313,356
/ CURRENT FILING DATE: 2005-12-21
/ PRIOR APPLICATION NUMBER: US 60/286,764
/ PRIOR FILING DATE: 2001-04-26
/ NUMBER OF SEQ ID NOS: 80
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 28
/ LENGTH: 8
/ TYPE: PRM
/ ORGANISM: bacteriophage T7
US-11-313-356-28
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Query Match          100.0%; Score 47; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.6e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 DYKDDDDK 8
        |||||
Db       1 DYKDDDDK 8
```

```
RESULT 9
US-11-328-747-16
/ Sequence 16, Application US/11328747
/ Publication No. US20060105409A1
/ GENERAL INFORMATION:
/ APPLICANT: Issakani, Sarkiz D.
/ APPLICANT: Huang, Jianing
/ APPLICANT: Sneung, Julie
/ APPLICANT: Pray, Todd R.
/ TITLE OF INVENTION: Ubiquitin Ligase Assay
/ FILE REFERENCE: 021044-007010US
/ CURRENT APPLICATION NUMBER: US/11/328,747
/ CURRENT FILING DATE: 2006-01-09
/ PRIOR APPLICATION NUMBER: US/10/835,096
/ PRIOR FILING DATE: 2004-04-28
/ PRIOR APPLICATION NUMBER: US/09/826,112
/ PRIOR FILING DATE: 2001-04-03
/ PRIOR APPLICATION NUMBER: US 09/542,497
/ PRIOR FILING DATE: 2000-04-03
/ NUMBER OF SEQ ID NOS: 21
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SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 16  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: FLAG peptide  
US-11-328-747-16

Query Match 100.0%; Score 47; DB 7; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.6e+04;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
DB 1 DYKDDDDK 8

RESULT 10  
US-11-264-463-2  
Sequence 2, Application US/11264463  
Publication No. US20060110782A1  
GENERAL INFORMATION:  
APPLICANT: BERTOZZI, CAROLYN R.  
APPLICANT: AGARD, NICHOLAS J.  
APPLICANT: PRESCHER, JENNIFER A.  
APPLICANT: BASKIN, JEREMY MICHAEL  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR  
FILE REFERENCE: BERK-039  
CURRENT APPLICATION NUMBER: US/11/264,463  
CURRENT FILING DATE: 2005-10-31  
PRIOR APPLICATION NUMBER: 60/624,202  
PRIOR FILING DATE: 2004-11-01  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic epitope  
US-11-264-463-2

Query Match 100.0%; Score 47; DB 7; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.6e+04;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
DB 1 DYKDDDDK 8

RESULT 11  
US-11-128-422-16  
Sequence 16, Application US/11128422  
Publication No. US20060127985A1  
GENERAL INFORMATION:  
APPLICANT: Alderson, Mark R.  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Smith, Craig A.  
TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple 7.5.3  
SOFTWARE: Microsoft Word, Version #6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/11/128,422  
FILING DATE: 13-May-2005  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/236,918  
FILING DATE: 06-May-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/060,843  
FILING DATE: 07-May-1993  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Anderson, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2801-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: FLAG peptide  
US-11-128-422-16

Query Match 100.0%; Score 47; DB 7; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.6e+04;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
DB 1 DYKDDDDK 8

RESULT 12  
US-11-270-796-29  
Sequence 29, Application US/11270796  
Publication No. US20060134068A1  
GENERAL INFORMATION:  
APPLICANT: Dong, Jiani  
TITLE OF INVENTION: TREATMENT OF CANCER BY SIMULTANEOUS INHIBITION OF BRAF AND  
FILE REFERENCE: 02420/1201581-US1  
CURRENT APPLICATION NUMBER: US/11/270,796  
CURRENT FILING DATE: 2005-11-08  
PRIOR APPLICATION NUMBER: 60/592,592  
PRIOR FILING DATE: 2004-07-30  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 29  
LENGTH: 8  
TYPE: PRT  
ORGANISM: artificial  
FEATURE:  
OTHER INFORMATION: synthetic peptide tag  
US-11-270-796-29

Query Match 100.0%; Score 47; DB 7; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.6e+04;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
DB 1 DYKDDDDK 8

Db 1 DYKDDDDK 8

RESULT 13  
US-11-328-747-17  
; Sequence 17, Application US/11328747  
; Publication No. US20060105409A1  
; GENERAL INFORMATION:  
; APPLICANT: Issakani, Sarkiz D.  
; APPLICANT: Huang, Jianing  
; APPLICANT: Sheung, Julie  
; APPLICANT: Pray, Todd R.  
; APPLICANT: Rigol Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Ubiquitin Ligase Assay  
; FILE REFERENCE: 021044-007010US  
; CURRENT APPLICATION NUMBER: US/11/328,747  
; PRIOR FILING DATE: 2006-01-09  
; PRIOR APPLICATION NUMBER: US/10/835,096  
; PRIOR FILING DATE: 2004-04-28  
; PRIOR APPLICATION NUMBER: US/09/826,312  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: US 09/542,497  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: FLAG-Cys  
US-11-328-747-17

Query Match 100.0%; Score 47; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.6e+04;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8  
Db 1 DYKDDDDK 8

RESULT 14  
US-11-264-463-3  
; Sequence 3, Application US/11264463  
; Publication No. US20060110782A1  
; GENERAL INFORMATION:  
; APPLICANT: BERTOZZI, CAROLYN R.  
; APPLICANT: AGARD, NICHOLAS J.  
; APPLICANT: PRESCHER, JENNIFER A.  
; APPLICANT: BASKIN, JEREMY MICHAEL  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR  
; TITLE OF INVENTION: MODIFICATION OF BIOMOLECULES  
; FILE REFERENCE: BERK-039  
; CURRENT APPLICATION NUMBER: US/11/264,463  
; CURRENT FILING DATE: 2005-10-31  
; PRIOR APPLICATION NUMBER: 60/624,202  
; PRIOR FILING DATE: 2004-11-01  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic epitope  
US-11-264-463-3

Query Match 100.0%; Score 47; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.6e+04;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8

Db 1 DYKDDDDK 8

RESULT 15  
US-11-251-734-20  
; Sequence 20, Application US/11251734  
; Publication No. US20060100134A1  
; GENERAL INFORMATION:  
; APPLICANT: AVANTIS PHARMACEUTICALS INC.  
; APPLICANT: GUO, Yong  
; APPLICANT: MORSE, Clarence C  
; APPLICANT: YAO, Zhengbin  
; TITLE OF INVENTION: MEMBRANE PENETRATING PEPTIDES AND USES THEREOF  
; FILE REFERENCE: HMR2053 US NP1  
; CURRENT APPLICATION NUMBER: US/11/251,734  
; PRIOR FILING DATE: 2005-10-17  
; PRIOR APPLICATION NUMBER: US 09/933,780  
; PRIOR FILING DATE: 2001-08-21  
; PRIOR APPLICATION NUMBER: US 60/227,647  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: GB 0103110.3  
; PRIOR FILING DATE: 2001-02-07  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 20  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
US-11-251-734-20

Query Match 100.0%; Score 47; DB 7; Length 19;  
Best Local Similarity 100.0%; Pred. No. 0.063;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8  
Db 3 DYKDDDDK 10

RESULT 16  
US-10-821-930-26  
; Sequence 26, Application US/10821930  
; Publication No. US20060133994A1  
; GENERAL INFORMATION:  
; APPLICANT: NERI, Dario  
; APPLICANT: TARLI, Lorenzo  
; APPLICANT: VITTI, Francesca  
; APPLICANT: BIRCHLER, Manfred  
; TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES  
; TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF  
; TITLE OF INVENTION: ANGIOGENESIS  
; FILE REFERENCE: SCH-1733P2  
; CURRENT APPLICATION NUMBER: US/10/821,930  
; CURRENT FILING DATE: 2004-04-12  
; PRIOR APPLICATION NUMBER: US/09/512,082  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 09/300,425  
; PRIOR FILING DATE: 1999-04-28  
; PRIOR APPLICATION NUMBER: 09/075,338  
; PRIOR FILING DATE: 1998-05-11  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: peptide construct  
US-10-821-930-26

Query Match 100.0%; Score 47; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.066;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DYKDDDDK 8  
Db 7 DYKDDDDK 14

RESULT 17  
US-11-251-734-18  
; Sequence 18, Application US/11251734  
; Publication No. US20060100134A1  
; GENERAL INFORMATION:  
; APPLICANT: AVENTIS PHARMACEUTICALS INC.  
; APPLICANT: GUO, Yong  
; APPLICANT: MORSE, Clarence C  
; APPLICANT: YAO, Zhengbin  
; TITLE OF INVENTION: MEMBRANE PENETRATING PEPTIDES AND USES THEREOF  
; FILE REFERENCE: HMR2053 US NP1  
; CURRENT APPLICATION NUMBER: US/11/251,734  
; PRIOR FILING DATE: 2005-10-17  
; PRIOR APPLICATION NUMBER: US 09/933,780  
; PRIOR FILING DATE: 2001-08-21  
; PRIOR APPLICATION NUMBER: US 60/227,647  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: GB 0103110.3  
; PRIOR FILING DATE: 2001-02-07  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 18  
; LENGTH: 23  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
US-11-251-734-18

Query Match 100.0%; Score 47; DB 7; Length 23;  
Best Local Similarity 100.0%; Pred. No. 0.077;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 3 DYKDDDDK 10

RESULT 18  
US-11-251-734-19  
; Sequence 19, Application US/11251734  
; Publication No. US20060100134A1  
; GENERAL INFORMATION:  
; APPLICANT: AVENTIS PHARMACEUTICALS INC.  
; APPLICANT: GUO, Yong  
; APPLICANT: MORSE, Clarence C  
; APPLICANT: YAO, Zhengbin  
; TITLE OF INVENTION: MEMBRANE PENETRATING PEPTIDES AND USES THEREOF  
; FILE REFERENCE: HMR2053 US NP1  
; CURRENT APPLICATION NUMBER: US/11/251,734  
; PRIOR FILING DATE: 2005-10-17  
; PRIOR APPLICATION NUMBER: US 09/933,780  
; PRIOR FILING DATE: 2001-08-21  
; PRIOR APPLICATION NUMBER: US 60/227,647  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: GB 0103110.3  
; PRIOR FILING DATE: 2001-02-07  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 19  
; LENGTH: 23  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

OTHER INFORMATION: Synthetic peptide  
US-11-251-734-19

Query Match 100.0%; Score 47; DB 7; Length 23;  
Best Local Similarity 100.0%; Pred. No. 0.077;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 3 DYKDDDDK 10

RESULT 19  
US-11-328-747-14  
; Sequence 14, Application US/11328747  
; Publication No. US20060105409A1  
; GENERAL INFORMATION:  
; APPLICANT: Issakani, Sarkiz D.  
; APPLICANT: Huang, Jiansing  
; APPLICANT: Sheung, Julie  
; APPLICANT: Pray, Todd R.  
; TITLE OF INVENTION: Ubiquitin Ligase Assay  
; FILE REFERENCE: 021044-007010US  
; CURRENT APPLICATION NUMBER: US/11/328,747  
; PRIOR FILING DATE: 2006-01-09  
; PRIOR APPLICATION NUMBER: US/10/835,096  
; PRIOR FILING DATE: 2004-04-28  
; PRIOR APPLICATION NUMBER: US/09/826,312  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: US 09/542,497  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 84  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: FLAG-ubiquitin  
US-11-328-747-14

Query Match 100.0%; Score 47; DB 7; Length 84;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8  
Db 2 DYKDDDDK 9

RESULT 20  
US-11-090-563-14  
; Sequence 14, Application US/11090563  
; Publication No. US20060115864A1  
; GENERAL INFORMATION:  
; APPLICANT: Issakani, Sarkiz D.  
; APPLICANT: Huang, Jiansing  
; APPLICANT: Sheung, Julie  
; APPLICANT: Pray, Todd R.  
; TITLE OF INVENTION: Assays for Identifying Ubiquitin Agents and for  
; TITLE OF INVENTION: Identifying Agents that Modify the Activity of  
; FILE REFERENCE: 021044-007061US  
; CURRENT APPLICATION NUMBER: US/11/090,563  
; PRIOR FILING DATE: 2005-03-25  
; PRIOR APPLICATION NUMBER: US 09/542,497  
; PRIOR FILING DATE: 2000-04-03  
; PRIOR APPLICATION NUMBER: US 09/826,312  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: US 60/291,863  
; PRIOR FILING DATE: 2001-05-18

```

; PRIOR APPLICATION NUMBER: US 10/091,139
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 10/091,174
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 10/108,767
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 10/109,460
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 10/152,156
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:FLAG-ubiquitin
US-11-090-563-14
```

```
Query Match          100.0%; Score 47; DB 7; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.3; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYKDDDDK 8
        |||||
Db      2 DYKDDDDK 9
```

```

RESULT 21
; Sequence 15, Application US/11328747
; Publication No. US20060105409A1
; GENERAL INFORMATION:
; APPLICANT: Issakani, Sarkiz D.
; APPLICANT: Huang, Jianing
; APPLICANT: Sheung, Julie
; APPLICANT: Pray, Todd R.
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: Ubiquitin Ligase Assay
; FILE REFERENCE: 021044-007010US
; CURRENT APPLICATION NUMBER: US/11/328,747
; PRIOR FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: US/10/835,096
; PRIOR FILING DATE: 2004-04-28
; PRIOR APPLICATION NUMBER: US/09/826,312
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 09/542,497
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:FLAG-Cys-ubiquitin
US-11-328-747-15
```

```
Query Match          100.0%; Score 47; DB 7; Length 85;
Best Local Similarity 100.0%; Pred. No. 0.31; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYKDDDDK 8
        |||||
Db      2 DYKDDDDK 9
```

```

RESULT 22
US-11-090-563-15
; Sequence 15, Application US/11090563
; Publication No. US20060115864A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Issakani, Sarkiz D.
; APPLICANT: Huang, Jianing
; APPLICANT: Sheung, Julie
; APPLICANT: Pray, Todd R.
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: Assays for Identifying Ubiquitin Agents and for
; TITLE OF INVENTION: Identifying Agents That Modify the Activity of
; FILE REFERENCE: 021044-007061US
; CURRENT APPLICATION NUMBER: US/11/090,563
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/542,497
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 09/826,312
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/291,863
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 10/091,139
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 10/091,174
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 10/108,767
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 10/109,460
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 10/152,156
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:FLAG-Cys-ubiquitin
US-11-090-563-15
```

```
Query Match          100.0%; Score 47; DB 7; Length 85;
Best Local Similarity 100.0%; Pred. No. 0.31; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYKDDDDK 8
        |||||
Db      2 DYKDDDDK 9
```

```

RESULT 23
; Sequence 16, Application US/11328747
; Publication No. US20060105409A1
; GENERAL INFORMATION:
; APPLICANT: Issakani, Sarkiz D.
; APPLICANT: Huang, Jianing
; APPLICANT: Sheung, Julie
; APPLICANT: Pray, Todd R.
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: Ubiquitin Ligase Assay
; FILE REFERENCE: 021044-007010US
; CURRENT APPLICATION NUMBER: US/11/328,747
; PRIOR FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: US/10/835,096
; PRIOR FILING DATE: 2004-04-28
; PRIOR APPLICATION NUMBER: US/09/826,312
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 09/542,497
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 86
; TYPE: PRT
```

ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial  
OTHER INFORMATION: Sequence: FLAG-Ala-Cys-ubiquitin  
US-11-328-747-18

Query Match 100.0%; Score 47; DB 7; Length 86;  
Best Local Similarity 100.0%; Pred. No. 0.31;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8  
Db 2 DYKDDDK 9

RESULT 24  
US-10-971-483-12  
Sequence 12, Application US/10971483  
Publication No. US2006008934A1  
GENERAL INFORMATION:  
APPLICANT: Columbia University  
APPLICANT: Greene, Lloyd A.  
APPLICANT: Angelastro, James M.  
TITLE OF INVENTION: METHODS FOR REGULATING THE GROWTH AND/OR  
TITLE OF INVENTION: SURVIVAL OF TUMOR CELLS AND STEM CELLS BY MODULATING THE  
FILE REFERENCE: 070050.2879 Greene  
CURRENT APPLICATION NUMBER: US/10/971,483  
PRIOR FILING DATE: 2004-10-22  
PRIOR APPLICATION NUMBER: US 10/809,312  
PRIOR FILING DATE: 2004-03-24  
PRIOR APPLICATION NUMBER: US 60/460,242  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12  
LENGTH: 99  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic tag  
US-10-971-483-12

Query Match 100.0%; Score 47; DB 6; Length 99;  
Best Local Similarity 100.0%; Pred. No. 0.36;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8  
Db 2 DYKDDDK 9

RESULT 25  
US-11-180-855-3  
Sequence 3, Application US/11180855  
Publication No. US20060088912A1  
GENERAL INFORMATION:  
APPLICANT: YAN, GOUYING  
APPLICANT: XIE, YUHONG  
APPLICANT: PAULSEN, JANET E  
APPLICANT: ZHANG, JIMIN  
APPLICANT: ROOKEY, DIONNA  
APPLICANT: BATES, BRIAN  
APPLICANT: LU, ZHIJIAN  
APPLICANT: MARK, ROBERT  
APPLICANT: CAMPOS, SUSIE J  
TITLE OF INVENTION: Compositions and Methods of Purifying Myelin-Associated  
TITLE OF INVENTION: Glycoprotein (MAG)  
FILE REFERENCE: 102729-29  
CURRENT APPLICATION NUMBER: US/11/180,855  
PRIOR FILING DATE: 2005-07-13  
PRIOR APPLICATION NUMBER: US 60/587,893  
PRIOR FILING DATE: 2004-07-14

PRIOR APPLICATION NUMBER: US 60/588,239  
PRIOR FILING DATE: 2004-07-15  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 3  
LENGTH: 340  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-180-855-3

Query Match 100.0%; Score 47; DB 7; Length 340;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8  
Db 332 DYKDDDK 339

RESULT 26  
US-11-180-855-2  
Sequence 2, Application US/11180855  
Publication No. US20060088912A1  
GENERAL INFORMATION:  
APPLICANT: YAN, GOUYING  
APPLICANT: XIE, YUHONG  
APPLICANT: PAULSEN, JANET E  
APPLICANT: ZHANG, JIMIN  
APPLICANT: ROOKEY, DIONNA  
APPLICANT: BATES, BRIAN  
APPLICANT: LU, ZHIJIAN  
APPLICANT: MARK, ROBERT  
APPLICANT: CAMPOS, SUSIE J  
TITLE OF INVENTION: Compositions and Methods of Purifying Myelin-Associated  
TITLE OF INVENTION: Glycoprotein (MAG)  
FILE REFERENCE: 102729-29  
CURRENT APPLICATION NUMBER: US/11/180,855  
CURRENT FILING DATE: 2005-07-13  
PRIOR FILING DATE: 2004-07-14  
PRIOR APPLICATION NUMBER: US 60/587,893  
PRIOR FILING DATE: 2004-07-15  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 2  
LENGTH: 531  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-180-855-2

Query Match 100.0%; Score 47; DB 7; Length 531;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8  
Db 523 DYKDDDK 530

RESULT 27  
US-11-267-837A-6  
Sequence 6, Application US/11267837A  
Publication No. US20060105952A1  
GENERAL INFORMATION:  
APPLICANT: Allison, Anthony  
TITLE OF INVENTION: Modified Annexin Proteins and Methods for Their Use in Organ  
TITLE OF INVENTION: Transplantation  
FILE REFERENCE: SURR. 90/CIP2  
CURRENT APPLICATION NUMBER: US/11/267,837A  
CURRENT FILING DATE: 2005-11-03  
PRIOR APPLICATION NUMBER: 60/270,402  
PRIOR FILING DATE: 2001-02-21  
PRIOR APPLICATION NUMBER: 11/078,231

```
; PRIOR FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: 10/080,370
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/552,428
; PRIOR FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: 60/579,589
; PRIOR FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: 60/332,582
; PRIOR FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 671
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)..(15)
; OTHER INFORMATION: The 'Xaa' at location 15 stands for Ser.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (335)..(335)
; OTHER INFORMATION: The 'Xaa' at location 335 stands for Lys, Asn, Arg, Ser, Thr,
; OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
; OTHER INFORMATION: Cys, or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (352)..(352)
; OTHER INFORMATION: The 'Xaa' at location 352 stands for Lys, Asn, Arg, Ser, Thr,
; OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
; OTHER INFORMATION: Cys, or Phe.
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-267-837A-6
```

```
Query Match          100.0%; Score 47; DB 7; Length 671;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYKDDDDK 8
        |||||
Db       2 DYKDDDDK 9
```

```
RESULT 28
US-11-134-228A-6
; Sequence 6, Application US/11134228A
; Publication No. US20060105320A1
; GENERAL INFORMATION:
; APPLICANT: Lindquist et al.
; TITLE OF INVENTION: ELECTRICAL CONDUCTORS AND DEVICES FROM PRION-LIKE PROTEINS
; FILE REFERENCE: 30554/40155A
; CURRENT APPLICATION NUMBER: US/11/134,228A
; PRIOR FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,277
; PRIOR FILING DATE: 2004-05-20
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: FLAG peptide
US-11-134-228A-6
```

```
Query Match          91.5%; Score 43; DB 7; Length 8;
Best Local Similarity 87.5%; Pred. No. 9.6e+04;
Matches      7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYKDDDDK 8
        |||||
Db       1 DYKDDDDK 8
```

```
RESULT 29
US-10-484-105-4
; Sequence 4, Application US/10484105
; Publication No. US20060127893A1
; GENERAL INFORMATION:
; APPLICANT: Universitat Zurich
; TITLE OF INVENTION: Modification of Human Variable Domains
; FILE REFERENCE: P 2289 US S3
; CURRENT APPLICATION NUMBER: US/10/484,105
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: EP 01 11 6756.6
; PRIOR FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-484-105-4
```

```
Query Match          89.4%; Score 42; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.6e+04;
Matches      7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYKDDDD 7
        |||||
Db       1 DYKDDDD 7
```

```
RESULT 30
US-11-299-013-17
; Sequence 17, Application US/11299013
; Publication No. US2006008878A1
; GENERAL INFORMATION:
; APPLICANT: BRIZZARD, BILLY L
; APPLICANT: HERMAN, RON
; TITLE OF INVENTION: PURIFICATION OF RECOMBINANT PROTEINS FUSED TO MULTIPLE EPITOPES
; FILE REFERENCE: SGM6933.7
; CURRENT APPLICATION NUMBER: US/11/299,013
; PRIOR FILING DATE: 2005-12-09
; PRIOR APPLICATION NUMBER: US 09/415,000
; PRIOR FILING DATE: 1999-10-08
; PRIOR FILING DATE: 1999-10-03
; PRIOR APPLICATION NUMBER: US 09/970,308
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthesized inventive sequence
US-11-299-013-17
```

```
Query Match          89.4%; Score 42; DB 7; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches      7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYKDDDD 7
        |||||
Db       16 DYKDDDD 22
```

```
RESULT 31
US-10-953-349-29832
; Sequence 29832, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
```

```

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29832
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Trifolium aestivum
US-10-953-349-29832
```

```
Query Match      83.0%; Score 39; DB 6; Length 91;
Best Local Similarity 75.0%; Pred. No. 5.5;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 DYKDDDK 8
Db      16 DYEDDDK 23
```

```

RESULT 32
US-10-953-349-29831
; Sequence 29831, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29831
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Trifolium aestivum
US-10-953-349-29831
```

```
Query Match      83.0%; Score 39; DB 6; Length 92;
Best Local Similarity 75.0%; Pred. No. 5.6;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 DYKDDDK 8
Db      17 DYEDDDK 24
```

```

RESULT 33
US-10-953-349-33141
; Sequence 33141, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33141
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-33141
```

```
Query Match      83.0%; Score 39; DB 6; Length 428;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 DYKDDDK 8
Db      16 DYEDDDK 23
```

```

RESULT 34
US-10-953-349-33140
; Sequence 33140, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33140
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-33140
```

```
Query Match      83.0%; Score 39; DB 6; Length 429;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 DYKDDDK 8
Db      17 DYEDDDK 24
```

```

RESULT 35
US-10-953-349-33139
; Sequence 33139, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33139
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-33139
```

```
Query Match      83.0%; Score 39; DB 6; Length 463;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 DYKDDDK 8
Db      51 DYEDDDK 58
```

```

RESULT 36
US-10-953-349-6317
; Sequence 6317, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
```

```
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 6317
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-6317

Query Match
Best Local Similarity 80.9%; Score 38; DB 6; Length 275;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
Db 192 DYNDDEK 199

RESULT 37
US-10-953-349-6316
; Sequence 6316, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 6316
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-6316

Query Match
Best Local Similarity 80.9%; Score 38; DB 6; Length 294;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
Db 211 DYNDDEK 218

RESULT 38
US-10-953-349-6315
; Sequence 6315, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 6315
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-6315

Query Match
Best Local Similarity 80.9%; Score 38; DB 6; Length 315;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
Db 232 DYNDDEK 239

RESULT 39
```

```
US-10-449-902-39313
; Sequence 39313, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 39313
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-39313

Query Match
Best Local Similarity 78.7%; Score 37; DB 6; Length 164;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
Db 147 DYSDDD 153

RESULT 40
US-10-953-349-21221
; Sequence 21221, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 21221
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-21221

Query Match
Best Local Similarity 78.7%; Score 37; DB 6; Length 389;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
Db 142 DYDDDDQ 149

RESULT 41
US-10-953-349-21220
; Sequence 21220, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
```



SOFTWARE: PatentIn version 3.3  
SEQ ID NO 21220  
LENGTH: 433  
TYPE: PRT  
ORGANISM: Glycine max  
US-10-953-349-21220

Query Match 78.7%; Score 37; DB 6; Length 433;  
Best Local Similarity 75.0%; Pred. No. 58;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
DB 186 DYDDDDQ 193

RESULT 42  
US-10-449-902-45116  
Sequence 45116, Application US/10449902  
Publication No. US20060123505A1  
GENERAL INFORMATION:  
APPLICANT: National Institute of Agrobiological Sciences.  
APPLICANT: Bio-oriented Technology Research Advancement Institution.  
APPLICANT: The Institute of Physical and Chemical Research.  
APPLICANT: Foundation for Advancement of International Science.  
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF  
FILE REFERENCE: MOA-A0205Y1-US  
CURRENT APPLICATION NUMBER: US/10/449, 902  
CURRENT FILING DATE: 2003-05-29  
PRIOR APPLICATION NUMBER: JP 2002-203269  
PRIOR FILING DATE: 2002-05-30  
PRIOR APPLICATION NUMBER: JP 2002-383870  
PRIOR FILING DATE: 2002-12-11  
NUMBER OF SEQ ID NOS: 56791  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 45116  
LENGTH: 567  
TYPE: PRT  
ORGANISM: Oryza sativa  
US-10-449-902-45116

Query Match 78.7%; Score 37; DB 6; Length 567;  
Best Local Similarity 75.0%; Pred. No. 78;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
DB 44 DYDDDDQ 51

RESULT 43  
US-09-756-0978-66  
Sequence 66, Application US/09756097B  
Publication No. US20060088938A1  
GENERAL INFORMATION:  
APPLICANT: Mitchell, Lloyd G.  
APPLICANT: Garcia-Blanco, Mariano A.  
APPLICANT: Puttareju, Madalah  
APPLICANT: Mansfield, Gary S.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR USE IN  
FILE REFERENCE: A1304-B-A-C 072874.0138  
CURRENT APPLICATION NUMBER: US/09/756, 0978  
CURRENT FILING DATE: 2001-01-08  
PRIOR APPLICATION NUMBER: 09/158, 863  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 09/133, 717  
PRIOR FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: 09/087, 233  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 08/766, 354  
PRIOR FILING DATE: 1996-12-13  
PRIOR APPLICATION NUMBER: 60/008, 317

PRIOR FILING DATE: 1995-12-15  
NUMBER OF SEQ ID NOS: 105  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 66  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: C terminal residues from glutathione -S-  
US-09-756-0978-66

Query Match 76.6%; Score 36; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9,6e+04;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDD 6  
DB 1 DYKDD 6

RESULT 44  
US-10-449-902-29232  
Sequence 29232, Application US/10449902  
Publication No. US20060123505A1  
GENERAL INFORMATION:  
APPLICANT: National Institute of Agrobiological Sciences.  
APPLICANT: Bio-oriented Technology Research Advancement Institution.  
APPLICANT: The Institute of Physical and Chemical Research.  
APPLICANT: Foundation for Advancement of International Science.  
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF  
FILE REFERENCE: MOA-A0205Y1-US  
CURRENT APPLICATION NUMBER: US/10/449, 902  
CURRENT FILING DATE: 2003-05-29  
PRIOR APPLICATION NUMBER: JP 2002-203269  
PRIOR FILING DATE: 2002-05-30  
PRIOR APPLICATION NUMBER: JP 2002-383870  
PRIOR FILING DATE: 2002-12-11  
NUMBER OF SEQ ID NOS: 56791  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 29232  
LENGTH: 194  
TYPE: PRT  
ORGANISM: Oryza sativa  
US-10-449-902-29232

Query Match 76.6%; Score 36; DB 6; Length 194;  
Best Local Similarity 75.0%; Pred. No. 35;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
DB 171 DYDEDDQ 178

RESULT 45  
US-10-449-902-49424  
Sequence 49424, Application US/10449902  
Publication No. US20060123505A1  
GENERAL INFORMATION:  
APPLICANT: National Institute of Agrobiological Sciences.  
APPLICANT: Bio-oriented Technology Research Advancement Institution.  
APPLICANT: The Institute of Physical and Chemical Research.  
APPLICANT: Foundation for Advancement of International Science.  
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF  
FILE REFERENCE: MOA-A0205Y1-US  
CURRENT APPLICATION NUMBER: US/10/449, 902  
CURRENT FILING DATE: 2003-05-29  
PRIOR APPLICATION NUMBER: JP 2002-203269  
PRIOR FILING DATE: 2002-05-30  
PRIOR APPLICATION NUMBER: JP 2002-383870  
PRIOR FILING DATE: 2002-12-11  
NUMBER OF SEQ ID NOS: 56791

;; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 49424  
; LENGTH: 194  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-449-902-49424

Query Match 76.6%; Score 36; DB 6; Length 194;  
Best Local Similarity 75.0%; Pred. No. 35;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
|||  
Db 171 DYLDDEDK 178

RESULT 46  
US-10-449-902-54492  
; Sequence 54492, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; PRIOR FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 54492  
; LENGTH: 411  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-449-902-54492

Query Match 76.6%; Score 36; DB 6; Length 411;  
Best Local Similarity 85.7%; Pred. No. 78;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
|||  
Db 139 DYDDDD 145

RESULT 47  
US-10-449-902-40889  
; Sequence 40889, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; PRIOR FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40889  
; LENGTH: 533  
; TYPE: PRT  
; ORGANISM: Oryza sativa

US-10-449-902-40889

Query Match 76.6%; Score 36; DB 6; Length 533;  
Best Local Similarity 85.7%; Pred. No. 1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
|||  
Db 523 DYTDDD 529

RESULT 48  
US-11-267-837A-9  
; Sequence 9, Application US/11267837A  
; Publication No. US20060105952A1  
; GENERAL INFORMATION:  
; APPLICANT: Allison, Anthony  
; TITLE OF INVENTION: Modified Annexin Proteins and Methods for Their Use in Organ  
; FILE REFERENCE: SURR-90/CIP2  
; CURRENT APPLICATION NUMBER: US/11/267,837A  
; PRIOR APPLICATION NUMBER: 60/270,402  
; PRIOR FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: 11/078,231  
; PRIOR FILING DATE: 2005-03-10  
; PRIOR APPLICATION NUMBER: 10/080,370  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: 60/552,428  
; PRIOR FILING DATE: 2004-03-11  
; PRIOR APPLICATION NUMBER: 60/579,589  
; PRIOR FILING DATE: 2004-03-11  
; PRIOR APPLICATION NUMBER: 60/332,582  
; PRIOR FILING DATE: 2001-11-21  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 9  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: purification tag  
US-11-267-837A-9

Query Match 74.5%; Score 35; DB 7; Length 8;  
Best Local Similarity 85.7%; Pred. No. 9.6e+04;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
|||  
Db 1 DYLDDD 7

RESULT 49  
US-10-449-902-34551  
; Sequence 34551, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; PRIOR FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 34551

LENGTH: 204  
TYPE: PRT  
ORGANISM: Oryza sativa  
US-10-449-902-34551

Query Match 74.5%; Score 35; DB 6; Length 204;  
Best Local Similarity 85.7%; Pred. No. 53;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
Db 162 DYDDDD 168

RESULT 50  
US-10-449-902-31822  
Sequence 31822, Application US/10449902  
Publication No. US20060123505A1  
GENERAL INFORMATION:  
APPLICANT: National Institute of Agrobiological Sciences.  
APPLICANT: Bio-oriented Technology Research Advancement Institution.  
APPLICANT: The Institute of Physical and Chemical Research.  
TITLE OF INVENTION: FOUNDATION FOR ADVANCEMENT OF INTERNATIONAL SCIENCE.  
FILE REFERENCE: MOA-A0205Y1-US  
CURRENT FILING DATE: 2003-05-29  
PRIOR APPLICATION NUMBER: JP 2002-203269  
PRIOR FILING DATE: 2002-05-30  
PRIOR APPLICATION NUMBER: JP 2002-383870  
NUMBER OF SEQ ID NOS: 56791  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 31822  
LENGTH: 342  
TYPE: PRT  
ORGANISM: Oryza sativa  
US-10-449-902-31822

Query Match 74.5%; Score 35; DB 6; Length 342;  
Best Local Similarity 85.7%; Pred. No. 92;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
Db 69 DYGDddd 75

RESULT 51  
US-10-449-902-40463  
Sequence 40463, Application US/10449902  
Publication No. US20060123505A1  
GENERAL INFORMATION:  
APPLICANT: National Institute of Agrobiological Sciences.  
APPLICANT: Bio-oriented Technology Research Advancement Institution.  
APPLICANT: The Institute of Physical and Chemical Research.  
TITLE OF INVENTION: FOUNDATION FOR ADVANCEMENT OF INTERNATIONAL SCIENCE.  
FILE REFERENCE: MOA-A0205Y1-US  
CURRENT APPLICATION NUMBER: US/10/449,902  
PRIOR FILING DATE: 2003-05-29  
PRIOR APPLICATION NUMBER: JP 2002-203269  
PRIOR FILING DATE: 2002-05-30  
PRIOR APPLICATION NUMBER: JP 2002-383870  
NUMBER OF SEQ ID NOS: 56791  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 40463  
LENGTH: 342  
TYPE: PRT  
ORGANISM: Oryza sativa  
US-10-449-902-40463

Query Match 74.5%; Score 35; DB 6; Length 342;  
Best Local Similarity 85.7%; Pred. No. 92;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
Db 69 DYGDddd 75

RESULT 52  
US-10-449-902-44996  
Sequence 44996, Application US/10449902  
Publication No. US20060123505A1  
GENERAL INFORMATION:  
APPLICANT: National Institute of Agrobiological Sciences.  
APPLICANT: Bio-oriented Technology Research Advancement Institution.  
APPLICANT: The Institute of Physical and Chemical Research.  
TITLE OF INVENTION: FOUNDATION FOR ADVANCEMENT OF INTERNATIONAL SCIENCE.  
FILE REFERENCE: MOA-A0205Y1-US  
CURRENT APPLICATION NUMBER: US/10/449,902  
CURRENT FILING DATE: 2003-05-29  
PRIOR APPLICATION NUMBER: JP 2002-203269  
PRIOR FILING DATE: 2002-05-30  
PRIOR APPLICATION NUMBER: JP 2002-383870  
NUMBER OF SEQ ID NOS: 56791  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 44996  
LENGTH: 351  
TYPE: PRT  
ORGANISM: Oryza sativa  
US-10-449-902-44996

Query Match 74.5%; Score 35; DB 6; Length 351;  
Best Local Similarity 85.7%; Pred. No. 94;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
Db 69 DYGDddd 75

RESULT 53  
US-10-449-902-46241  
Sequence 46241, Application US/10449902  
Publication No. US20060123505A1  
GENERAL INFORMATION:  
APPLICANT: National Institute of Agrobiological Sciences.  
APPLICANT: Bio-oriented Technology Research Advancement Institution.  
APPLICANT: The Institute of Physical and Chemical Research.  
TITLE OF INVENTION: FOUNDATION FOR ADVANCEMENT OF INTERNATIONAL SCIENCE.  
FILE REFERENCE: MOA-A0205Y1-US  
CURRENT APPLICATION NUMBER: US/10/449,902  
CURRENT FILING DATE: 2003-05-29  
PRIOR APPLICATION NUMBER: JP 2002-203269  
PRIOR FILING DATE: 2002-05-30  
PRIOR APPLICATION NUMBER: JP 2002-383870  
NUMBER OF SEQ ID NOS: 56791  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 46241  
LENGTH: 734  
TYPE: PRT  
ORGANISM: Oryza sativa  
US-10-449-902-46241

Query Match 74.5%; Score 35; DB 6; Length 734;  
Best Local Similarity 85.7%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7

Db 713 DYLDLDD 719

```

RESULT 54
US-10-953-349-18302
; Sequence 18302, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18302
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18302

```

Query Match 72.3%; Score 34; DB 6; Length 133;  
 Best Local Similarity 71.4%; Pred. No. 48;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDDK 8  
 Db 108 YKDEDDR 114

```

RESULT 55
US-10-953-349-39990
; Sequence 39990, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39990
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-39990

```

Query Match 72.3%; Score 34; DB 6; Length 133;  
 Best Local Similarity 71.4%; Pred. No. 48;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDDK 8  
 Db 108 YKDEDDR 114

```

RESULT 56
US-10-953-349-6258
; Sequence 6258, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3

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; SEQ ID NO 6258
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-6258

```

Query Match 72.3%; Score 34; DB 6; Length 150;  
 Best Local Similarity 71.4%; Pred. No. 54;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
 Db 132 DYDEDD 138

```

RESULT 57
US-10-953-349-6257
; Sequence 6257, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6257
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-6257

```

Query Match 72.3%; Score 34; DB 6; Length 163;  
 Best Local Similarity 71.4%; Pred. No. 59;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
 Db 145 DYDEDD 151

```

RESULT 58
US-10-449-902-31740
; Sequence 31740, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31740
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-31740

```

Query Match 72.3%; Score 34; DB 6; Length 219;  
 Best Local Similarity 75.0%; Pred. No. 81;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8

Db 123 DEBDDDK 130

RESULT 59  
US-10-449-902-40441

Sequence 40441, Application US/10449902  
Publication No. US20060123505A1

GENERAL INFORMATION:

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institution.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

FILE REFERENCE: MOA-A0205Y1-US

CURRENT APPLICATION NUMBER: US/10/449,902

PRIOR FILING DATE: 2003-05-29

PRIOR APPLICATION NUMBER: JP 2002-203269

PRIOR FILING DATE: 2002-05-30

PRIOR APPLICATION NUMBER: JP 2002-383870

PRIOR FILING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 56791

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 40441

LENGTH: 219

TYPE: PRT

ORGANISM: Oryza sativa

US-10-449-902-40441

Query Match

Best Local Similarity 72.3%; Score 34; DB 6; Length 219;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8

Db 123 DEBDDDK 130

RESULT 60

US-10-953-349-6256

Sequence 6256, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:

APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

FILE REFERENCE: 2750-1579PUS2

CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT FILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOFTWARE: PatentIn version 3.3

SEQ ID NO 6256

LENGTH: 222

TYPE: PRT

ORGANISM: Arabidopsis thaliana

US-10-953-349-6256

Query Match

Best Local Similarity 72.3%; Score 34; DB 6; Length 222;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7

Db 204 DYEDDD 210

RESULT 61

US-10-953-349-2040

Sequence 2040, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:

APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: ENCODED THERBY

FILE REFERENCE: 2750-1579PUS2

CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT FILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOFTWARE: PatentIn version 3.3

SEQ ID NO 2040

LENGTH: 229

TYPE: PRT

ORGANISM: Arabidopsis thaliana

US-10-953-349-2040

Query Match

Best Local Similarity 72.3%; Score 34; DB 6; Length 229;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7

Db 183 DYEDDD 189

RESULT 62

US-10-449-902-41697

Sequence 41697, Application US/10449902

Publication No. US20060123505A1

GENERAL INFORMATION:

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institution.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

FILE REFERENCE: MOA-A0205Y1-US

CURRENT APPLICATION NUMBER: US/10/449,902

PRIOR FILING DATE: 2003-05-29

PRIOR APPLICATION NUMBER: JP 2002-203269

PRIOR FILING DATE: 2002-05-30

PRIOR APPLICATION NUMBER: JP 2002-383870

PRIOR FILING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 56791

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 41697

LENGTH: 294

TYPE: PRT

ORGANISM: Oryza sativa

US-10-449-902-41697

Query Match

Best Local Similarity 72.3%; Score 34; DB 6; Length 294;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DYKDDDK 8

Db 31 DYKDDDK 38

RESULT 63

US-10-953-349-36044

Sequence 36044, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:

APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

FILE REFERENCE: 2750-1579PUS2

CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT FILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOFTWARE: PatentIn version 3.3

SEQ ID NO 36044

LENGTH: 301

TYPE: PRT

ORGANISM: Zea mays subsp. mays

US-10-953-349-36044

Query Match 72.3%; Score 34; DB 6; Length 301;  
Best Local Similarity 85.7%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
| | | | |  
Db 71 DMKDDDD 77

RESULT 64  
US-10-953-349-2039  
; Sequence 2039, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2039  
; LENGTH: 338  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-953-349-2039

Query Match 72.3%; Score 34; DB 6; Length 338;  
Best Local Similarity 71.4%; Pred. No. 1.3e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
| | | | |  
Db 292 DYEDDED 298

RESULT 65  
US-10-953-349-2038  
; Sequence 2038, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2038  
; LENGTH: 340  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-953-349-2038

Query Match 72.3%; Score 34; DB 6; Length 340;  
Best Local Similarity 71.4%; Pred. No. 1.3e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
| | | | |  
Db 294 DYEDDED 300

RESULT 66  
US-10-953-349-5131  
; Sequence 5131, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; TITLE OF INVENTION: ENCODED THERBY  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 5131  
; LENGTH: 362  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-953-349-5131

Query Match 72.3%; Score 34; DB 6; Length 362;  
Best Local Similarity 71.4%; Pred. No. 1.4e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
| | | | |  
Db 310 DYEDDDE 316

RESULT 67  
US-10-449-902-52372  
; Sequence 52372, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: The Institute of Technology Research Advancement Institution.  
; APPLICANT: Foundation for Advancement of Physical and Chemical Research.  
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USBS THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 52372  
; LENGTH: 373  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-449-902-52372

Query Match 72.3%; Score 34; DB 6; Length 373;  
Best Local Similarity 75.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 8  
| | | | |  
Db 26 DAKDDDE 33

RESULT 68  
US-10-449-902-43294  
; Sequence 43294, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USBS THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791

SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 43294  
LENGTH: 410  
TYPE: PRT  
ORGANISM: Oryza sativa  
US-10-449-902-43294

Query Match 72.3%; Score 34; DB 6; Length 410;  
Best Local Similarity 62.5%; Pred. No. 1.6e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
DB 261 DFDSDDE 268

RESULT 69  
US-10-449-902-42067  
Sequence 42067, Application US/10449902  
Publication No. US20060123505A1  
GENERAL INFORMATION:  
APPLICANT: National Institute of Agrobiological Sciences.  
APPLICANT: Bio-oriented Technology Research Advancement Institution.  
APPLICANT: The Institute of Physical and Chemical Research.  
APPLICANT: Foundation for Advancement of International Science.  
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF  
FILE REFERENCE: MOA-A0205Y1-US  
CURRENT APPLICATION NUMBER: US/10/449,902  
CURRENT FILING DATE: 2003-05-29  
PRIOR APPLICATION NUMBER: JP 2002-203269  
PRIOR FILING DATE: 2002-05-30  
PRIOR APPLICATION NUMBER: JP 2002-383870  
PRIOR FILING DATE: 2002-12-11  
NUMBER OF SEQ ID NOS: 56791  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 42067  
LENGTH: 437  
TYPE: PRT  
ORGANISM: Oryza sativa  
US-10-449-902-42067

Query Match 72.3%; Score 34; DB 6; Length 437;  
Best Local Similarity 75.0%; Pred. No. 1.7e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
DB 134 DAKDDDE 141

RESULT 70  
US-10-449-902-50266  
Sequence 50266, Application US/10449902  
Publication No. US20060123505A1  
GENERAL INFORMATION:  
APPLICANT: National Institute of Agrobiological Sciences.  
APPLICANT: Bio-oriented Technology Research Advancement Institution.  
APPLICANT: The Institute of Physical and Chemical Research.  
APPLICANT: Foundation for Advancement of International Science.  
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF  
FILE REFERENCE: MOA-A0205Y1-US  
CURRENT APPLICATION NUMBER: US/10/449,902  
CURRENT FILING DATE: 2003-05-29  
PRIOR APPLICATION NUMBER: JP 2002-203269  
PRIOR FILING DATE: 2002-05-30  
PRIOR APPLICATION NUMBER: JP 2002-383870  
PRIOR FILING DATE: 2002-12-11  
NUMBER OF SEQ ID NOS: 56791  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 50266  
LENGTH: 487  
TYPE: PRT  
ORGANISM: Oryza sativa

US-10-449-902-50266

Query Match 72.3%; Score 34; DB 6; Length 497;  
Best Local Similarity 71.4%; Pred. No. 1.9e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
DB 23 DFDQDDD 29

RESULT 71  
US-10-449-902-44569  
Sequence 44569, Application US/10449902  
Publication No. US20060123505A1  
GENERAL INFORMATION:  
APPLICANT: National Institute of Agrobiological Sciences.  
APPLICANT: Bio-oriented Technology Research Advancement Institution.  
APPLICANT: The Institute of Physical and Chemical Research.  
APPLICANT: Foundation for Advancement of International Science.  
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF  
FILE REFERENCE: MOA-A0205Y1-US  
CURRENT APPLICATION NUMBER: US/10/449,902  
CURRENT FILING DATE: 2003-05-29  
PRIOR APPLICATION NUMBER: JP 2002-203269  
PRIOR FILING DATE: 2002-05-30  
PRIOR APPLICATION NUMBER: JP 2002-383870  
PRIOR FILING DATE: 2002-12-11  
NUMBER OF SEQ ID NOS: 56791  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 44569  
LENGTH: 520  
TYPE: PRT  
ORGANISM: Oryza sativa  
US-10-449-902-44569

Query Match 72.3%; Score 34; DB 6; Length 520;  
Best Local Similarity 71.4%; Pred. No. 2e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
DB 23 DFDQDDD 29

RESULT 72  
US-10-449-902-45621  
Sequence 45621, Application US/10449902  
Publication No. US20060123505A1  
GENERAL INFORMATION:  
APPLICANT: National Institute of Agrobiological Sciences.  
APPLICANT: Bio-oriented Technology Research Advancement Institution.  
APPLICANT: The Institute of Physical and Chemical Research.  
APPLICANT: Foundation for Advancement of International Science.  
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF  
FILE REFERENCE: MOA-A0205Y1-US  
CURRENT APPLICATION NUMBER: US/10/449,902  
CURRENT FILING DATE: 2003-05-29  
PRIOR APPLICATION NUMBER: JP 2002-203269  
PRIOR FILING DATE: 2002-05-30  
PRIOR APPLICATION NUMBER: JP 2002-383870  
PRIOR FILING DATE: 2002-12-11  
NUMBER OF SEQ ID NOS: 56791  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 45621  
LENGTH: 521  
TYPE: PRT  
ORGANISM: Oryza sativa  
US-10-449-902-45621

Query Match 72.3%; Score 34; DB 6; Length 521;  
Best Local Similarity 71.4%; Pred. No. 2e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
|:|:|:|:  
Db 23 DFQDDDD 29

## RESULT 73

US-10-449-902-45113  
; Sequence 45113, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; PRIOR FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 45113  
; LENGTH: 684  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-449-902-45113

Query Match 72.3%; Score 34; DB 6; Length 684;  
Best Local Similarity 71.4%; Pred. No. 2,7e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDD 8  
|:|:|:|:  
Db 294 YEDDDDR 300

RESULT 74  
US-10-953-349-21280  
; Sequence 21280, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 21280  
; LENGTH: 75  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-21280

Query Match 70.2%; Score 33; DB 6; Length 75;  
Best Local Similarity 75.0%; Pred. No. 37;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 8  
|:|:|:|:  
Db 47 DDKDDDE 54

RESULT 75  
US-10-449-902-30504  
; Sequence 30504, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; PRIOR FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 30504  
; LENGTH: 145  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-449-902-30504

Query Match 70.2%; Score 33; DB 6; Length 145;  
Best Local Similarity 85.7%; Pred. No. 75;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
|:|:|:|:  
Db 44 DAKDDDD 50

RESULT 76  
US-10-449-902-34122  
; Sequence 34122, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 34122  
; LENGTH: 171  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-449-902-34122

Query Match 70.2%; Score 33; DB 6; Length 171;  
Best Local Similarity 62.5%; Pred. No. 89;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 8  
|:|:|:|:  
Db 41 DYDDDEE 48

RESULT 77  
US-10-953-349-27604  
; Sequence 27604, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349



;; CURRENT FILING DATE: 2004-09-30  
;; NUMBER OF SEQ ID NOS: 40252  
;; SOFTWARE: PatentIn version 3.3  
;; SEQ ID NO 27604  
;; LENGTH: 203  
;; TYPE: PRT  
;; ORGANISM: Triticum aestivum  
US-10-953-349-27604

Query Match 70.2%; Score 33; DB 6; Length 203;  
Best Local Similarity 85.7%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DYKDDDD 7  
Db 42 DAKDDDD 48

RESULT 78  
US-10-449-902-50940  
; Sequence 50940, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 50940  
; LENGTH: 221  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-449-902-50940

Query Match 70.2%; Score 33; DB 6; Length 221;  
Best Local Similarity 85.7%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DYKDDDD 7  
Db 44 DAKDDDD 50

RESULT 79  
US-10-449-902-30872  
; Sequence 30872, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 30872  
; LENGTH: 431

;; TYPE: PRT  
;; ORGANISM: Oryza sativa  
US-10-449-902-30872

Query Match 70.2%; Score 33; DB 6; Length 431;  
Best Local Similarity 71.4%; Pred. No. 2.4e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDD 7  
Db 206 NFKDDDD 212

RESULT 80  
US-10-449-902-37911  
; Sequence 37911, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 37911  
; LENGTH: 508  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-449-902-37911

Query Match 70.2%; Score 33; DB 6; Length 508;  
Best Local Similarity 75.0%; Pred. No. 2.8e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DYKDDDD 8  
Db 495 DDKDDDE 502

RESULT 81  
US-10-471-571A-3230  
; Sequence 3230, Application US/10471571A  
; Publication No. US20060115490A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE: P026927WO  
; CURRENT APPLICATION NUMBER: US/10/471,571A  
; CURRENT FILING DATE: 2003-09-12  
; PRIOR APPLICATION NUMBER: GB-0107661.1  
; PRIOR FILING DATE: 2001-03-27  
; NUMBER OF SEQ ID NOS: 5642  
; SOFTWARE: SeqWin99, version 1.03  
; SEQ ID NO 3230  
; LENGTH: 553  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)...(553)  
; OTHER INFORMATION: arglyl-tRNA synthetase  
US-10-471-571A-3230

Query Match 70.2%; Score 33; DB 6; Length 553;  
Best Local Similarity 62.5%; Pred. No. 3.1e+02;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8

Db 296 DFRDDKDR 303

RESULT 82

US-10-449-902-40941  
; Sequence 40941, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40941  
; LENGTH: 770  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-449-902-40941

Query Match 70.2%; Score 33; DB 6; Length 770;  
Best Local Similarity 62.5%; Pred. No. 4.4e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8

Db 738 DFSDNDK 745

RESULT 83  
US-10-449-902-31438  
; Sequence 31438, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31438  
; LENGTH: 876  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-449-902-31438

Query Match 70.2%; Score 33; DB 6; Length 876;  
Best Local Similarity 71.4%; Pred. No. 5e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDK 8

Db 818 YKDEDE 824

RESULT 84

US-10-449-902-56037  
; Sequence 56037, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 56037  
; LENGTH: 936  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-449-902-56037

Query Match 70.2%; Score 33; DB 6; Length 936;  
Best Local Similarity 71.4%; Pred. No. 5.4e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDK 8

Db 878 YKDEDE 884

RESULT 85  
US-10-449-902-52762  
; Sequence 52762, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 52762  
; LENGTH: 1179  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-449-902-52762

Query Match 70.2%; Score 33; DB 6; Length 1179;  
Best Local Similarity 62.5%; Pred. No. 6.9e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8

Db 87 EYDDDD 94

RESULT 86  
US-10-449-902-53947  
; Sequence 53947, Application US/10449902

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; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53947
; LENGTH: 1180
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-53947

```

```

Query Match      70.2%; Score 33; DB 6; Length 1180;
Best Local Similarity 71.4%; Pred. No. 6.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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```

QY      1 DYKDDDD 7
        :|:|:|:|
Db      500 NFKDDDD 506

```

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RESULT 87
US-11-289-102-378
; Sequence 378, Application US/11289102
; Publication No. US20060121511A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Hyerim
; APPLICANT: Shaw, Peter M.
; APPLICANT: Clark, Edwin
; TITLE OF INVENTION: MICROTUBULE-STABILIZING AGENTS
; FILE REFERENCE: 10338 NP
; CURRENT APPLICATION NUMBER: US/11/289,102
; CURRENT FILING DATE: 2005-11-29
; PRIOR APPLICATION NUMBER: US 60/631,993
; PRIOR FILING DATE: 2004-11-30
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 378
; LENGTH: 1230
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-289-102-378

```

```

Query Match      70.2%; Score 33; DB 7; Length 1230;
Best Local Similarity 71.4%; Pred. No. 7.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 DYKDDDD 7
        :|:|:|:|
Db      338 EYSDDDD 344

```

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RESULT 88
US-11-074-497-41
; Sequence 41, Application US/11074497
; Publication No. US2006012135A1
; GENERAL INFORMATION:
; APPLICANT: Geerts, Hugo
; APPLICANT: Maure, Stefan
; APPLICANT: Cik, Miroslav
; APPLICANT: Meert, Theo
; APPLICANT: Ver Donck, Luc

```

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; TITLE OF INVENTION: NEUTROTROPHIC GROWTH FACTOR
; FILE REFERENCE: 43962-010700
; CURRENT APPLICATION NUMBER: US/11/074,497
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US/09/357,349
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: 09/327,668
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 09/248,772
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: GB 9815283.8
; PRIOR FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Plasmid NH2-terminal
US-11-074-497-41

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Query Match      68.1%; Score 32; DB 7; Length 39;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY      1 DYKDDDK 8
        :|:|:|:|
Db      24 DLYDDDK 31

```

```

RESULT 89
US-10-449-902-43449
; Sequence 43449, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43449
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-43449

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```

Query Match      68.1%; Score 32; DB 6; Length 74;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      2 YKDDDD 7
        :|:|:|:|
Db      55 YKDEDD 60

```

```

RESULT 90
US-10-449-902-33753
; Sequence 33753, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.

```

```
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 33753
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-33753

Query Match      68.1%; Score 32; DB 6; Length 80;
Best Local Similarity 83.3%; Pred. No. 56;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 DYKDDDD 7
Db      22 YEDDDD 27

RESULT 91
US-10-449-902-36276
; Sequence 36276, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; FILE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 36276
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-36276

Query Match      68.1%; Score 32; DB 6; Length 146;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 DYKDDDD 7
Db      131 EYDDDDD 137

RESULT 92
US-10-953-349-6227
; Sequence 6227, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCER-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
```

```
; SEQ ID NO 6227
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-6227

Query Match      68.1%; Score 32; DB 6; Length 203;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 DYKDDDDK 8
Db      34 DSDDDDK 41

RESULT 93
US-10-449-902-29282
; Sequence 29282, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; FILE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 29282
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-29282

Query Match      68.1%; Score 32; DB 6; Length 205;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 DYKDDDD 7
Db      44 DYKDDDD 50

RESULT 94
US-10-516-753-74
; Sequence 74, Application US/10516753
; Publication No. US20060123506A1
; GENERAL INFORMATION:
; APPLICANT: Hannoufa, Abdelali
; APPLICANT: Lydiatte, Derek J.
; APPLICANT: Gao, Ming-Jun
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION USING CHROMATIN REMODELLING FACTOR
; FILE REFERENCE: 270.78USMO
; CURRENT APPLICATION NUMBER: US/10/516,753
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: PCT/CA2003/000822
; PRIOR FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: US 60/387,088
; PRIOR FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 74
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Arabidopsis
; FEATURE:
; OTHER INFORMATION: atKCL2
```

US-10-516-753-74

Query Match 68.1%; Score 32; DB 6; Length 221;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDD 6  
|:|:|  
Db 170 DYEDDD 175

RESULT 95

US-10-953-349-6226  
; Sequence 6226, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 6226  
; LENGTH: 231  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-953-349-6226

Query Match 68.1%; Score 32; DB 6; Length 231;  
Best Local Similarity 75.0%; Pred. No. 1.7e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
|:|:|  
Db 62 DSDDDDK 69

RESULT 96

US-10-953-349-16219  
; Sequence 16219, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 16219  
; LENGTH: 234  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-16219

Query Match 68.1%; Score 32; DB 6; Length 234;  
Best Local Similarity 71.4%; Pred. No. 1.8e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
|:|:|  
Db 12 DFDDDD 18

RESULT 97

US-10-953-349-16218  
; Sequence 16218, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 16218  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-16218

Query Match 68.1%; Score 32; DB 6; Length 240;  
Best Local Similarity 71.4%; Pred. No. 1.8e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
|:|:|  
Db 18 DFDDDD 24

RESULT 98

US-10-953-349-31660  
; Sequence 31660, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 31660  
; LENGTH: 252  
; TYPE: PRT  
; ORGANISM: Trifolium aestivum  
US-10-953-349-31660

Query Match 68.1%; Score 32; DB 6; Length 252;  
Best Local Similarity 62.5%; Pred. No. 1.9e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DYKDDDK 8  
|:|:|  
Db 139 DYSDDD 146

RESULT 99

US-10-953-349-20549  
; Sequence 20549, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 20549  
; LENGTH: 255  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-20549

Query Match 68.1%; Score 32; DB 6; Length 255;  
Best Local Similarity 71.4%; Pred. No. 1.9e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7  
 | : |||  
 Db 121 DFDDDDD 127

RESULT 100  
 US-10-953-349-31659  
 ; Sequence 31659, Application US/10953349  
 ; Publication No. US20060107345A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ALEXANDROV, Nikolai et al.  
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
 ; TITLE OF INVENTION: ENCODED THERBY  
 ; FILE REFERENCE: 2750-1579PUS2  
 ; CURRENT APPLICATION NUMBER: US/10/953,349  
 ; CURRENT FILING DATE: 2004-09-30  
 ; NUMBER OF SEQ ID NOS: 40252  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 31659  
 ; LENGTH: 260  
 ; TYPE: PRT  
 ; ORGANISM: Triticum aestivum  
 ; US-10-953-349-31659

Query Match 68.1%; Score 32; DB 6; Length 260;  
 Best Local Similarity 62.5%; Pred. No. 2e+02;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 DYKDDDDK 8  
 | : |||  
 Db 147 DYSSDDDE 154

Search completed: June 29, 2006, 11:56:19  
 Job time : 25 secs